



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 179398

TO: Patricia Duffy
Location: REM/3B05/3C18
Art Unit: 1645
Thursday, February 16, 2006
Case Serial Number: 09/900766

From: Toby Port
Location: Biotech-Chem Library
REM-1A59
Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Examiner Duffy,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port
X22523



STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact*:

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☒ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library, Remsen Bldg.



STIC-Biotech/ChemLib

179308

From: Duffy, Patricia
Sent: Thursday, February 09, 2006 4:42 PM
To: STIC-Biotech/ChemLib
Subject: SEQ search

In re: 09/900,766

Please search SEQ ID NO:1 and 7.
Plesae print out top 75 hits for each.
Please include both a commercial and interference search

Thank you,

Pat Duffy
REMSSEN 3B05; mailbox 3C18
571-272-0855

RECEIVED
FEB 13 2006
STIC

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 15, 2006, 20:08:10 ; Search time 201.229 Seconds
(without alignments)
1467.298 Million cell updates/sec

Title: US-09-900-766-1
Perfect score: 3522
Sequence: 1 EVOLQSGPDLVKPGASVKI.....EATHKTSPIVKSPFNRNES 672

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : A Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3522	100.0	672	6	ABP58454
2	1832.5	52.0	478	8	ADN97499
3	1832.5	52.0	509	8	ADN97517
4	1653	46.9	552	8	ADN97513
5	1644	46.7	573	4	AAG64459
6	1321.5	37.5	669	9	ADY97271
7	1218	34.6	233	6	ABP58455
8	1130	32.1	233	6	ABP58457
9	1113	31.6	245	2	AAW35375
10	1107	31.4	233	6	ABP58456
11	1107	31.4	257	4	AAU14103
12	1107	31.4	257	6	ABO10268
13	1107	31.4	257	8	ADF98830
14	1096.5	31.1	720	4	AAG65572
15	1095.5	31.1	603	9	ADM44587
16	1093.5	31.0	621	9	ADM44588
17	1093	31.0	230	4	ABP67339
18	1091	31.0	245	2	AAW35374
19	1072	30.4	248	6	ABU79072
20	1072	30.4	248	7	ADF43296
21	1072	30.4	248	9	AEA02990
22	1069	30.4	592	4	ABP3838
23	1069	30.4	595	2	AAW86003
24	1064	30.2	469	8	ADR59118

98	950.5	27.0	621	9	ADW44596	Adw44596 PRIMATE	171	912	25.9	238	5	AAE18371	Human pen
99	949.5	27.0	467	9	ADV26107	Adv26107 Mouse OKT	172	912	25.9	238	5	ABG76346	Mouse DAV
100	948.5	27.0	467	9	ADW18833	Adw18833 Murine OK	173	912	25.9	238	5	ABG76755	DAV-1 ant
101	948.5	26.9	244	9	ADR59117	Adr59117 Anti-K88/	174	912	25.9	448	2	AAK43673	Mouse ant
102	948	26.9	214	3	AAU78253	Aau78253 Mouse agg	175	911	25.9	234	9	ADK39101	Mouse mon
103	948	26.9	233	6	ABP58458	Abp58458 Staphyloc	176	911	25.9	234	9	ADK39138	Mouse mon
104	948	26.9	257	4	AAU14104	Aau14104 Peptide s	177	910	25.8	214	6	ABP96756	TSH recep
105	948	26.9	257	6	ABO10269	Abol10269 S. aureus	178	910	25.8	214	6	ABP96755	TSH recep
106	948	26.9	257	7	ADW44368	Adw44368 Staphyloc	179	910	25.8	214	9	AEC20774	M-CSF spe
107	948	26.9	257	8	ADH10956	Adh10956 Enterotox	180	910	25.8	218	6	ABP96773	TSH recep
108	948	26.9	257	8	ADH10956	Adh10956 Enterotox	181	910	25.8	218	6	ABP96773	TSH recep
109	947	26.9	214	9	AEC20772	Aec20772 M-CSF spe	182	909.5	25.8	254	2	AAV30117	Murine an
110	945	26.8	234	6	AAO29870	Aao29870 Mouse ant	183	909.5	25.8	254	2	AAV30119	Murine an
111	945	26.8	234	7	ADU79788	Adj79788 TRA-8 ant	184	909.5	25.8	254	9	ADW10850	Polypepti
112	944.5	26.8	209	6	ABP96752	Abp96752 TSH recep	185	909	25.8	272	9	AEA29814	Mouse ZMC
113	944.5	26.8	209	6	ABP96751	Abp96751 TSH recep	186	909	25.8	448	2	AAK06476	Heavy cha
114	944.5	26.8	239	2	AAW67087	Aaw67087 Mab 55.1	187	908.5	25.8	219	8	ADP84966	Murine an
115	944	26.8	233	2	AAW67338	Aaw67338 Staphyloc	188	908.5	25.8	219	8	ADP84966	Murine an
116	944	26.8	233	8	ADI95318	Adi95318 OSPF-rela	189	908	25.8	257	3	AAV70102	Staphyloc
117	942	26.7	233	2	AAW45011	Aar45011 Staphyloc	190	907.5	25.8	216	8	ADU86562	Immunoglo
118	941.5	26.7	219	2	AAW76086	Aar76086 Mab 55.1	191	907	25.8	222	2	AAW01751	MH1 monoc
119	941	26.7	233	2	AAW35373	Aaw35373 Staphyloc	192	906	25.7	214	8	ADW41870	Amino aci
120	941	26.7	233	4	AAW67338	Aab67338 Staphyloc	193	904.5	25.7	219	3	AAW68994	Amino aci
121	940	26.7	243	8	ADT77694	Adt77694 Monoclon	194	904.5	25.7	238	2	AAV17416	Mouse imm
122	940	26.6	234	5	AAU72802	Aau72802 TRA-8 lig	195	904	25.7	214	6	ABP96763	TSH recep
123	935	26.5	257	6	ABU79068	Abu79068 S. aureus	196	904	25.7	214	6	ABP96764	TSH recep
124	935	26.5	257	7	ADF43288	Adf43288 Staphyloc	197	904	25.7	448	2	AAW99643	Anti-bGH
125	935	26.5	257	9	AEA02982	Aea02982 Staphyloc	198	903.5	25.7	219	8	ADU15725	Murine an
126	933	26.5	222	2	AAW15934	Aaw15934 Antibody	199	903	25.6	233	3	AAV70103	Mutant Sc
127	933	26.5	233	5	ABB76234	Abb76234 Staphyloc	200	902.5	25.6	219	8	ADR19323	Murine Ig
128	932.5	26.5	218	7	ADW05274	Adw05274 Female mo	201	901.5	25.6	219	8	ADW41874	Amino aci
129	932.5	26.4	218	8	ADM80365	Adm80365 Murine ho	202	901	25.6	218	2	AAW75459	Mouse ant
130	931	26.4	223	1	AAW40031	Aap40031 Kappa ant	203	901	25.6	218	2	AAW75457	Mouse ant
131	926	26.3	451	8	ADN97545	Adn97545 Artificia	204	900.5	25.6	215	8	ADO19050	Murine an
132	925	26.3	257	5	ABB79501	Abb79501 Staphyloc	205	900.5	25.6	462	6	AAO29869	Mouse ant
133	925	26.3	257	6	ABU10081	Abu10081 Staphyloc	206	900.5	25.6	462	7	ADJ79787	TRA-8 ant
134	925	26.3	257	7	ABU62334	Abu62334 S. aureus	207	900.5	25.6	464	5	AAU72801	Anti-K88/
135	925	26.3	257	7	AAE37676	Aae37676 Protein #	208	898.5	25.5	240	8	ADR59121	Anti-K88/
136	923.5	26.2	219	9	ADZ00217	Adz00217 Mouse OKT	209	897.5	25.5	215	8	ADW19052	Murine an
137	923.5	26.2	219	9	ADZ00217	Adz00217 Mouse OKT	210	897.5	25.5	223	2	AAW75458	Mouse ant
138	921	26.1	233	5	AAW54463	Aay54463 Amino aci	211	897.5	25.5	474	9	ADW86668	FLJ32028
139	921	26.1	233	5	ABB79502	Abb79502 Staphyloc	212	896	25.4	214	9	AEC20765	M-CSF spe
140	921	26.1	233	6	ABU10082	Abu10082 Staphyloc	213	895	25.4	214	6	ABP96759	TSH recep
141	921	26.1	233	7	ABU62335	Abu62335 S. aureus	214	895	25.4	214	6	ABP96760	TSH recep
142	921	26.1	233	7	AAE37677	Aae37677 Protein #	215	895	25.4	216	2	AAW15935	Antibody
143	921	26.1	233	9	ADY93173	Ady93173 Bacterial	216	895	25.4	216	6	ABP96776	TSH recep
144	919.5	26.1	219	2	AAW44495	Aar44495 Sequence	217	894	25.4	216	6	ABP96775	TSH recep
145	918.5	26.1	465	8	ADT77691	Adt77691 Monoclon	218	894	25.4	218	8	ADN97507	Artificia
146	917.5	26.1	219	6	ABP96777	Abp96777 TSH recep	219	894	25.4	712	8	ADN97543	Artificia
147	917.5	26.1	219	6	ABP96778	Abp96778 TSH recep	220	893.5	25.4	219	2	AAW53597	Amino aci
148	917	26.0	233	6	ABU10099	Abu10099 Staphyloc	221	893.5	25.4	233	9	ADW97106	Murine ma
149	916.5	26.0	238	2	AAW31752	Aaw31752 L chain s	222	893.5	25.4	233	9	ADW97102	Murine ma
150	916.5	26.0	238	2	AAW71889	Aaw71889 Anti-huma	223	893.5	25.4	470	8	AEA27481	Monoclon
151	916.5	26.0	238	3	AAW12909	Aaw12909 Anti-huma	224	892.5	25.3	463	9	AAW90837	3B1 singl
152	916	26.0	454	5	ABB76124	Abb76124 Recombina	225	892.5	25.3	599	2	AAW90837	3B1 singl
153	916	26.0	462	5	ABB76126	Abb76126 Recombina	226	892	25.3	232	9	ADW97131	Murine ma
154	915.5	26.0	234	2	AAW30123	Aay30123 Murine an	227	891	25.3	214	9	AEC20776	M-CSF spe
155	915.5	26.0	254	2	AAW30121	Aay30121 Murine an	228	891	25.3	215	3	AAW78254	Mouse agg
156	915.5	26.0	254	9	ADW10852	Adw10852 BotFab5 h	229	891	25.3	218	6	ABP96770	TSH recep
157	915.5	26.0	231	8	ADW10854	Adw10854 BotFab20	230	891	25.3	218	6	ABP96769	TSH recep
158	915	26.0	254	8	ADW98824	Adw98824 Staphyloc	231	890.5	25.3	215	8	ADN97547	Artificia
159	915	26.0	238	2	AAW83042	Aaw83042 Anti-Fag	232	890.5	25.3	483	8	ADN97549	Artificia
160	915	26.0	238	3	AAW14748	Aaw14748 Mouse ant	233	890	25.3	214	6	ABP96766	TSH recep
161	915	26.0	238	3	AAW90898	Aaw90898 Murine an	234	890	25.3	214	6	ABP96765	TSH recep
162	915	26.0	238	5	ABB74913	Abb74913 Humanised	235	889.5	25.3	235	2	AAW06178	Murine A5
163	915	26.0	238	5	ABB74867	Abb74867 Humanised	236	889.5	25.3	235	2	AAW06178	Murine A5
164	914.5	26.0	219	2	AAW59416	Aar59416 cD9 antib	237	889	25.2	467	6	AAE38408	Mouse vir
165	914.5	26.0	219	8	ADP84965	Adp84965 Murine Ig	238	888	25.2	214	6	ABP96762	TSH recep
166	914.5	26.0	220	9	ABE08093	Abp08093 Murine Ig	239	888	25.2	214	6	ABP96761	TSH recep
167	913	25.9	448	2	AAW97376	Aar97376 Murine an	240	888	25.2	214	8	ADU15723	Murine an
168	912.5	25.9	235	2	AAW47449	Aar47449 T84.12 l1	241	888	25.2	438	8	ADU15726	Murine an
169	912.5	25.9	235	2	AAW47451	Aar47451 T84.12 l4	242	886	25.2	237	7	ADW57549	Human Pro
170	912	25.9	233	6	ABU10098	Abu10098 Staphyloc	243	886	25.2	237	7	ADD47098	Human Pro

QY 301 ATSEYEGSSVDLYGAYYQACGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQ 360
Db 245 HRDDPPPTASDI----- 256
QY 361 TTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRLIVFHSSEGSTVS 420
Db 257 -----GKRGKRGD----- 265
QY 421 YDLFDAQQGYPTDLLRIYRDNNTTSSLSLSLYLTTISVMTQTPSSLVLSAGDRVIT 480
Db 266 -----IVMTQSHKFMSTSVGDRVSIT 286
QY 481 CKASQSVNDVAMYQKPGQSPKLLISYTSRRYAGVDPFSGSGYGTDFTLTSSVQAE 540
Db 287 CKASQDVNTAVAMYQKPGHSPKLLIYSASFRYTGVPDRFTGNRSCTDFTTSSVQAE 346
QY 541 AAVYFCQDYNSTPTFGGGTKLEIKRADAAPTYSIFPPSSEQLTSGGASVVCFLNNFPYK 600
Db 347 LAVYCCQHYTTPPTFGGGTKLEIKRADAAPTYSIFPPSSEQLTSGGASVVCFLNNFPYK 406
QY 601 DINVKWKIDGSRQNGVLNSWTQDSDKSTYSMSSTLTLTCKDEYERHNSYTCETHKTST 660
Db 407 DINVKWKIDGSRQNGVLNSWTQDSDKSTYSMSSTLTLTCKDEYERHNSYTCETHKTST 466
QY 661 SPIVKSFRNE 671
Db 467 SPIVKSFRNE 477
RESULT 3
ADN97517
ID ADN97517 standard; protein; 509 AA.
AC ADN97517;
XX
DT 01-JUL-2004 (first entry)
DE Artificial protein construction protein #17.
XX
KW artificial proprotein; propeptide; protein engineering; antibody.
XX
OS Unidentified.
XX
PN WO2004031362-A2.
XX
PD 15-APR-2004.
XX
PF 03-OCT-2003; 2003WO-US031420.
XX
PR 03-OCT-2002; 2002US-0415940P.
XX
PA (LARG-) LARGE SCALE BIOLOGY CORP.
XX
PI Reini SJ, Edwards P;
XX
DR WPI; 2004-330170/30.
XX
DR N-PSDB; ADN97516.
XX
PT New artificial proprotein comprises three peptide sequences, useful for
PT artificial multimeric protein engineering in eukaryotes.
XX
XX
PS Example 12; SEQ ID NO 90; 244pp; English.
XX
CC The invention relates to an artificial proprotein comprising three
CC peptide sequences: a first peptide sequence of interest, a propeptide
CC sequence attached to the C-terminus of the first peptide sequence of
CC interest, and a second peptide of interest attached to the C-terminus of
CC the propeptide sequence. The artificial proprotein and polynucleotides
CC are useful for artificial multimeric protein engineering, e.g. antibodies
CC and antibody fragments in eukaryotes. This sequence corresponds to a
CC protein used in the generation of the protein of the invention.
XX

SQ Sequence 509 AA;
Query Match 52.0%; Score 1832.5; DB 8; Length 509;
Best Local Similarity 56.5%; Pred. No. 1.1e-100;
Matches 379; Conservative 32; Mismatches 65; Indels 195; Gaps 5;
QY 1 EVLQSQGPDLPKASVKISCKASGYSFTGYMHWKQSPGKGLEWIGRINPNNGVTLY 60
Db 33 QVQLQQSGPDLKPGASLKLCTASGFNIDKTIHWVKQRPQEGGLEWIGRIYPTNGVTRY 92
QY 61 NQFEKDKATLTVDSKSTTAYMELRSITSDSAVYCARSTMIINYMVDYQGCGTSVTVSS 120
Db 93 DPKFDKATITADTSSNTAYLQVRSITSDTAVYCSRWGGDGFYANDYWGQGSASVTVSS 152
QY 121 AKTTPSPVYPLAPGSAQAQNSMTVLGCLVKGYFPEPTVTWNSGSLSSGVTTPFAVLQSD 180
Db 153 AKTTPSPVYPLAPGSAQAQNSMTVLGCLVKGYFPEPTVTWNSGSLSSGVTTPFAVLQSD 212
QY 181 LYTLSSSVTPSPSTWSPSETVTCNVAHPASSTKVDKIVPRDSGGPSEKSEINEKDLRKK 240
Db 213 LYTLSSSVTPSPSTWSPSETVTCNVAHPASSTKVDKIVPRDCG-----GK 258
QY 241 SELOQTALGNLKOIYYNNSKAITSSSEKADQFLTNTLLFKGPTFGHPWYNLDDLGLSTA 300
Db 259 RTIQDSA-----TDT-----VDLGAE 275
QY 301 ATSEYEGSSVDLYGAYYQACGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQ 360
Db 276 HRDDPPPTASDI----- 287
QY 361 TTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRLIVFHSSEGSTVS 420
Db 288 -----GKRGKRGD----- 296
QY 421 YDLFDAQQGYPTDLLRIYRDNNTTSSLSLSLYLTTISVMTQTPSSLVLSAGDRVIT 480
Db 297 -----IVMTQSHKFMSTSVGDRVSIT 317
QY 481 CKASQSVNDVAMYQKPGQSPKLLISYTSRRYAGVDPFSGSGYGTDFTLTSSVQAE 540
Db 318 CKASQDVNTAVAMYQKPGHSPKLLIYSASFRYTGVPDRFTGNRSCTDFTTSSVQAE 377
QY 541 AAVYFCQDYNSTPTFGGGTKLEIKRADAAPTYSIFPPSSEQLTSGGASVVCFLNNFPYK 600
Db 378 LAVYCCQHYTTPPTFGGGTKLEIKRADAAPTYSIFPPSSEQLTSGGASVVCFLNNFPYK 437
QY 601 DINVKWKIDGSRQNGVLNSWTQDSDKSTYSMSSTLTLTCKDEYERHNSYTCETHKTST 660
Db 438 DINVKWKIDGSRQNGVLNSWTQDSDKSTYSMSSTLTLTCKDEYERHNSYTCETHKTST 497
QY 661 SPIVKSFRNE 671
Db 498 SPIVKSFRNE 508
RESULT 4
ADN97513
ID ADN97513 standard; protein; 552 AA.
XX
AC ADN97513;
XX
DT 01-JUL-2004 (first entry)
XX
DE Artificial protein construction protein #15.
XX
KW artificial proprotein; propeptide; protein engineering; antibody.
XX
OS Unidentified.
XX
PN WO2004031362-A2.
XX
PD 15-APR-2004.
XX


```
Db 187 SVTVSSAKTTTPSYPLAPGSAQTNSMVTGLCLVKGYPPEPVTVTWNSGSLSSGVHTFP 246
Qy 175 AVLQSDLYTLSSSVTPSPSTWPTVTCNVAHPASSTKVDKIVPRDSGGPSEKSEBINE 234
Db 247 AVLQSDLYTLSSSVTPSPSTWPTVTCNVAHPASSTKVDKIVPRD----- 293
Qy 235 KDLRKSELOGTALGNLKOIYYNSKAITSEKSAOQFLNTLLFKGFTTGHFWYNDLLV 294
Db 294 -----CTSDAEST----- 301
Qy 295 DLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINL 354
Db 302 -----TVSKTENLSGGSSVIEFRAGY-----LFF 326
Qy 355 WIDG-KOTVTPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRLIVFHS 413
Db 327 WMEAMKOSTI----- 336
Qy 414 SEGSTVSYDLFDAGQGYPTDLLRIYRDNNTISSTLSISLYLT-----TSIVMTQPT 467
Db 337 -----LMLLLLLLTPVTKAMAEVMTQPTL 362
Qy 468 SLLVSAGDRVTITCKASQSV--SND-----VAVYQKPGQSPKLLISYTSRYAGVPRDFSG 522
Db 363 SLPVSLGDQASISCRSQTIVHSGDYLDFWFLQKPGQSPKLLIYKVSNRFSGVPRDFSG 422
Qy 523 SGVGTDTLTLTSSVQAEADAVYFCQDYNPPTFGGTTKLEIKRADAAPTIVSIFPPSSEQ 582
Db 423 SSGGTDTLTLKISRVEADLGVYFCQGHVPTFGGTTKLEIKRADAAPTIVSIFPPSSEQ 482
Qy 583 LTSGGASVVCFLNNFYFKDINVKWKIDGSRQNGVLSWTDQDSKSTYSMSSTLTITKD 642
Db 483 LTSGGASVVCFLNNFYFKDINVKWKIDGSRQNGVLSWTDQDSKSTYSMSSTLTITKD 542
Qy 643 EYERHNSYTCEATHKTSTSPVKSFNRE 671
Db 543 EYERHNSYTCEATHKTSTSPVKSFNRE 571

RESULT 6
ADY97271
ID ADY97271 standard; protein; 669 AA.
AC ADY97271;
XX
XX
DT 16-JUN-2005 (first entry)
DE Exemplary antibody fusion protein SEQ ID NO:3.
KW antibody engineering; fusion protein; cytostatic; antimicrobial;
KW virucide; antibacterial; cancer; infection.
XX
XX Synthetic.
XX
XX US2005069552-A1.
XX
XX 31-MAR-2005.
XX
XX 28-JUL-2004; 2004US-00900928.
XX
XX 28-JUL-2003; 2003US-0490569P.
XX
XX (BLEC/) BLECK G T.
XX (YORK/) YORK D.
XX (COLL/) COLLINS I.
XX
XX Bleck GT, York D, Collins I;
XX
XX WPI; 2005-261600/27.
XX N-PSDB; ADY97269.
XX
XX Composition useful as cancer vaccine, comprises polypeptide having
```

```
PT antibody heavy chain fused to antibody light chain, or multivalent
PT antibody having two polypeptides with antibody heavy chain fused to
PT antibody light chain.
XX
XX Disclosure; SEQ ID NO 3; 101pp; English.
XX
CC The invention describes a composition (I) comprising: (a) a polypeptide
CC comprising at least one antibody heavy chain fused to at least one
CC antibody light chain; or (b) a multivalent antibody comprising at least
CC two polypeptides, where each of the polypeptides comprises at least one
CC antibody heavy chain fused to at least one antibody light chain. Also
CC described: (1) a composition (II) comprising a nucleic acid comprising at
CC least one antibody heavy chain gene and at least one antibody light chain
CC gene, where the nucleic acid encodes a polypeptide comprising at least
CC one antibody heavy chain fused to at least one antibody light chain; (2)
CC a method (M1) of binding an antigen, involves providing a polypeptide
CC comprising at least one antibody heavy chain fused to at least one
CC antibody light chain, and contacting the polypeptide with a sample having
CC an antigen under conditions such that the polypeptide binds to the
CC antigen; (3) a method (M2), which involves providing a vector comprising
CC a bicistronic expression construct comprising genes encoding an antibody
CC heavy chain gene and an antibody light chain gene, and altering the
CC nucleic acid sequence of a splice acceptor sequence or a splice donor
CC sequence in the antibody light chain gene or the antibody heavy chain
CC gene under conditions such that splicing is prevented at the splice
CC acceptor sequence or donor sequence; (4) a nucleic acid sequence produced
CC by (M2); (5) a vector (III) comprising a modified antibody heavy or light
CC gene, where modification eliminates a splice donor or acceptor sequence
CC in antibody heavy or light chain gene; and (6) a host cell comprising
CC in a mixture or determining the presence or absence of expression of a
CC particular protein. (I) is also useful as vaccine for treating cancer and
CC infections caused by pathogens e.g. virus or bacteria. The present
CC sequence represents an exemplary antibody fusion protein from the present
CC invention.
XX
SQ Sequence 669 AA;
```

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Query Match 37.5%; Score 1321.5; DB 9; Length 669;
Best Local Similarity 40.8%; Pred. No. 3.9e-70;
Matches 303; Conservative 94; Mismatches 199; Indels 147; Gaps 17;

Qy 1 EVOLQSGDPLVKPGASVKISCKASGYSFTGYNMHWKQSPGKLEWIGRINPNNGVTLY 60
Db 1 EVOLVESGGGVQGRSLRLSCASGDFDFTYMWVWRQAPGKLEWIGRHPDSSTNY 60
Qy 61 NQKFQKATLTVDKSSSTTAYMELSLTSEDSAVYCYARSTMTIYNVMDYQGTSVTVSS 120
Db 61 APSLKDRFTISRDNAXNTLFLQMDSLRPEDTGYFCA-SLYFGFPWPAYWGQGPVTVSS 119
Qy 121 AKTTTPSVYPLAPGSAQAQNTSMVTGLCLVKGYPPEPVTVTWNSGSLSSGVHTFPVLQSD 180
Db 120 ASTKGFSVFLAPSSKSTSGTAAALGCLVKDYFPEPTVTVSMNSGALTSGVHTFPAVLQSS 179
Qy 181 -LYTLSSSVTPSPSTWPTVTCNVAHPASSTKVDKIVPRDS-----GG 224
Db 180 GLYSLSSVTPSPSSSLGTQYICNVNHPKPSNTKDKVEPKSCDKTHTCTCPAPELGG 239
Qy 225 PSEKSEINEKD---LRKSELOGTALGNLKOIYYNSKAITSEKSAOQFLNTLLFKG 281
Db 240 PSVFLFPKPKDTLMISRTPEVTCVVVD-----VSHEDPEVK----- 277
Qy 282 FFTGHPWYND-LLVDLGLSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHD 340
Db 278 -----NWYVDGVEVHNKTKPREEQYNSTYRVVSVL-----TVLHQ 313
Qy 341 NNRLTEKKVPINLWIDGK-----TTVPIDK-----VKTSKEV 375
Db 314 D-----WLNKGEYCKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM 360
Qy 376 TVQVELDLQARHYLHGKFGLYNSDSFGKVGQRLIVFHSSEGS-----TVSVDLFDAGQY 430
Db 361 TKQVSLTCL-----VKGFPD-----IAVEWESNGQPENNYKTTTPPVLDSDGSF 406
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QY 431 -----PDILLRIYRDNNTTISSTLSISLYLTT--SIWMTQTPS 468
 Db 407 FLYSKLTVDKSRWQGNVFCSSVHEALHNHYTKLSLSLSPGILFHATQADIQLTQSPSS 466
 QY 469 LLVSAGDRVTITCKASQSVNDVAVYQOKPQSPKLLISYTSRSYAGVDPDRFSGSGYGTD 528
 Db 467 LNSVGRVTITCKASQDVGTSVAVYQOKPKAPKLLIYWTSTRHGVSRFSGSGGTD 526
 QY 529 FTLTSSVQAEADAAYVFCQDYNSPPTFGGTTKLEIKRADAAPTVAIFPPSSQLTSGGA 588
 Db 527 FTFITSSLPEDIATVYCOQ-YSLYRSFGQTKVEIKRTVAAPSVFIFPPSDQLKSGTA 585
 QY 589 SVVCFLLNFPKDVNKWIDGSEKONGVLSNWDQSDKSTYSMSSTLTLTQDEYERHN 648
 Db 586 SVVCLLNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKSTYSLSSTLTLSKADYERKH 645
 QY 649 SYTCEATHKTSTSPVIVKSFNRNE 671
 Db 646 VVACEVTHQGLSSPVTKSFNRGE 668
 RESULT 7
 ID ABP58455 standard; protein; 233 AA.
 XX AC ABP58455;
 XX 14-APR-2003 (first entry)
 DT Engineered superantigen SEA/E-120 for human cancer therapy.
 DE Superantigen; staphylococcal enterotoxin; antibody; cancer; tumour;
 KW cytostatic; vaccine; SEA/E-120; mutant; mutein.
 XX Staphylococcus sp.
 OS Synthetic.
 XX Key Location/Qualifiers
 FT Misc-difference 20 /note= "wild-type Arg substituted by Gly"
 FT Misc-difference 21 /note= "wild-type Asn substituted by Thr"
 FT Misc-difference 24 /note= "wild-type Ser substituted by Gly"
 FT Misc-difference 27 /note= "wild-type Arg substituted by Lys"
 FT Misc-difference 79 /note= "wild-type Lys substituted by Glu"
 FT Misc-difference 81 /note= "wild-type Lys substituted by Glu"
 FT Misc-difference 83 /note= "wild-type Lys substituted by Ser"
 FT Misc-difference 84 /note= "wild-type Lys substituted by Ser"
 FT Misc-difference 227 /note= "wild-type Asp substituted by Ser"
 XX WO2003002143-A1.
 PN 09-JAN-2003.
 XX 19-JUN-2002; 2002WO-SE001188.
 PF 28-JUN-2001; 2001SE-00002327.
 XX (ACTI-) ACTIVE BIOTECH AB.
 XX Forsberg G, Erlandsson E, Antonsson P, Walsee B;
 PI WPI; 2003-201467/19.
 XX Conjugate for therapy, has bacterial superantigen with a region in T-cell

PT receptor and four regions to determine binding to class II major
 PT histocompatibility complex, antibody to cancer associated cell surface
 PT structure.
 XX Claim 8; Fig 2; 102pp; English.
 XX The present sequence is the protein sequence of engineered staphylococcal
 CC superantigen SEA/E-120. The superantigen is derived from staphylococcal
 CC enterotoxin E (SEE) by the incorporation of the following amino acid
 CC substitutions to reduce seroreactivity whilst maintaining production
 CC levels and biological activity: R20G, N21R, S24G, K27K, K79E, K81E, K83S
 CC and D227S. SEA/E-120 has been genetically fused to the Fab moiety of the
 CC tumour reactive antibody 5T4 to form a claimed conjugate (see ABP58454)
 CC designed to target and destroy cancer cells, including cancer of the
 CC lung, breast, colon, kidney, pancreas, ovary, stomach, cervix and
 CC prostate (claimed)
 XX SQ Sequence 233 AA;
 Query Match 34.6%; Score 1218; DB 6; Length 233;
 Best Local Similarity 100.0%; Pred. No. 1.6e-64;
 Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 226 SEKSEINEKDLRKSELGQTALGNLKOIYYNSKAITSEKSADQFLNTLLFKGFFTG 285
 Db 1 SEKSEINEKDLRKSELGQTALGNLKOIYYNSKAITSEKSADQFLNTLLFKGFFTG 60
 QY 286 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 345
 Db 61 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
 QY 346 EEKKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVKQ 405
 Db 121 EEKKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVKQ 180
 QY 406 RGLIVFHSSEGSTSVSYDLFDAQGYQYPTDLLRIYRDNNTTISSTLSISLYLTT 458
 Db 181 RGLIVFHSSEGSTSVSYDLFDAQGYQYPTDLLRIYRDNNTTISSTLSISLYLTT 233
 RESULT 8
 ID ABP58457 standard; protein; 233 AA.
 XX AC ABP58457;
 XX 14-APR-2003 (first entry)
 DT Engineered superantigen SEA/E-18 for human cancer therapy.
 DE Superantigen; staphylococcal enterotoxin; antibody; cancer; tumour;
 KW cytostatic; vaccine; SEA/E-18; mutant; mutein.
 XX Staphylococcus sp.
 OS Synthetic.
 XX WO2003002143-A1.
 PN 09-JAN-2003.
 XX 19-JUN-2002; 2002WO-SE001188.
 PF 28-JUN-2001; 2001SE-00002327.
 XX (ACTI-) ACTIVE BIOTECH AB.
 XX Forsberg G, Erlandsson E, Antonsson P, Walsee B;
 PI WPI; 2003-201467/19.
 XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
 PT receptor and four regions to determine binding to class II major
 PT histocompatibility complex, antibody to cancer associated cell surface

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PT structure.
PS Example 3; Fig 3; 102pp; English.
XX
XX
CC The present sequence is the protein sequence of engineered staphylococcal
CC superantigen SEA/E-18. The superantigen is based on staphylococcal
CC enterotoxin E (SEE, see ABP58456) except for 4 amino acid residues close
CC to the N-terminal that were from enterotoxin A and one substitution in
CC the C-terminal part, D227A. Models of new superantigen variants were
CC constructed using the SEA/E-18 model as the template. These include the
CC new engineered superantigen SEA/E-120 (see ABP58455), which has been
CC genetically fused to the Fab moiety of the tumour reactive antibody 574
CC to form a conjugate (see ABP58454) polypeptide. The conjugate is a
CC claimed example of novel conjugates and an antibody comprising an
CC engineered bacterial superantigen and an antibody moiety. The conjugates
CC are designed to target and destroy cancer cells, including cancer of the
CC lung, breast, colon, kidney, pancreas, ovary, stomach, cervix and
CC prostate (claimed)
XX
SQ Sequence 233 AA;
    Query Match          32.1%; Score 1130; DB 6; Length 233;
    Best Local Similarity 91.4%; Pred. No. 2.7e-59;
    Matches 213; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
    QY 226 SEKSEINEKDLRKSELOQTALGNLKKQIYYNSKAITSEKSGADQFLTNTLLFKGFFTG 285
    Db 1 SEKSEINEKDLRKSELOQTALGNLKKQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
    QY 286 HPWYNDLLVDLGSTATSEYEGSSVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
    Db 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
    QY 346 EEKVPINLWIDGKQTTVPIDKVTSKKEVTQVELDLQARHYLHGKFGVNSDFGKQV 405
    Db 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTQVELDLQARHYLHGKFGVNSDFGKQV 180
    QY 406 RGLIVFHSSEGSTSVSYDLFDAQGGYQPTDLLRIYRDNTTISSTLSISLYTT 458
    Db 181 RGLIVFHSSEGSTSVSYDLFDAQGGYQPTDLLRIYRDNTINSENHLALYLYTT 233
    RESULT 9
    AAW35375
    ID AAW35375 standard; peptide; 245 AA.
    AC AAW35375;
    XX
    XX 20-APR-1998 (first entry)
    DE Staphylococcus enterotoxin SEE modified superantigen.
    XX SEE; SEA; Staphylococcus enterotoxin; superantigen; conjugate; treatment;
    KW cancer; infection; autoimmune disease; antibody; modified.
    XX
    OS Staphylococcus sp.
    XX
    PH Key Location/Qualifiers
    FT Misc-difference 20 /label= R20G
    FT /note= "wild-type Arg is replaced by Gly"
    FT Misc-difference 21 /label= N21T
    FT /note= "wild-type Asn is replaced by Thr"
    FT Misc-difference 24 /label= S24G
    FT /note= "wild-type Ser is replaced by Gly"
    FT Misc-difference 27 /label= R27K
    FT /note= "wild-type Arg is replaced by Lys"
    XX
    PN W09736932-A1.
    XX

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PD 09-OCT-1997.
XX
XX 26-MAR-1997; 97WO-SE000537.
XX
XX 29-MAR-1996; 96SE-00001245.
PR 12-AUG-1996; 96US-00695692.
XX
XX (PHAA ) PHARMACIA & UPJOHN AB.
XX
XX Antonsson P, Hansson J, Bjoerk P, Dohlstén M, Kalland T;
XX Abrahamsen L, Forsberg G;
XX MPI; 1997-503052/46.
XX
XX Conjugate of target seeking moiety and modified superantigen - useful for
XX activating the immune system to treat cancer, viral infections, parasitic
XX infestations and autoimmune diseases.
XX
XX Claim 5; Page; 58pp; English.
XX
XX This is a modified Staphylococcus enterotoxin SEE superantigen. The wild-
XX type SEE superantigen is modified to be used in a novel conjugate. The
XX novel conjugate comprises a target seeking moiety and a modified wild
XX type superantigen. This modified superantigen retains its ability to
XX activate a subset of T cells, even though 1 or more wild-type amino acid
XX residues in at least 1 region which functions in determining binding to T
XX cell receptor (TCR) and activation of a subset of T cells has/have been
XX replaced. Such a modified superantigen can optionally be used as part of
XX a conjugate with a target seeking moiety, for activating the immune
XX system to treat a mammalian disease. A pharmaceutical composition can be
XX prepared comprising a modified antibody (preferably a Fab fragment fused
XX to a peptide moiety providing activation of T cells in Vbeta specific
XX manner) in which cysteines providing for interchain cysteine linkages in
XX the native antibody have been replaced (preferably by serine residues) to
XX prohibit cysteine formation. The modified wild-type superantigen is used
XX for treating cancer, viral infections, parasitic infestations and
XX autoimmune disease. The modified wild type superantigen has a lower
XX immunogenicity and reactivity with neutralising antibodies and has fewer
XX side-effects when used as a drug, compared to wild type superantigen.
XX Note: This sequence is not provided in the specification. It has been
XX created by modifying the wild-type SEE superantigen sequence in Pages 38-
XX 39 of the specification
XX
XX Sequence 245 AA;
    Query Match          31.6%; Score 1113; DB 2; Length 245;
    Best Local Similarity 86.9%; Pred. No. 2.9e-58;
    Matches 213; Conservative 8; Mismatches 12; Indels 12; Gaps 1;
    QY 226 SEKSEINEKDLRKSELOQTALGNLKKQIYYNSKAITSEKSGADQFLTNTLLFKGFFTG 285
    Db 1 SEKSEINEKDLRKSELOQTALGNLKKQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
    QY 286 HPWYNDLLVDLGSTATSEYEGSSVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
    Db 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
    QY 346 EEKVPINLWIDGKQTTVPIDKVTSKKEVTQVELDLQARHYLHGKFGVNSDFGKQV 405
    Db 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTQVELDLQARHYLHGKFGVNSDFGKQV 180
    QY 406 RGLIVFHSSEGSTSVSYDLFDAQGGYQPTDLLRIYRDNTTISSTLSISLYTT 453
    Db 181 RGLIVFHSSEGSTSVSYDLFDAQGGYQPTDLLRIYRDNTINSENHLIDLYTINSENHLIDL 240
    QY 454 YLYTT 458
    Db 241 YLYTT 245
    RESULT 10
    ABP58456
    ID ABP58456 standard; protein; 233 AA.

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XX AC ABP58456;
XX DT 14-APR-2003 (first entry)
XX DE Staphylococcal enterotoxin E.
XX KW Superantigen; staphylococcal enterotoxin E; antibody; cancer; tumour;
XX OS cytostatic; vaccine.
XX PN Staphylococcus sp.
XX PD WO2003002143-A1.
XX XX 09-JAN-2003.
XX PF 19-JUN-2002; 2002WO-SE001188.
XX PR 28-JUN-2001; 2001SE-00002327.
XX PA (ACTI-) ACTIVE BIOTECH AB.
XX PI Forsberg G, Erlandsson E, Antonsson P, Walse B;
XX DR WPI; 2003-201467/19.
XX XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
PT receptor and four regions to determine binding to class II major
PT histocompatibility complex, antibody to cancer associated cell surface
PT structure.
XX PS Example 3; Fig 4; 102pp; English.
XX CC The present sequence is the protein sequence of staphylococcal
CC enterotoxin SEE. The invention provides novel conjugates (see ABP58454)
CC for human cancer therapy. These comprise an engineered bacterial
CC superantigen, such as novel SEA/E-120 (see ABP58455), which is based on
CC SEE, and an antibody moiety, such as tumour reactive antibody 574. The
CC superantigen is engineered to reduce seroreactivity whilst maintaining
CC biological activity and production levels. The conjugates are designed to
CC target and destroy cancer cells, including cancer of the lung, breast,
CC colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
XX Sequence 233 AA;
XX SQ
Query Match 31.4%; Score 1107; DB 6; Length 233;
Best Local Similarity 89.7%; Pred. No. 6.3e-58;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKSELOQTALGNLKQIYYNSKAITSEKSDAOFPLNTLLFKGFFTG 285
Db 1 SEKSEINEKDLRKSELOQTALGNLSNRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
QY 286 HPWYNDLLVDLGSSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTAQWYGGVTLHDNNRLT 345
Db 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTAQWYGGVTLHDNNRLT 120
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 406 RGLIVPHSSEGSTVSYDLFDAQOQYPTLLRIYRDNTTISSTSLSLVLYTT 458
Db 181 RGLIVPHSSEGSTVSYDLFDAQOQYPTLLRIYRDNTTINSENHLDLYLYTT 233
RESULT 11
ID AAU14103
XX AAU14103 standard; peptide; 257 AA.
XX AC AAU14103;
XX DT 21-NOV-2001 (first entry)

XX DE Peptide sequence from Staphylococcus aureus enterotoxin type E.
XX KW Anti-retroviral; DP178-like; DP107-like; enterotoxin type E;
XX KW antifusogenic; antiviral; HIV transmission.
XX OS Staphylococcus aureus.
XX PN WO200151673-A2.
XX PD 19-JUL-2001.
XX PF 05-JUL-2000; 2000WO-US035727.
XX XX 09-JUL-1999; 99US-00350841.
XX PR (TRIM-) TRIMERIS INC.
XX PA Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
XX DR WPI; 2001-442157/47.
XX XX Identifying a compound that inhibits the formation of or disrupts a
PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral
PT or intracellular modulatory activity, by detecting the formation of a
PT DP107/DP178 complex.
XX PS Disclosure; Fig 41; 259pp; English.
XX CC The present invention relates to peptides which exhibit anti-retroviral
CC activity. The peptides of the invention (AAU12559-AAU14009) comprise
CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to
CC amino acids 639-673 of the transmembrane protein gp41 from human
CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide
CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention
CC also relates to a method of identifying compounds that inhibit the
CC formation of or disrupts a DP107/DP178 complex. The method comprises
CC detecting the formation of a DP107/DP178 complex, both in the presence or
CC absence of a test compound, in a reaction mixture containing DP107 and
CC DP178 peptides. The method is useful for identifying compounds, including
CC small molecule compounds, which may themselves exhibit antifusogenic,
CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like
CC peptides are useful to inhibit human and non-human retroviral,
CC particularly HIV, transmission to uninfected cells. The present sequence
CC represents a peptide sequence from Staphylococcus aureus enterotoxin type
XX E
XX SQ
Sequence 257 AA;
Query Match 31.4%; Score 1107; DB 4; Length 257;
Best Local Similarity 89.7%; Pred. No. 7.1e-58;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKSELOQTALGNLKQIYYNSKAITSEKSDAOFPLNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELOQTALGNLSNRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 286 HPWYNDLLVDLGSSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTAQWYGGVTLHDNNRLT 345
Db 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTAQWYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVPHSSEGSTVSYDLFDAQOQYPTLLRIYRDNTTISSTSLSLVLYTT 458
Db 205 RGLIVPHSSEGSTVSYDLFDAQOQYPTLLRIYRDNTTINSENHLDLYLYTT 257
RESULT 12
ID ABO10268
XX ABO10268 standard; protein; 257 AA.

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XX AC ABO10268;
XX DT 19-AUG-2003 (first entry)
XX DE S. aureus enterotoxin E.
XX KW HIV; DP107; DP178; glycoprotein 41; antiviral; virucide; EBV;
XX KW Epstein-Barr virus infection; heptad repeat motif.
XX OS Staphylococcus aureus.
XX PN US6518013-B1.
XX PD 11-FEB-2003.
XX PF 07-JUN-1995; 95US-00485546.
XX PR 07-JUN-1993; 93US-00073028.
XX PR 07-JUN-1994; 94US-00255208.
XX PR 20-DEC-1994; 94US-00360107.
XX PA (TRIM-) TRIMERIS INC.
XX PI Barney SO, Lambert DM, Petteway SR;
XX DR WPI; 2003-465599/44.
XX PT Inhibiting transmission of Epstein-Barr virus to a cell, by contacting
XX PT the cell with a peptide consisting of a region of Epstein-Barr virus
XX PS protein.
XX PS Example; Fig 41; 716pp; English.
XX CC The invention relates to inhibiting (M) transmission of an Epstein-Barr
XX CC virus to a cell, comprising contacting the cell with an effective
XX CC concentration of a peptide consisting of a region of 16-39 consecutive
XX CC amino acids of an Epstein-Barr virus protein for an effective period of
XX CC time, where the region is recognised by one or more of AL1MOT15,
XX CC 107x178x4 or PLZIP sequence search motifs, the peptide further comprises
XX CC an amino terminal X, and a carboxy terminal Z in which X comprises an
XX CC amino group, acetyl group, 9-fluorenylmethoxy-carbonyl group, hydrophobic
XX CC group or macromolecular carrier group, and Z comprises a carboxyl group,
XX CC amido group, hydrophobic group, or macromolecular carrier group, and
XX CC fusion of the virus to the cell is inhibited. The peptides were
XX CC identified by analysing the structure/motifs present in the HIV-1
XX CC glycoprotein 41 anti-HIV peptides DP107 and DP178. These heptad repeat
XX CC motif containing peptides were used to design the motifs cited above,
XX CC which in turn were used to analyse proteins from other pathogenic
XX CC organisms and HIV isolates, looking for DP107/178 structural analogues.
XX CC The method is useful for inhibiting transmission of Epstein-Barr virus to
XX CC a cell and Epstein-Barr virus infection. The present sequence is a
XX CC protein from a pathogenic organism analysed for regions analogous to
XX CC DP107 or DP178
XX SQ Sequence 257 AA;
Query Match 31.4%; Score 1107; DB 6; Length 257;
Best Local Similarity 89.7%; Pred. No. 7.1e-58;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKKSLOQTALGNLKOIYYNSKAITSEKSAQDPLTNTLLFKGFTG 285
DB 25 SEKSEINEKDLRKKSLOQNALNLRIQIYYNEKAITENKESDDQFLENTLLFKGFTG 84
QY 286 HPWNLLVDLGGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
DB 85 HPWNLLVDLGGKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 346 EEKKVPINLWDGKQTTPIDKVKTSKKEVTVQELDLQARHLYHGKGLNSDSFGKQV 405
DB 145 EEKKVPINLWDGKQTTPIDKVKTSKKEVTVQELDLQARHLYHGKGLNSDSFGKQV 204
QY 406 RGLIVFHSSEGSTSVSYDLFDQAQGVDPDTLLRIYRDNNTTSSLSLSLYLTT 458
DB 205 RGLIVFHSSEGSTSVSYDLFDQAQGVDPDTLLRIYRDNKNKTINSENHLIDLXYLTT 257
RESULT 13
ADF89830
ID ADF89830 standard; protein; 257 AA.
XX AC ADF89830;
XX DT 26-FEB-2004 (first entry)
XX DE Staphylococcal enterotoxin E (SEE) superantigen.
XX KW Superantigen; SAG; Staphylococcal enterotoxin; SE; SEE; cytostatic;
XX KW gene therapy; cancer.
XX OS Staphylococcus sp.
XX PN W02003094846-A2.
XX PD 20-NOV-2003.
XX PF 08-MAY-2003; 2003WO-US014381.
XX PR 08-MAY-2002; 2002US-0378988P.
XX PR 15-JUN-2002; 2002US-0389366P.
XX PR 28-AUG-2002; 2002US-0406697P.
XX PR 29-AUG-2002; 2002US-0406750P.
XX PR 01-OCT-2002; 2002US-0415310P.
XX PR 02-OCT-2002; 2002US-0415400P.
XX PR 09-JAN-2003; 2003US-0438686P.
XX PA (TERM/) TERMAN D S.
XX PI Terman DS;
XX DR WPI; 2004-011997/01.
XX PT Treating a subject with cancer or malignant diseases comprises
XX PT intratumoral, intrathecal or intracavitary administration of an amount of
XX PT a superantigen composition to the subject.
XX PS Disclosure; SEQ ID NO 7; 91pp; English.
XX CC The invention relates to treating a subject with cancer. The method
XX CC involves administering an amount of a superantigen (SAG) composition
XX CC comprising a molecule selected from: a native SAG protein; its
XX CC biologically active fragment or a biologically active homologue or a
XX CC biologically active fusion protein comprising the SAG or its fragment or
XX CC homologue fused to a fusion partner polypeptide or peptide. The SAG is
XX CC selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic
XX CC exotoxin, Y. pseudotuberculosis SAG, Mycoplasma arthritides SAG and
XX CC Clostridium perfringens exotoxin. The method is useful in treating cancer
XX CC or malignant diseases such as malignant pleural effusion, ascites,
XX CC pericardial effusion or meningeal carcinomatosis. The present sequence
XX CC represents a Staphylococcal enterotoxin E (SEE) superantigen.
XX SQ Sequence 257 AA;
Query Match 31.4%; Score 1107; DB 8; Length 257;
Best Local Similarity 89.7%; Pred. No. 7.1e-58;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKKSLOQTALGNLKOIYYNSKAITSEKSAQDPLTNTLLFKGFTG 285
DB 25 SEKSEINEKDLRKKSLOQNALNLRIQIYYNEKAITENKESDDQFLENTLLFKGFTG 84
QY 286 HPWNLLVDLGGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
DB 85 HPWNLLVDLGGKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
```

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QY 346 EEKVPINLWIDKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKQV 405
Db 145 EEKVPINLWIDGRQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKQV 204
QY 406 RGLIVFHSSEGSTSVSYDLFDAQSQYPTDLLRIYRDNTTISSTLSLSLYTT 458
Db 205 RGLIVFHSSEGSTSVSYDLFDAQSQYPTDLLRIYRDNTTINSENLHIDLVLTT 257

RESULT 14
AAG65572
ID AAG65572 standard; protein; 720 AA.
AC AAG65572;
DT 30-NOV-2001 (first entry)
DE Amino acid sequence of a plasmid pCAH9-B8d.
KW Gene library; immunoglobulin; antibody library.
XX Synthetic.
XX WO200162907-A1.
PN 30-AUG-2001.
PD 22-FEB-2001; 2001WO-JP001298.
PF 22-FEB-2000; 2000JP-00050543.
PR (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
PA Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M;
PI Okuno Y, Shiraki K;
XX WPI; 2001-565420/63.
DR N-PSDB; AAH47738.
XX Producing gene libraries and antibody libraries, involves selecting a
PT light chain that binds to a heavy chain product to produce a functional
PT formation, and producing a gene library of the light chain variable
PT regions.
XX Example; Fig 3-6; 181pp; Japanese.
XX The invention relates to producing gene libraries, comprising
CC immunoglobulin light and heavy variable region. The method involves
CC selecting light chain that binds with the heavy chain product to produce
CC a functional conformation, producing a gene library comprising a
CC collection of these light chain variable genes, and combining with gene
CC library of heavy chain variable genes. The method is used for production
CC of gene and antibody libraries. The present sequence represents the amino
CC acid sequence of a plasmid pCAH9-B8d
XX
SQ Sequence 720 AA;
Query Match 31.1%; Score 1096.5; DB 4; Length 720;
Best Local Similarity 37.9%; Pred. No. 1e-56;
Matches 256; Conservative 39; Mismatches 55; Indels 325; Gaps 9;
QY 1 EVOLQSGPDLVKPGASVKISKASGYFTGYVMHWKQSPGKLEWIGRINPNNGVTLY 60
Db 23 QVQLQSGHAEVLPFGASVKLSCTASGFINIKDTTHHWKQRPKG----- 66
QY 61 NQKFKDKATLTVDKSSTTAYMELRSLTSDSAVYICARSTMITNY---VMDYWGQTSVT 117
Db 67 -----LTSEDATVYYCA-----GYDYGNFYWGQGTIVT 95
QY 118 VSSAKTTPPSVPLAPGSAQAQTNMWTLCGLVKGYPPEPVTVTWNSGSLSSGVHTTFAVL 177
Db 96 VSSASTKPSVPLAPGSPSSKSTSGTAALGCLVKDYPPEPVTVTWNSGALTSVHTTFAVL 155
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QY 178 QSD-LYTLSSSVTPSSSTWPSSETVCNVAHPASSTKVKDKKIVPRDSGGPSEKSEINEKD 236
Db 156 QSSGLYSLSSVTVTPSSSLGTGYICNVNHNKSNKTKVDKKVEPK----- 199
QY 237 LRKKSSELOCTALGNLKKIYYNKAITSSEKSADQFLTNLLFKGFTTGHFWNDLLVDL 296
Db 200 ----- 199
QY 297 GSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTAChMYGGVTLHDNNRLTEKKVPINLWI 356
Db 200 -----SCHH----- 203
QY 357 DGKQITVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGKGLIVFHSSEG 416
Db 204 -----HHHMKYLLPTAAA-----GLLL----- 221
QY 417 STVSYDLFDAQSQYPTDLLRIYRDNTTISSTLSLSLYTYTTSIVMTQPTSLLSVAGDR 476
Db 222 -----LAAQPAMATSDIELTQSPASLSASVGET 249
QY 477 VTIITCASOSVSNDAWYQKQSPKLLISYTSRYAGVPDRFSGSGYGTDFTLTISSV 536
Db 250 VTITCRASGNIIHNYLA----- 265
QY 537 QAEDAAVYFCQDYNSPPTFGGGTKLEIKRADAAPTVISIFPPSSSEQLTSGGASVVCFLNN 596
Db 266 -----KLEIKRADAAPTVISIFPPSSSEQLTSGGASVVCFLNS 301
QY 597 FYPKQINVKWKIDGSRQNGVLNSWTDQSKDSTYSMSSTLTLTQDEYERHNSYTCEATH 656
Db 302 FYPKQINVKWKIDGSRQNGVLNSWTDQSKDSTYSMSSTLTLTQDEYERHNSYTCEATH 361
QY 657 KTSTSPVKSENRNE 671
Db 362 KTSTSPVKSENRNE 376

RESULT 15
ADW44587
ID ADW44587 standard; protein; 603 AA.
AC AC
XX ADW44587;
DT 24-MAR-2005 (first entry)
XX Antibody huCC49 heavy chain (CH2 domain deleted).
DE
XX Antibody engineering; bispecific antibody; Cytostatic; Immunosuppressive;
KW Antinflammatory; Gastrointestinal-Gen.; Dermatological; Antiulcer;
KW Antirheumatic; Antiarthritic; Nephrotropic; Antithyroid; Thyromimetic;
KW Muscular-Gen.; Neuroprotective; Antianemic; CNS-Gen.; Respiratory-Gen.;
KW Vulnerary; cancer; neoplasm; lymphoma; autoimmune disease; inflammation;
KW huCC49; Tag72; heavy chain variable region.
XX
OS Mus sp.
OS Homo sapiens.
OS Synthetic.
OS Chimeric.
XX WO2005000899-A2.
PN PN
XX 06-JAN-2005.
PD 28-JUN-2004; 2004WO-US020945.
PF 27-JUN-2003; 2003US-0483877P.
PR 03-OCT-2003; 2003US-0508810P.
PR 28-OCT-2003; 2003US-051531P.
PR 30-OCT-2003; 2003US-0516030P.
XX (BIOG-) BIOGEN IDEC MA INC.
PA Glaser S, Reff M, Yang T, Wu X, Chinn P;
PI
```


XX	Glaser S, Reff M, Yang T, Wu X, Chinn P;	
PI	WPI; 2005-058133/06.	
DR	N-PSDB; ADW44585.	
XX	New composition comprising polypeptide dimers comprising at least four	
PT	binding sites and at least two polypeptide chains linked via at least one	
PT	interchain disulfide linkage, useful for treating e.g., cancer or	
PT	autoimmune diseases.	
XX	Claim 34; SEQ ID NO 20; 172pp; English.	
XX	The invention relates to a composition comprising polypeptide dimers	
CC	comprising at least four binding sites and at least two polypeptide	
CC	chains, where the polypeptide chains comprise at least one heavy chain	
CC	portion and a synthetic connecting peptide, and where greater than about	
CC	50% of the dimers comprise polypeptide chains that are linked via at	
CC	least one interchain disulfide linkage, or comprising minibody molecules	
CC	comprising two polypeptide chains, where the polypeptide chains comprise	
CC	a heavy chain portion and a synthetic connecting peptide, where the	
CC	polypeptide chains lack all or part of a CH2 domain, and where greater	
CC	than about 50% of the molecules are present in a form in which one of the	
CC	polypeptide chains are linked via at least one interchain disulfide	
CC	linkage. Also included are a nucleic acid molecule comprising a	
CC	nucleotide sequence encoding a polypeptide chain as defined above, a host	
CC	cell comprising a vector and a binding molecule comprising CH2 deleted	
CC	heavy and light chains of the antibodies huCC49 and PRIMATIZED p388. The	
CC	synthetic connecting peptide comprises a (Gly-Ser) ⁿ linker attached to a	
CC	portion of a hinge region from IgG1, IgG3 or IgG4. The molecules are	
CC	bispecific and comprise at least one binding site specific for a soluble	
CC	ligand or for a cell surface molecule. The molecules comprise two binding	
CC	sites specific for a tumor cell antigen and two binding sites specific	
CC	for a prodrug. The synthetic connecting peptide comprises a proline	
CC	residue at position 243, Kabat numbering system. The synthetic connecting	
CC	peptide further comprises an alanine residue at position 244 and a	
CC	proline residue at position 245, Kabat numbering system. The polypeptide	
CC	dimers are tetraivalent minibody molecules. The composition is useful for	
CC	treating a subject that would benefit from treatment with an antigen	
CC	binding molecule, where the subject is suffering from cancer, lymphoma,	
CC	an autoimmune disease or disorder, or an inflammatory disease or disorder	
CC	The composition is useful for treating autoimmune diseases such as	
CC	Crohn's disease, inflammatory bowel disease, systemic lupus	
CC	erythematosus, ulcerative colitis, rheumatoid arthritis, Goodpasture's	
CC	syndrome, Grave's disease, Hashimoto's thyroiditis, pemphigus vulgaris,	
CC	myasthenia gravis, scleroderma, autoimmune hemolytic anemia, pernicious	
CC	anemia, Sjogren's syndrome, neurological disorders such as multiple	
CC	sclerosis, and inflammatory diseases or disorders such as cystic	
CC	fibrosis, sinusitis, gastroenteritis, drug reactions and burns. The	
CC	polypeptide is useful for diagnostic or therapeutic purposes. The binding	
CC	molecules are also useful for pretargeting applications for	
CC	chemotherapeutic drug delivery. The present sequence represents a heavy	
CC	chain variable region (optionally CH2 domain deleted) from the anti-Rag72	
CC	antibody huCC49.	
XX	Sequence 621 AA;	
SQ		
Query Match 31.0%; Score 1093.5; DB 9; Length 621;		
Best Local Similarity 41.0%; Pred. No. 1.3e-56;		
Matches 279; Conservative 74; Mismatches 182; Indels 145; Gaps 20;		
Qy	1 EVQLQSGDPLVPGASVKISCKASGYSTGYTHWVKVQSPGKGLWIGRIHPNNGVTILY 60	
Db	1 QVQLVQSGAEVHPGASVKISCKASGYFTDTHAIHWVKQNPQGRLEWIGYFSPGNDDFKY 60	
Qy	61 NQKFKDKATLTVDKSTTAYMELRSLTSEDSAVYYCARSTMITNYMDYWGQGTSTVTS 120	
Db	61 NERFKGATLTADTASTAYVELLSRSEDATYFCTRSLN-----MAYWGQGLTVTSS 115	
Qy	121 AKTTPPSVPLAPGSAAQNTNMYTLGCLVKGYPEPVTVTWNSGSISSGVHTPEPAVLQSD 180	
Db	116 ASTKGPVSFPLAPSSKSTSGGTAALGCLVKDYPEPVTVTWNSGALTSGVHTPEPAVLQSS 175	
Qy	181 -LYTLSSSVTPSPSTVTCNVAHPASSTKVDKKIVPRDSGG-----PSEKSEEI 232	
Db	176 GLYSLSVVTPFSSSLGTQTYICNVNHRPSNTKVKVEPKSCDKTHTCTPPEPEKSCDT 235	
Qy	233 NEKDLRKKSLEQGTALGNL-----KQIYYNYSKAITSEKSGADQFLTN-----TLLEKGF 282	
Db	236 PPPCPRCAPAPGGSGGGSGGQPRPQVY-----TLPPSRDELTKKQVSLTCLVKGF 287	
Qy	283 FTGHPWYNLLVDLSTAASTSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNN 342	
Db	288 YP-----SDIAV-----EWE-----SNGQP-----ENN 305	
Qy	343 RLTEKKVPIINLWDGK---QTTVPIDKVKTSKEVTVOELDQA---RHYLHGKFGLYNS 397	
Db	306 ----YKTPPVLDSDGSPFLYSKLTVDKSRWQGNVFCVMHEALHNHYTKSLSPG 361	
Qy	398 DSFGGKVGKRLIVFHSSSEGSTVSVDLFDAGQGYPDTLRLIYRDNTTISSTLSISLYLT 457	
Db	362 KSGGGSGGG-----GSGGG-----SNDVANYQOKPGOSP KLLISYTS 511	
Qy	458 TSIVMTQPTSLVLSAGDRVTITCKASQSV-----SNDVANYQOKPGOSP KLLISYTS 511	
Db	378 SDIVMSQSDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQOKPGOSP KLLIYWASA 437	
Qy	512 RVAGVPDRFSGSGYGTDTFTLTSSVQAEADAAVYFCQDYNSPPTFGGKLEIKRADAAP 571	
Db	438 RESGVDPDRFSGSGSGTDTFTLTSSVQAEADVAVYCOQYISYPLTFGAGTKLELKGSGG 497	
Qy	572 TVSIFFPSPSE-QLTSGGASW-----CFLNNFPKIDINVKM-KIDGSRQN--GVL 618	
Db	498 GGGSGGGGSGVQLVQSGAEVWPKGASVKISCKASGYFTDTHAIHWVKQNPQGRLEWIGYF 557	
Qy	619 NSWTQDSDKSTYSMSSTLT 638	
Db	558 SPGNDDFKYNERFKGKATLT 577	
RESULT 17		
AAB67339		
ID	AAB67339 standard; peptide; 230 AA.	
XX	AAB67339;	
XX	23-APR-2001 (first entry)	
XX	Staphylococcus aureus enterotoxin E protein.	
XX	Tumour; cancer; immune; enterotoxin.	
XX	Staphylococcus aureus.	
XX	US6180097-B1.	
XX	30-JAN-2001.	
XX	30-OCT-1998; 98US-00183437.	
XX	03-OCT-1989; 89US-00416530.	
XX	17-JAN-1990; 90US-00466577.	
XX	17-JAN-1991; 91WO-US000342.	
XX	01-JUN-1992; 92US-00891718.	
XX	02-MAR-1993; 93US-00025144.	
XX	31-JAN-1994; 94US-00189424.	
XX	19-JUN-1995; 95US-00491746.	
XX	(TERM/) TERMAN D S.	
XX	Terman DS;	
XX	WPI; 2001-158657/16.	
XX	Tumor cell capable of stimulating antitumor immune reactivity in vitro or	
PT	in vivo comprises exogenous nucleic acids encoding a superantigen and a	

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PT costimulatory molecule.
XX Disclosure; Fig 2; 16pp; English.
XX
XX The present invention relates to a tumour cell capable of stimulating
CC antitumor immune reactivity in vitro or in vivo contains and expresses an
CC exogenous nucleic acid molecule encoding a superantigen or its active
CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
CC molecule that activates T cells in conjunction with an antigenic
CC stimulus. The invention may be used for cancer therapy by stimulating an
CC anticancer immune response in vivo or ex vivo
XX
XX Sequence 230 AA;
SQ
Query Match 31.0%; Score 1093; DB 4; Length 230;
Best Local Similarity 89.6%; Pred. No. 4.2e-57;
Matches 206; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
QY 229 SEINEKDLRKKSSELOQTALGNLKOIYYNYSKAITSEKSDAQFLNTLLFKGFFTGHPW 288
DB 1 SEINEKDLRKKSSELOQTALGNLKOIYYNYSKAITSEKSDAQFLNTLLFKGFFTGHPW 60
QY 289 YNDLLVDLGSSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEK 348
DB 61 YNDLLVDLGSSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEK 120
QY 349 KVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQVQGL 408
DB 121 KVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQVQGL 180
QY 409 IVFHSSEGSTSVSYDLFDAQGYPTLLRIYRDNTTISSTLSLSLYTT 458
DB 181 IVFHSSEGSTSVSYDLFDAQGYPTLLRIYRDNTTISSTLSLSLYTT 230
RESULT 18
AAW35374
ID AAW35374 standard; peptide; 245 AA.
XX
XX AAW35374;
XX
XX 20-APR-1998 (first entry)
XX
XX Staphylococcus enterotoxin SEE wild-type superantigen.
DE
XX SEE; SEA; Staphylococcus enterotoxin; superantigen; conjugate; treatment;
XX cancer; infection; autoimmune disease; antibody.
XX
XX Staphylococcus sp.
XX
XX Key Location/Qualifiers
FH Misc-difference 20 /note= "can be mutated at this position"
FT FT Misc-difference 21 /note= "can be mutated at this position"
FT FT Misc-difference 24 /note= "can be mutated at this position"
FT FT Misc-difference 27 /note= "can be mutated at this position"
XX
XX WO9736932-A1.
PN
XX
XX 09-OCT-1997.
XX
XX 26-MAR-1997; 97WO-SE000537.
XX
XX 29-MAR-1996; 96SE-00001245.
PR
XX 12-AUG-1996; 96US-00695692.
XX
XX (PHAA ) PHARMACIA & UPJOHN AB.
XX
XX Antonsson P, Hansson J, Bjoerk P, Dohlstén M, Kalland T;
PI Abrahamsen L, Forsberg G;

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XX WPI; 1997-503052/46.
XX
XX Conjugate of target seeking moiety and modified superantigen - useful for
PT activating the immune system to treat cancer, viral infections, parasitic
PT infestations and autoimmune diseases.
XX
XX Claim 4; Page 38-39; 58pp; English.
XX
XX This is the wild-type Staphylococcus enterotoxin SEE superantigen. This
CC SEE superantigen can be modified to be used in a novel conjugate. The
CC novel conjugate comprises a target seeking moiety and a modified wild
CC type superantigen. The modified superantigen retains its ability to
CC activate a subset of T cells, even though 1 or more wild-type amino acid
CC residues in at least 1 region which functions in determining binding to T
CC cell receptor (TCR) and activation of a subset of T cells has/have been
CC replaced. Such a modified superantigen can optionally be used as part of
CC a conjugate with a target seeking moiety, for activating the immune
CC system to treat a mammalian disease. A pharmaceutical composition can be
CC prepared comprising a modified antibody (preferably a Fab fragment fused
CC to a peptide moiety providing activation of T cells in Vbeta specific
CC manner) in which cysteines providing for interchain cysteine linkages in
CC the native antibody have been replaced (preferably by serine residues) to
CC prohibit cysteine formation. The modified wild-type superantigen is used
CC for treating cancer, viral infections, parasitic infestations and
CC autoimmune disease. The modified wild type superantigen has a lower
CC immunogenicity and reactivity with neutralising antibodies and has fewer
CC side-effects when used as a drug, compared to wild type superantigen
XX
XX Sequence 245 AA;
SQ
Query Match 31.0%; Score 1091; DB 2; Length 245;
Best Local Similarity 85.3%; Pred. No. 6e-57;
Matches 209; Conservative 9; Mismatches 15; Indels 12; Gaps 1;
QY 226 SEKSEINEKDLRKKSSELOQTALGNLKOIYYNYSKAITSEKSDAQFLNTLLFKGFFTG 285
DB 1 SEKSEINEKDLRKKSSELOQTALGNLKOIYYNYSKAITSEKSDAQFLNTLLFKGFFTG 60
QY 286 HPWYNDLLVDLGSSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
DB 61 HPWYNDLLVDLGSSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
QY 346 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
DB 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 406 RGLIVFHSSEGSTSVSYDLFDAQGYPTLLRIYRDNTTISSTLSLSLYTT 453
DB 181 RGLIVFHSSEGSTSVSYDLFDAQGYPTLLRIYRDNTTISSTLSLSLYTT 240
QY 454 YLYTT 458
DB 241 YLYTT 245
RESULT 19
ABU79072
ID ABU79072 standard; protein; 248 AA.
XX
XX AC ABU79072;
XX
XX 18-JUN-2003 (first entry)
XX
XX S. aureus SEE (staphylococcus enterotoxin E) protein.
DE
XX Superantigen; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis;
KW gene therapy; mammalian cell receptor; tumour associated lipid; anergy;
KW T cell; antigen presenting cell; tumouricidal immunocyte; cytostatic;
KW APC; antitumour.
XX
XX Staphylococcus aureus.
OS
XX
XX

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Qy 226 SEKSEINEKDLRKSELOQTALCNLQIYYNYSKAITSEKSDQFLTNLLFKGPF 285
Db 25 SEKSEINEKDLRKSELOQTALCNLQIYYNYSKAITSEKSDQFLTNLLFKGPF 84
Qy 286 HPWYNDLLVLDGSAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 345
Db 85 HPWYNDLLVLDGSAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 144
Qy 346 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGGKVQ 405
Db 145 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGGKVQ 204
Qy 406 RGLIVHSSSEGSTVSYDLFDAQGYPTDILLRIYRDNTTISSTSL 449
Db 205 RGLIVHSSSEGSTVSYDLFDAQGYPTDILLRIYRDNTTINSENL 248
RESULT 21
AEA02990
ID AEA02990 standard; protein; 248 AA.
XX
AC AEA02990;
XX
DT 28-JUL-2005 (first entry)
XX
DE Staphylococcal enterotoxin E (SEE) amino acid sequence SEQ ID NO:16.
XX
KW tumor; neoplasm; gene therapy; immunotherapy; cytostatic;
KW Staphylococcal enterotoxin E.
XX
OS Staphylococcus sp.
XX
PN US2005112141-A1.
XX
PD 26-MAY-2005.
XX
PF 08-SEP-2004; 2004US-00937758.
XX
PR 30-AUG-2000; 2000US-00650884.
XX
PA (TERM/) TERMAN D S.
XX
PI Terman DS;
XX
DR WPI; 2005-394926/40.
DR N-PSDB; AEA02989.
XX
PT New composition for treating a tumor or neoplastic disease in a subject
PT comprises conjugates comprising superantigen polypeptides or nucleic
PT acids with other molecules that produce a tumoricidal response.
XX
PS Example 3; SEQ ID NO 16; 125pp; English.
XX
CC The invention relates to a composition for treating a tumor or neoplastic
CC disease in a subject. Also described: (1) a mammalian cell comprising an
CC exogenous nucleic acid encoding a superantigen expressed in the cell,
CC which cell also produces or expresses all alpha-anomers of
CC monoglycosylceramide or diglycosylceramide, where expression of the
CC superantigen and the mono- or diglycosylceramide is capable of eliciting
CC an antitumor immune response in a mammal into which the cell is
CC introduced; (2) treating a tumor or neoplastic disease in a subject; (3)
CC preparing a population of immunotherapeutic T or natural killer T (NKT)
CC cells useful to treat a tumor or neoplastic disease in a subject; (4) an
CC apoptotic cell preparation or lysate useful for treating a tumor or
CC neoplastic disease in a subject, comprising a cell population that has
CC been transfected with naked DNA encoding a superantigen, and treated to
CC undergo apoptosis or lysis; and (5) a cell that has ingested or been
CC transfected with the above apoptotic preparation or lysate, thus,
CC rendering the cell effective in presenting material expressed from
CC transfecting nucleic acid or material ingested to the immune system of a
CC mammal to elicit an anti-tumor immune response. The composition and
CC methods are useful for treating tumors or neoplastic diseases. The
CC present sequence represents a Staphylococcal enterotoxin E (SEE) protein

CC sequence, which is used in an example from the present invention. Note -
CC the sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from the
CC USPTO web site.
XX
SQ Sequence 248 AA;
Query Match 30.4%; Score 1072; DB 9; Length 248;
Best Local Similarity 90.2%; Pred. No. 8.2e-56;
Matches 202; Conservative 9; Mismatches 13; Indels 0; Gaps 0;
Qy 226 SEKSEINEKDLRKSELOQTALCNLQIYYNYSKAITSEKSDQFLTNLLFKGPF 285
Db 25 SEKSEINEKDLRKSELOQTALCNLQIYYNYSKAITSEKSDQFLTNLLFKGPF 84
Qy 286 HPWYNDLLVLDGSAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 345
Db 85 HPWYNDLLVLDGSAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 144
Qy 346 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGGKVQ 405
Db 145 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGGKVQ 204
Qy 406 RGLIVHSSSEGSTVSYDLFDAQGYPTDILLRIYRDNTTISSTSL 449
Db 205 RGLIVHSSSEGSTVSYDLFDAQGYPTDILLRIYRDNTTINSENL 248
RESULT 22
AAB83838
ID AAB83838 standard; protein; 592 AA.
XX
AC AAB83838;
XX
DT 23-JUL-2001 (first entry)
XX
DE Amino acid sequence of an Ig-5T4 fusion protein.
XX
KW Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
KW hypersensitivity; autoimmune disease; central nervous system disorder;
KW Parkinson's disease; periodontal disease; cardiopulmonary disease;
KW cardiovascular disease; gastrointestinal disorder; infection; diabetes;
KW Helicobacter-related disease; immune disorder.
XX
OS Synthetic.
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Misc-difference 503
FT /note= "Met encoded by CTG"
XX
PN WO200136486-A2.
XX
PD 25-MAY-2001.
XX
PF 13-NOV-2000; 2000WO-GB004317.
XX
PR 18-NOV-1999; 99WO-GB003859.
PR 15-FEB-2000; 2000GB-00003527.
PR 02-MAR-2000; 2000GB-00005071.
XX
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PI Kingman A, Kingman SM, Bebbington CR, Carroll MW, Ellard FM;
PI Myers KA;
XX
DR WPI; 2001-343805/36.
DR N-PSDB; AAF89733.
XX
PT Use of single chain antibody capable of recognizing a disease associated
PT molecule for manufacturing a medicament for preventing and/or treating a
PT disease condition associated with disease associated molecule.
XX

PS Disclosure; Fig 6; 118pp; English.
XX The specification describes the use of a single chain antibody (ScFv),
CC which is capable of recognizing a disease associated molecule in the
CC manufacture of a medicament for the prevention and treatment of a disease
CC condition. The ScFv antibody is useful in the manufacture of a
CC medicament, for affecting a disease in vivo, for preparing a
CC pharmaceutical composition, for in vivo imaging and/or for adjuvant
CC treatment of a disease. The ScFv antibody is also useful for treating
CC inflammatory diseases including arthritis, hypersensitivity, autoimmune
CC diseases, cancers, central nervous system disorders including Parkinson's
CC disease, periodontal diseases, cardiopulmonary diseases, cardiovascular
CC diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
CC related diseases, and other immune disorders. The present sequence
XX represents an Ig-574 fusion protein
SQ Sequence 592 AA;

Query Match 30.4%; Score 1069; DB 4; Length 592;
Best Local Similarity 37.9%; Pred. No. 3.5e-55;
Matches 254; Conservative 20; Mismatches 60; Indels 336; Gaps 9;

QY 1 EVQLQSGDPLVKPGASVKISKASGYSTGYTHMVKQSPGKLEWIGRINPNNGVTL 60
DB 20 EVQLQSGDPLVKPGASVKISKASGYSTGYTHMVKQSPGKLEWIGRINPNNGVTL 79
QY 61 NQKFKDKAILTVDKSSTTAYMELRSLTSDSAVYCARSTMTITNYMDYWGQTSVTSS 120
DB 80 NQKFKDKAILTVDKSSTTAYMELRSLTSDSAVYCARSTMTITNYMDYWGQTSVTSS- 138
QY 121 AKTTPSPVPLAPGSAQAQNSMTLGLVKGYPEPVTYTNWNSGSLSSGVHTFPVQLQSD 180
DB 139 ----- 138
QY 181 LYTSSSVTPSPSTWPSSTVTCNVAHPASSTKVDKIKVPRDGGPSEKSEINEKDLRKK 240
DB 139 -----SGG----- 141
QY 241 SELQGTALGNLKOIYYNSKAITSEKSAQDFLTNTLLFKGPTGHPWYNLLDLGSTA 300
DB 142 ----- 141
QY 301 ATSEYEGSSVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLTEKKVPINLWDGKQ 360
DB 142 -----GGSGGGT-----GG----- 151
QY 361 TTVPIDKVKTSKEVTVQELDLQARHYLHGKFLGYNDSFGGKVGRLIVFHSSEGSTVS 420
DB 152 -----GG----- 153
QY 421 YDLFDAQQGVPTDLLRIYRDNNTISSTLSISLYLTTSIVMTQTPTSLVNSAGDRTTIT 480
DB 154 -----SSIVMTQTPTFLVNSAGDRTTIT 176
QY 481 CRASQSVNDVAVYQKPGQPKLLIYTSRRVAGVDRFSGSGYGTDFTLTISVQAE 540
DB 177 CRASQSVNDVAVYQKPGQPKLLIYTSRRVAGVDRFSGSGYGTDFTLTISVQAE 236
QY 541 AAVYFCQDYNPPTFGGKTKLEIKRADA-APTVSIFFPSSEQLTSGGASVWVFLNFP 599
DB 237 LAVYFCQDYNPPTFGGKTKLEIKRASKTGPSVFFLAPSSKTSGGTAALGCLVKDYFP 296
QY 600 KDINVKW-----IDGERQNGVLNWDQSDKSTYSMSSTLTLTVDKDEVERHNSYCEAT 655
DB 297 EPTVTSWNSGALTSGVHTFPVQLQS-----SGLYSLSSVTVTPSSSLGT-QTYICNVN 348
QY 656 HKTSTSPIVK 665
DB 349 HKPSNTKVDK 358

RESULT 23
AAW86003

ID AAW86003 standard; protein; 595 AA.
XX
AC AAW86003;
XX
XX 15-MAR-1999 (first entry)
DT
XX Anti-574 single chain antibody 574Sabl.
DE
XX Tumour interacting protein; cancer; gene therapy; vector; 574 antigen;
KW monoclonal antibody; single chain antibody; mouse; human; 574Sabl.
XX
OS Mus sp.
OS Homo sapiens.
OS Synthetic.
OS Chimeric.
XX
PN W09855607-A2.
XX
PD 10-DEC-1998.
XX
XX 04-JUN-1998; 98WO-GB001627.
PF
XX 04-JUN-1997; 97GB-00011579.
PR
XX 20-JUN-1997; 97GB-00013150.
PR
XX 04-JUL-1997; 97GB-00014230.
PR
XX (OXFO-) OXFORD BIOMEDICA UK LTD.
PA
XX Kingsman SM, Bebbington CR, Ellard FM, Carroll MW, Myers KA;
PI
XX WPI; 1999-059910/05.
DR
XX N-PSDB; AAV80291.
DR
XX
PT New vector encoding a tumour interacting protein for treating cancer -
PT contains a desired nucleotide sequence and/or protein which recognises
PT tumours, and is used as a gene delivery system to treat cancer.
XX
XX Example 1; Fig 1B; 82pp; English.
XX
CC This is the amino acid sequence of a single chain antibody (Sabl), termed
CC 574Sabl, comprising an scFv derived from murine monoclonal antibody 574
CC (see AAW86002) and the human g1 constant region. cDNA (see AAV80291)
CC encoding the Sabl has been inserted into vector pCineo to allow expression
CC in mammalian cells. The trophoblast cell surface antigen defined by 574
CC is expressed at high levels on the cells of a wide variety of human
CC tumours. The invention relates to a vector comprising a nucleotide
CC sequence coding for a tumour interacting protein (TIP) and optionally a
CC nucleotide sequence of interest (NOI) which encodes a protein of interest
CC (POI), the vector being capable of delivering the NOI and/or POI to the
CC tumour recognised by the TIP. Delivery can be in vivo or ex vivo. The
CC vector is used to treat cancer, and may also used as a gene delivery
CC system for introducing at least 1 gene encoding a TIP (preferably a
CC tumour binding protein) into a haematopoietic cell lineage
XX
SQ Sequence 595 AA;
Query Match 30.4%; Score 1069; DB 2; Length 595;
Best Local Similarity 37.9%; Pred. No. 3.5e-55;
Matches 254; Conservative 20; Mismatches 60; Indels 336; Gaps 9;
QY 1 EVQLQSGDPLVKPGASVKISKASGYSTGYTHMVKQSPGKLEWIGRINPNNGVTL 60
DB 23 EVQLQSGDPLVKPGASVKISKASGYSTGYTHMVKQSPGKLEWIGRINPNNGVTL 82
QY 61 NQKFKDKAILTVDKSSTTAYMELRSLTSDSAVYCARSTMTITNYMDYWGQTSVTSS 120
DB 83 NQKFKDKAILTVDKSSTTAYMELRSLTSDSAVYCARSTMTITNYMDYWGQTSVTSS- 141
QY 121 AKTTPSPVPLAPGSAQAQNSMTLGLVKGYPEPVTYTNWNSGSLSSGVHTFPVQLQSD 180
DB 142 ----- 141
QY 181 LYTSSSVTPSPSTWPSSTVTCNVAHPASSTKVDKIKVPRDGGPSEKSEINEKDLRKK 240

Db	142	-----		SGG	144
Qy	241	SELQGTALGNLKOIYYNKAITSSEKSAOQFLTNLLPGFTTGHWNVDLLVLDGSTA	300		
Db	145	-----			144
Qy	301	ATSEYEGSSVDLYGAYYGQAGGTPNKTAQMYGGVTLHDNNRLTEKKVPINLWIDGKQ	360		
Db	145	-----	GGSGGGT	GG	154
Qy	361	TTVPIDKVTSKKEVTVQELDLQARHYLHGKFLGYNLSDSPGGKQVQRLIVFHSSEGSTVS	420		
Db	155	-----	GG	GG	156
Qy	421	YDLFDAQQYVPTLLRIYRDNNTTISSTLSISLYLYTTSIVMTQTPTSLVLSAGDRVTIT	480		
Db	157	-----	SSIVMTQTPTFLVLSAGDRVTIT	SSIVMTQTPTFLVLSAGDRVTIT	179
Qy	481	CKASQSVSNDAVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDTFTLTSSVQAE	540		
Db	180	CKASQSVSNDAVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDTFTLTSSVQAE	239		
Qy	541	AAVYFQQDYNPPTFGGTTKLEIKRADA-APTIVSIPPPSSEQLTSGGASVWCFLANFYP	599		
Db	240	LAVYFQQDYNPPTFGGTTKLEIKRADA-APTIVSIPPPSSEQLTSGGASVWCFLANFYP	299		
Qy	600	KDINVKW-----IDGSRQNGVLNSWTQDQSKDSTYSMSSTLTLTKDYEYERHNSYTCEAT	655		
Db	300	EPTVSNWNGALYSGVHTFPAVLQS-----SGLYSLSVVTVTPSSSLGT-QTYICNVN	351		
Qy	656	HKTSTSPIVK 665			
Db	352	HKPSNTKVDK 361			
RESULT 24					
ADR59118					
ID ADR59118 standard; protein; 469 AA.					
AC ADR59118;					
DT 18-NOV-2004 (first entry)					
DE Anti-K88/K99 antibody related protein, SEQ ID 69.					
KW Gastrointestinal; antibody; heavy chain; light chain; variable region;					
KW enterotoxigenic Escherichia coli; ETEC; K88 antigen; K99 antigen;					
KW animal food; enteric disease.					
OS Mus sp.					
XX WO2004074491-A2.					
XX 02-SEP-2004.					
XX 16-FEB-2004; 2004WO-EP001427.					
XX 18-FEB-2003; 2003US-0448429P.					
XX (SYGN) SYNGENTA PARTICIPATIONS AG.					
XX Brown D, Campos M, Dalmia B, Demarest S, Hansen G, Heifetz PB;					
XX WPI; 2004-635583/61.					
XX Novel immunoglobulin heavy chain comprising bovine CH3 or CH2 domain,					
XX murine CH2CH3 domain or human CH2CH3 domain, useful in treatment or					
XX prevention of enteric disease in animal.					
XX Claim 58; SEQ ID NO 69; 165pp; English.					
XX The present invention relates to coding sequences for mammalian antibody					
CC					

CC	heavy and light chains directed against enterotoxigenic Escherichia coli (ETEC), in particular, ETEC of a strain possessing the K88 or K99 antigen. The heavy and light chain sequences are useful for producing transgenic plants, which express the K88 or K99 antibody. The transgenic plants are useful for producing animal feed, food product, animal feed additive, feed pre-mix or nutritional supplement and are also useful for treating or preventing enteric disease in an animal. The present sequence was used in an example from the invention.				
XX					
QY	Sequence 469 AA;				
Query Match 30.2%; Score 1064; DB 8; Length 469;					
Best Local Similarity 37.8%; Pred. No. 5.3e-55;					
Matches 252; Conservative 52; Mismatches 114; Indels 248; Gaps 13;					
QY	1	EVQLQQSGDPLVKPGASVKISKASGYFTGYVMHWKSPGKLEWIGRINPNNGVTLY	60		
DB	20	EVQLQQSGPELVKPGASVKISKASDYSLTDTYMHVWKQSHGESLEWIGYINFGATNY	79		
QY	61	NQKPKDKATLTVDKSSSTTAYMELRSLTSEDSAVYYCARSTMTITNYVMDYMQGTSVTSS	120		
DB	80	NQKPKDKATLTVDTSSTTVYMQFNLSLTSEDSAVYYCVREALLRNAYMDYMQGTSVTSS	139		
QY	121	AKTTPSPVPLAPGSAQAQNSMTLGLVKGYPEPPTVTVNWSGSLSSGVHTFPAVLQSD	180		
DB	140	AKTTPSPVPLAPGSAQAQNSMTLGLVKGYPEPPTVTVNWSGSLSSGVHTFPAVLQSD	199		
QY	181	LYTLSSSVTPSPSTWSPSETVTCNVNVAHPASTKVDKIVPRDSDGSPSEKSEINEKDLRKK	240		
DB	200	LYTLSSSVTPSPSTWSPSETVTCNVNVAHPASTKVDKIVPRDCG-----	242		
QY	241	SELQGTALGNLKOIYYNKAITSSEKSAOQFLTNLLPGFTTGHFWYNDLLVLDGSTA	300		
DB	243	CKPCICTVPEVSSVFIPPK-----PKDVLITL-----	271		
QY	301	ATSEYEGSSVDLYGAYYGQAGGTPNKTAQMYGGVTLHDNNRLTEKKVPINLWIDGKQ	360		
DB	272	-----TP-KVTCVVVDIS-----KDDPEVQFSFVD-----	296		
QY	361	TTVPIDKVTSKKEV-----TVQELDLQARHYLHGK-FGL-VNSDSFGKGQVORGLIVF	411		
DB	297	-DVEVHTAQTPREQFNSTFRSVSELPIMHQDLNGKEFKCRVNSAFAPIEK-----	350		
QY	412	HSSEGSTSVYDLFDAQQYVPTLLRIYRDNNTTISSTLSISLYLYTTSIVMTQTPTSLV	471		
DB	351	-----TISKT-----	355		
QY	472	SAGDRVTITCKASQSVSNDAVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDTFL	531		
DB	356	-----	355		
QY	532	TISSVQAEAAVYFCQDYNPPTFGGTTKLEIKRADAAPTIVSIPPPSSSEQLTSGGASV	591		
DB	356	-----KGRPKADQVYTIPTPKQMAKDKVSLT	382		
QY	592	CFLNFPKIDINVKWIKDGSERQNGVLNSWTQDQSKDSTYSMSSTLTLTKDYEYERHNSYT	651		
DB	383	CMITDFPEDIIVEMQWNGQPAEN-YKNTQPIMDT-DGSYFYVYKLVNQSKEWAGNTFT	440		
QY	652	CEATHK 657			
DB	441	CSVLHE 446			
RESULT 25					
AAR76088					
ID AAR76088 standard; protein; 464 AA.					
XX	AAR76088;				
XX	25-MAR-2003 (revised)				
DT	21-NOV-1995 (first entry)				
XX					

XX DE Murine mAb 2471 heavy chain protein.

XX KW Screening; diagnosis; chemotherapy; cancer; cytostatic; neoplasm; prostatitis; andrology; genitourinary disease; inflammation; rheumatoid arthritis; antiarthritic; antirheumatic; immune disorder; musculoskeletal disease; antiinflammatory; autoimmune disease; immunosuppressive; cardiovascular disease; cardiovascular-gen.; cerebrovascular ischemia; scarring; vulnary; infection; myocardial infarction; cardiant; neurological disease; Alzheimer's disease; neuroprotective; neotropic; degeneration; hematological disease; organ transplant rejections; graft versus host disease; developmental disorder; antibody.

OS Mus sp.

XX WO2005010049-A2.

PN 03-FEB-2005.

PD 06-JUL-2004; 2004WO-US018921.

XX 09-JUL-2003; 2003US-0485820P.

PR (ELIL) LILLY & CO ELI.

XX Bradley HM, Kikly KK, Lancaster JS, Rowlinson SW;

PI WPI; 2005-123130/13.

DR N-PSDB; ADW97107.

XX Binding composition for treating diseases e.g. cancer, is capable of specifically binding to and neutralizing transforming growth factor (TGF) beta 1, comprises binding sites of anti-TGF beta antibodies designated 1021, 2471 and 3821.

XX Example 2; SEQ ID NO 8; 129pp; English.

XX The present invention relates to a binding composition which is capable of specifically binding to and neutralizing transforming growth factor (TGF) beta 1, comprises binding sites of anti-TGF beta 1 antibodies designated 1021, 2471 and 3821. The invention is useful for diagnosing, preventing and treating diseases chosen from cell proliferative (e.g. cancer), inflammatory (e.g. chronic prostatitis), autoimmune (e.g. rheumatoid arthritis), cardiovascular (e.g. stroke, myocardial scarring, infarction), neurological (e.g. Alzheimer's disease), fibrotic, blood diseases (e.g. agammaglobulinemia), organ rejection, graft-versus-host disease and developmental diseases. The present sequence is the murine mAb 2471 heavy chain protein.

XX Sequence 460 AA;

Query Match 29.8%; Score 1048; DB 9; Length 460;
Best Local Similarity 38.0%; Pred. No. 4.6e-54;
Matches 253; Conservative 51; Mismatches 110; Indels 252; Gaps 14;

QY 1 EVLOQSGDPLVKPGASVKISCKASGYFTGYMHVWVKQSPGKLEWIGRINPNWGLY 60

DB 21 EVLOQSGPELVKPGASVKISCKASGYFTDYMHVWVKQSHGKLEWLYIYPYNGDTGY 80

QY 61 NQKFKDKATLVDSKSTTAYMELSLTSDSAVYVCARSTMTNYMDYMGQGTSTVSS 120

DB 81 NQKFKSKATLVDSNSTAYMELSLTSDSAVYCVRG-----YWFAYWGQGLTVST 136

QY 121 AKTTPSVVPLAPGSAQAQNSMTLGLVKGYFPEPVTVTWNSGSLSSGVHTFPVQLSD 180

DB 137 AKTTPSVVPLAPGSAQAQNSMTLGLVKGYFPEPVTVTWNSGSLSSGVHTFPVQLSD 196

QY 181 LYTLSSSVTPSWTSETVTCNVAHPASSTKVYKIVPRDSGSPSEKSEINEKDLKK 240

DB 197 LYTLSSSVTPSWTSETVTCNVAHPASSTKVYKIVPRDCG----- 239

QY 241 SELQGTALGNLKIYYVNSKAITSSSEKSAQDLTNTLLPKGFTHPWNLDLVLGSTA 300

DB 240 CRPCICTVPEVSSVFIFPPK-----PKDVLITL----- 268

QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKACMYGGVTLHDNNRLTEKKVPINLWIDGKQ 360

DB 269 -----TP-KVTCVVVDIS-----KDDPEVQFSMFVD--- 293

QY 361 TTVPIDKVKTSKEV-----TVQELDLQARHHLHGK-FGL-YNSDSFGGKVQORGLIVP 411

DB 294 -DVEVHTAQTPREBQFNSTFRSVSELPIMHQDWLNGKEFKCEVNSAAPAPIEK----- 347

QY 412 HSSEGSTVSYDLFDAQGGYPTDLLRIYRDNTTISSTLSISLYLYTTSIVMTQPTTSLV 471

DB 348 -----TISK----- 352

QY 472 SAGDRVTITCKASQSVSNDAVYQKPGQSPKLLISYTSRYAGVDPDRSGSGYGTDTFL 531

DB 353 ----- 352

QY 532 TISSVQAEDAAYVFCQDYNPPTFGGKLEIKRADAAPTYSIFPPSSEQLTSGGASVV 591

DB 353 -----KGRPKAPQVYTIPTPKQMAKDKVSLT 379

QY 592 CFLNNFYPKDINVWKIDGSRQNGVLSNWTQDSDKSTYSMSSTLTLTCKDEYERHNSYT 651

DB 380 CMITDFPEDITVEMQWNGQPAEN-YKNTQPIMDT-DGSYFVYVSKLVNQQSKNWEAGNTFT 437

QY 652 CEATHK 657

DB 438 CSVLHE 443

RESULT 29

ABB76235

ID ABB76235 standard; protein; 230 AA.

XX AC ABB76235;

DT 09-AUG-2002 (first entry)

XX Staphylococcus aureus enterotoxin E.

DE Enterotoxin E; SEB; superantigen; antigen; tumour; cancer; antitumour; therapy.

KW Staphylococcus aureus.

OS

XX Key Location/Qualifiers

FT Misc-difference 120 /note= "given as 'J' in the specification"

FT Misc-difference 121 /note= "given as 'J' in the specification"

FT Misc-difference 123 /note= "given as 'O' in the specification"

FT Misc-difference 124 /note= "given as 'U' in the specification"

FT Misc-difference 125 /note= "given as 'V' in the specification"

XX US2002051765-A1.

PN 02-MAY-2002.

XX 19-DEC-2000; 2000US-00741503.

XX 03-OCT-1989; 89US-00416530.

PR 17-JAN-1990; 90US-00466577.

PR 17-JAN-1991; 91WO-US000342.

PR 01-JUN-1992; 92US-00891718.

PR 02-MAR-1993; 93US-00025144.

PR 31-JAN-1994; 94US-00189424.

PR 19-JUN-1995; 95US-00491746.

XX

Db 61 YNDLLVDKGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLTEEX 120
Qy 349 KVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQGL 408
Db 121 XVQXBWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQGL 180
Qy 409 IVPHSSEGSTVSVLDLFDAGQYQPTDLLRIYRDNTTSSLSLSLYLYTT 458
Db 181 IVPHSSEGSTVSVLDLFDAGQYQPTDLLRIYRDNTTSENHIDLYLYTT 230

RESULT 34
AAE18377
ID AAE18377 standard; protein; 597 AA.
XX AAE18377;
DT 07-MAY-2002 (first entry)
XX Human N-terminal DAV-1 heavy chain-mature TNF-alpha fusion protein.
DE Human; bifunctional molecule; monoclonal antibody; gene therapy; cancer;
KW vascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder;
KW hyperproliferative disorder; hormonal disorder; DAV-1 heavy chain;
KW cytotatic; vasotropic; ophthalmological; tumour necrosis factor-alpha;
KW TNF-alpha; fusion protein.
XX Homo sapiens.
OS Synthetic.
OS Chimeric.

XX Key Location/Qualifiers
FH Region 1..439
FT /note= "N-terminal portion of DAV-1 heavy chain"
FT Region 441..597
FT /note= "Human mature TNF-alpha"
XX WO200204522-A2.

XX 17-JAN-2002.
XX 09-JUL-2001; 2001WO-EP007878.
XX 10-JUL-2000; 2000US-00613017.
XX (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
PA (SCRI) SCRIPPS RES INST.
XX Nemerow GR, Li E;
XX WPI; 2002-171707/22.

XX New bifunctional molecules comprising an antibody or its antigen-binding
PT portion, and a targeting agent, useful for e.g. gene therapy, or for
PT promoting Adenoviral vector-mediated gene delivery to cells lacking av
PT integrins.

XX Claim 15; Page 98-99; 106pp; English.
XX The present invention relates to a bifunctional molecule comprising an
XX antibody or its antigen-binding portion, and a targeting agent where the
XX antibody specifically binds to an antigen in a protein that binds to av
XX integrin, and the targeting agent specifically binds to a cell surface
XX protein that activates the phosphatidylinositol 3 (PI3K) signalling
XX pathway. The bifunctional molecules are useful for gene therapy, for
XX promoting Adenoviral (Ad) vector-mediated gene delivery to cells lacking
XX av integrins, for enhancing Ad binding and internalisation, and in gene
XX delivery of by fibreless adenovirus particles. The bifunctional molecules
XX permit targeting of viral and bacterial vectors to cells that express
XX targeted receptors. Diseases that can be targeted include cancers,
XX vascular disorders, diabetic retinopathies, restenosis, ophthalmic
XX disorders, hyperproliferative disorders, and hormonal disorders. The

CC present sequence is human N-terminal DAV-1 heavy chain-mature tumour
CC necrosis factor-alpha (TNF-alpha) fusion protein which is used in the
CC invention
XX
SQ Sequence 597 AA;
Query Match 29.2%; Score 1028; DB 5; Length 597;
Best Local Similarity 37.2%; Pred. No. 9.7e-53;
Matches 253; Conservative 53; Mismatches 115; Indels 260; Gaps 15;
Qy 1 EVOLQSGDPLVKPGASVKISKASGYSTGYMHVVKOSPGKLEWIGRIINPNNGVLY 60
Db 20 EVOLQSGPELVKPGASVKISKASGYTFTDYNMHVVKOSHGKSLWIGYIYPIYKGGTGY 79
Qy 61 NQKFKDKATLTVDKSSTTAYMEIRSLTSEDSAVVYCARSTMTINVMYDVGQGSTVTSS 120
Db 80 NQKFKSKATLTDTSSSNTAYMEIRSLTSDASAVVYCARG-----IAYVQGGTLVTVA 132
Qy 121 AKTTTPSVVPLAPGSAQAQNSMTVLGCLVKGYFPEPTVTWNSGSLSSGVHTFPVQLQSD 180
Db 133 AKTTTPSVVPLAPGSAQAQNSMTVLGCLVKGYFPEPTVTWNSGSLSSGVHTFPVQLQSD 192
Qy 181 LYTLSSTVTPSSTWPSSETVTCNVAHPASSTKVDKIVPRDGGSPSEKSEINEKDLRKK 240
Db 193 LYTLSSTVTPSSTWPSSETVTCNVAHPASSTKVDKIVPRDCG----- 235
Qy 241 SELQGTALGNLKOIYYNSKAITSEKSAQDQLTLLFKGFFTGHPYNDLLVDLGSTA 300
Db 236 CRPCICTVPESSVFIFFPK-----PKDVLTTL----- 264
Qy 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLTBEKKVPIINLWDGKQ 360
Db 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD--- 289
Qy 361 TTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVQGLIYF 411
Db 290 -DVEVHTAQTPREEQFNSTFRSVSELPIHQDNLNGKEFKCRVNSAAPPAIEK----- 343
Qy 412 HSSEGSTVSYDLFDAQGYQPTDLLRIYRDNTTSSLSLSISLYLYTTSIVMTQPTSLLV 471
Db 344 -----TISKT----- 348
Qy 472 SAGDRVITITCKASQSVSNDVAVYQKPGQSKLLISYTSRYAGVPDRFSGGYGDTFTL 531
Db 349 ----- 348
Qy 532 TISSVQAEAAVYFCQDYNSPPTFGGKLEIKRADAAPTVISIPPPSEQLTSGGASVV 591
Db 349 -----KGRPKAPQVYTIPTPPKEQMAKDKVSLT 375
Qy 592 CFLNNFYPKDINVKMKIDGSEKQNGVLSNWTDDSKDSTYSMSSTLTLTDEYERHNSVT 651
Db 376 CMITDFFPEDITVEQWQNGQPAEN-YKNTQPIMDT-DGSIFVYSKLVNOKSNWEAGNTFI 433
Qy 652 CEATHKTSTSPVSKFNRNES 672
Db 434 CSVLHE-----FVRSRRTPS 449
RESULT 35
ABG76352
ID ABG76352 standard; protein; 597 AA.
XX
AC ABG76352;
XX
DT 23-OCT-2003 (revised)
DT 10-MAY-2003 (first entry)
XX
DE Mouse DAV-1 heavy chain-mature human TNF-alpha fusion protein.
XX Human; bifunctional molecule; antigen-binding portion; alpha integrin;
KW cell surface protein; phosphatidylinositol-3-OH kinase; PI3K;
KW signalling pathway; targeted gene therapy; delivery vector;

CC aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft
CC rejection. The present sequence represents the heavy chain of the murine
CC anti-human Fas monoclonal antibody HFE7A, which is produced by hybridoma
CC HFE7A (FERM-BP-5828)
XX
SQ Sequence 464 AA;

Query Match 29.1%; Score 1025.5; DB 3; Length 464;
Best Local Similarity 36.2%; Pred. No. 1e-52;
Matches 243; Conservative 64; Mismatches 106; Indels 259; Gaps 14;

QY 1 EVQLQSGDPLVKPGASVKLSCKASGYSTGYMHVWVKSPGKGLWIGRINPNNGVTLY 60
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 60
20 QVQLQPGAEVLKPGASVKLSCKASGYSTGYMHVWVKSPGKGLWIGRINPNNGVTLY 79
QY 61 NQKFKDKATLVTDKSTTAYMELRSTSEDSAVYYCARS-TMITNYMDVWGQTSVTYS 119
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 119
80 NQKFKGKATLVTDKSTTAYMELRSTSEDSAVYYCARNRDYNNWYFDVWGQTSVTYS 139
QY 120 SAKTTPPVVPLAPGSAAGTNSMTVLCGLVKGYFPEPVTVMNSGLSGVHTFPVAVLOS 179
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 179
140 SAKTTPPVVPLAPGSAAGTNSMTVLCGLVKGYFPEPVTVMNSGLSGVHTFPVAVLOS 199
QY 180 DLYTLSSSVTPSPSTVTCNVAHPASSTKVDKIVPRDSGGSEKSEINEKDLRK 239
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 239
200 DLYTLSSSVTPSPSTVTCNVAHPASSTKVDKIVPRDCG----- 243
QY 240 KSELQGTALGNLQIYYNKAITSSEKSAQDLTNTLLFKGFTGHWPWYNDLLVLDLST 299
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 299
244 -CKPCICTVPEVSSVFIFFPK-----PKDVLTLT----- 272
QY 300 AATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGK 359
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 359
273 -----TP-KVTCVVVDIS-----KDDPEVQSFVFD-- 297
QY 360 QTTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVKQGLIV 410
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 410
298 --DVEVHTAQTPRERQFNSTFRSVELPTIMHQNWLNGKEFKCRVNSAAPPAPIEK--- 351
QY 411 FHSSEGSTVSYDLFDAQGVPTLLRIYRDNNTTISLSLSISLYLVTTSIVMTQTPTSL 470
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 470
352 -----TISK----- 356
QY 471 VSAGDRVTITCKASQSVNDVAWYQKPGQSPKLLISYTSRYAGVDPFRFSGSGYGTDF 530
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 530
357 ----- 356
QY 531 LTISSVQAEADAIVFCQDYNSPPTGGGTLKIKRADAAPTVISIIPPSSQLTSGGASV 590
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 590
357 -----KGRKAPQVYITPPPKQMAKDKVSL 382
QY 591 VCFLNPFYKIDINVKKIDGSEKQ-----GVLSNWTDDQSKDSTYSMSSTLTLTCKDEYE 645
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 645
383 TCMITDFFEDITVEQWNGQPAENYKNTQPIMT-----NGSYFVYSKLVNQKSNWE 435
QY 646 RHNSYTCETATHK 657
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 657
436 AGNTFTCSVLHE 447

RESULT 38
AAW90897
ID AAW90897 standard; protein; 464 AA.
XX
AC AAW90897;

XX 08-AUG-2000 (first entry)
DT Murine anti-Fas antibody HFE7A heavy chain protein.
DE

XX Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;

KW nephrotropic; antifertility; neuroprotective; antiarteriosclerotic;
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus; HFE7A;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX
OS Mus musculus.

XX EP990663-A2.
XX 05-APR-2000.
XX 29-SEP-1999; 99EP-00307711.
XX 30-SEP-1998; 98JP-00276881.
XX 30-SEP-1998; 98JP-00276882.
XX (SANY) SANKYO CO LTD.

PI Serizawa N, Haryuyama H, Nakahara K, Tamaki I, Takahashi T;
XX WPI; 2000-258930/23.
DR N-PSDB; AAA11546.

XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT inflammatory or autoimmune disease, induces apoptosis selectively in
PT cells with abnormal Fas-Fas ligand systems.

XX Example reference 4; Page 100-102; 263pp; English.

CC This invention describes a novel humanized anti-Fas antibody-like
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence represents
CC a murine anti-Fas monoclonal antibody HFE7A heavy chain described in the
CC method of the invention

XX SQ Sequence 464 AA;

Query Match 29.1%; Score 1025.5; DB 3; Length 464;
Best Local Similarity 36.2%; Pred. No. 1e-52;
Matches 243; Conservative 64; Mismatches 106; Indels 259; Gaps 14;

QY 1 EVQLQSGDPLVKPGASVKLSCKASGYSTGYMHVWVKSPGKGLWIGRINPNNGVTLY 60
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 60
20 QVQLQPGAEVLKPGASVKLSCKASGYTFTSYMQWVKQRPQGLWIGRINPNNGVTLY 79
QY 61 NQKFKDKATLVTDKSTTAYMELRSTSEDSAVYYCARS-TMITNYMDVWGQTSVTYS 119
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 119

Db 80 NQKFKGKATLTVDTSSTAYMQLSLSLTSSEDSAVYYCARNRDYNNWYFDVWGTTGTTVTS 139

QY 120 SAKTTPPSVYPLAPGSAQTNSMVTLCGLVKGYPPEPVTVTWNSGSLSSGVHTFPFVAVLOS 179

Db 140 SAKTTPPSVYPLAPGSAQTNSMVTLCGLVKGYPPEPVTVTWNSGSLSSGVHTFPFVAVLOS 199

QY 180 DLYTLSSSVTVPSSTWPSSTVCNVAHPASSTKVDKKIYPRDSGGPSEKSEINEKDLRK 239

Db 200 DLYTLSSSVTVPSSTWPSSTVCNVAHPASSTKVDKKIYPRDCG----- 243

QY 240 KSELOQTALGNLQKIYYYNKSAITSEKSDAQLTNTLLFKGFTGHPWYNLLVDLGST 299

Db 244 -CKPCICTVPEVSSVFIFPPK-----PKDVLTTTL----- 272

QY 300 AATSEYEGSSVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEEKVPINLWIDGK 359

Db 273 -----TP-KVTCVVVDIS-----KDDPEVQFSWFDV-- 297

QY 360 QTTVPIDKVKTSKKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVQVGLIV 410

Db 298 --DVEVHTAQTPREBQFNSTFRSVSELPIHQNLWNGKEFKCRVNSAAPAPIEK----- 351

QY 411 FHSSEGSTVSYDLFDAQGYPDTLRLIYRDNTTISSTLSLSLYLTTTSIVMTQTPTSL 470

Db 352 -----TISKT----- 356

QY 471 VSAGDRVTITCKASQSVSNDVAWYQKPGSPKLLISYTSRYSYAGVDPDRFSGSGYGTDT 530

Db 357 ----- 356

QY 531 LTISSVQAEADAAYFCQDYNSPPTFGGKTKLEIKRADAAPTYSIFPPSSEQLTSGASV 590

Db 357 -----KGRPKAPQYVTTIPPKQMAKDKVSL 382

QY 591 VCFLNFPKIDINVKWKIDGSRQN-----GVLSNWTQDQSDKSTYSMSSTLTLTDEYE 645

Db 383 TCMITDFPEDITVEQWNGQPAENYKNTQPIMNT-----NGSYFVYSKLVQKSNWE 435

QY 646 RHNSYTCEATHK 657

Db 436 AGNTFTCSVLHE 447

RESULT 39

ABB74912

ID ABB74912 standard; peptide; 464 AA.

XX ABB74912;

XX 30-APR-2002 (first entry)

DE Humanised anti-Fas antibody related peptide SEQ ID NO 29.

XX Human; mouse; Fas/Fas ligand system; Fas; antibody; light chain;

KW heavy chain; apoptosis; antiallergic; immunosuppressive; apoptotic;

KW autoimmune disease; allergy; atopy.

XX Homo sapiens.

OS JP2001342149-A.

PN 11-DEC-2001.

PD 28-MAR-2001; 2001JP-00093243.

PF 29-MAR-2000; 2000JP-00091144.

XX (SANY) SANKYO CO LTD.

PA WPI; 2002-145114/19.

XX Drug for preventing or treating e.g. autoimmune disease or allergy,

PT comprises humanized anti-Fas antibody.

XX Example 6 (preparatory); Page 26; 154pp; Japanese.

PS The invention relates to a preventive or treating agent for diseases

CC caused by abnormality in the Fas/Fas ligand system containing, as the

CC active component, an antibody having a light chain subunit and a heavy

CC chain subunit and an activity of combining specifically with mammalian

CC Fas and an activity of inducing apoptosis in a cell expressing Fas. The

CC agent has antiallergic, immunosuppressive and apoptotic activity and is

CC used for preventing and treating autoimmune diseases, allergy, atopy and

CC others. The present sequence is that of a peptide useful to the invention

XX Sequence 464 AA;

Query Match 29.1%; Score 1025.5; DB 5; Length 464;

Best Local Similarity 36.2%; Pred. No. 1e-52;

Matches 243; Conservative 64; Mismatches 106; Indels 259; Gaps 14;

QY 1 EVQLQQSGDLPVKPGASVKISKASGYSTGYVMHWKQSPGKGLEWIGRIINPNNGVTLY 60

Db 20 QVQLQPGALVKPGASVKLSCKASGYTFTSYMQWVKQRPQGLEWIGELIDSDSYNY 79

QY 61 NQKFKDKATLTVDKSTTAYMELRSLTSSEDSAVYYCARS-TMITNYMDYWGOGTSTVTS 119

Db 80 NQKFKGKATLTVDTSSTAYMQLSLSLTSSEDSAVYYCARNRDYNNWYFDVWGTTVTS 139

QY 120 SAKTTPPSVYPLAPGSAQTNSMVTLCGLVKGYPPEPVTVTWNSGSLSSGVHTFPFVAVLOS 179

Db 140 SAKTTPPSVYPLAPGSAQTNSMVTLCGLVKGYPPEPVTVTWNSGSLSSGVHTFPFVAVLOS 199

QY 180 DLYTLSSSVTVPSSTWPSSTVCNVAHPASSTKVDKKIYPRDSGGPSEKSEINEKDLRK 239

Db 200 DLYTLSSSVTVPSSTWPSSTVCNVAHPASSTKVDKKIYPRDCG----- 243

QY 240 KSELOQTALGNLQKIYYYNKSAITSEKSDAQLTNTLLFKGFTGHPWYNLLVDLGST 299

Db 244 -CKPCICTVPEVSSVFIFPPK-----PKDVLTTTL----- 272

QY 300 AATSEYEGSSVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEEKVPINLWIDGK 359

Db 273 -----TP-KVTCVVVDIS-----KDDPEVQFSWFDV-- 297

QY 360 QTTVPIDKVKTSKKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVQVGLIV 410

Db 298 --DVEVHTAQTPREBQFNSTFRSVSELPIHQNLWNGKEFKCRVNSAAPAPIEK----- 351

QY 411 FHSSEGSTVSYDLFDAQGYPDTLRLIYRDNTTISSTLSLSLYLTTTSIVMTQTPTSL 470

Db 352 -----TISKT----- 356

QY 471 VSAGDRVTITCKASQSVSNDVAWYQKPGSPKLLISYTSRYSYAGVDPDRFSGSGYGTDT 530

Db 357 ----- 356

QY 531 LTISSVQAEADAAYFCQDYNSPPTFGGKTKLEIKRADAAPTYSIFPPSSEQLTSGASV 590

Db 357 -----KGRPKAPQYVTTIPPKQMAKDKVSL 382

QY 591 VCFLNFPKIDINVKWKIDGSRQN-----GVLSNWTQDQSDKSTYSMSSTLTLTDEYE 645

Db 383 TCMITDFPEDITVEQWNGQPAENYKNTQPIMNT-----NGSYFVYSKLVQKSNWE 435

QY 646 RHNSYTCEATHK 657

Db 436 AGNTFTCSVLHE 447

RESULT 40

ABB74866

ID ABB74866 standard; peptide; 464 AA.

XX ABB74866;

XX

DT	26-APR-2002	(first entry)
XX	Humanised anti-Fas antibody related peptide SEQ ID NO 32.	
XX	Human, mouse; humanised anti-Fas antibody; Fas/Fas ligand;	
XX	light chain subunit; apoptosis; immunosuppressive; antiallergic;	
KW	autoimmune disease; allergy; atopic.	
XX	Homo sapiens..	
OS	JP2001342148-A.	
XX	11-DEC-2001.	
PD	28-MAR-2001; 2001JP-00093106.	
XX	29-MAR-2000; 2000JP-00090918.	
XX	(SANY) SANKYO CO LTD.	
PA	WPI; 2002-145113/19.	
XX	Drug containing humanized anti-Fas antibody, used for preventing and	
PT	treating autoimmune diseases, allergy, and atopy.	
XX	Example 6 (Preparatory); Page 26; 194pp; Japanese.	
PS	The invention relates to a preventive or treating agent for diseases	
XX	caused by abnormality in Fas/Fas ligand system containing as the active	
CC	component an antibody having as the light chain subunit a polypeptide	
CC	containing residues 1-218 of one of 3, 239 residue amino acid sequences,	
CC	or residues 1-451 of one of 3, 470 residue amino acid sequences, all	
CC	fully defined in the specification and having an activity of combining	
CC	specifically with mammalian Fas and an activity of inducing apoptosis in	
CC	a cell expressing Fas. The agent has immunosuppressive and antiallergic	
CC	activity and is used for preventing and treating autoimmune diseases,	
CC	allergy, atopy and others. The present sequence is that of a peptide,	
CC	useful to the invention	
XX	Sequence 464 AA;	
SQ	Query Match 29.1%; Score 1025.5; DB 5; Length 464;	
	Best Local Similarity 36.2%; Pred. No. 1e-52;	
	Matches 243; Conservative 64; Mismatches 106; Indels 259; Gaps 14;	
Qy	1	EVQLQGGPDLVKPGASVKISCKASGYSFTGYMHVVKQSPGKLEWIGRINPNNGVTLY 60
Db	20	QVQLQQPGAEVLKPGASVKLSCKASGYTFTSYMQWVKQRPQGLEWIGIDPSDSVTNY 79
Qy	61	NQRPKDKATLTVDKSSITAYNELSLTSEDSAVVYCARS-TWITNYVDYWGQTSVTVS 119
Db	80	NQRPKGKATLTVDTSSTAYNQLSSTSEDSAVVYCARNRDYSNNVPDVMGTGTTVTVS 139
Qy	120	SAKTTPTSPVPLAPGSAQAQNSMTWLGLCVKGYPEPVTVTWNSGSLSSGVHTTTPAVLQS 179
Db	140	SAKTTPTSPVPLAPGSAQAQNSMTWLGLCVKGYPEPVTVTWNSGSLSSGVHTTTPAVLQS 199
Qy	180	DLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKVDKIVPRDSSGSPSEKSEINEKDLRK 239
Db	200	DLYTLSSSVTVPSSTWPSSTVTCNVAHPASSTKVDKIVPRDCG-----243
Qy	240	KSELQGTALGNLKIYYNNSKAITSSSEKSAOQFLTNTLLFKGFTGHPWYNLLVDLGST 299
Db	244	-CRPCICTVPEVSSVFIPPK-----PKDVITITL-----272
Qy	300	AATSEYEGSSVDLYGAYYGQACAGTGNKTAQMYGGVTLHDNRLITEEKKVPINLWIDGK 359
Db	273	-----TP-KVTCVVVDIS-----KODPEVQFSWFVD--297
Qy	360	QTTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-RGL-YNSDSPFGKVGQRLIV 410
Db	298	--DVEVHTAQTPQREEQFNSTFRSVSELPIMHQNWLNGKEFKCRVNSAAPPATIEK----351

XX	Query Match	29.1%; Score 1025.5; DB 9; Length 466;	
PF	Best Local Similarity	36.6%; Pred. No. 1e-52;	
XX	Matches 245; Conservative	61; Mismatches 112; Indels 251; Gaps 14;	
PR	25-MAR-2003; 2003KR-00018621.		
XX	25-MAR-2003; 2003KR-00018621.		
XX	(IMMU-) IMMUNOMICS CO LTD.		
PA	(KWON-) KWON B S.		
XX	Kim JY, Kwon BS, Kwon MH, Lee UH;		
PI	WPI; 2005-108831/12.		
DR	Humanized monoclonal polypeptide specific for human 4-lbb molecule and		
XX	pharmaceutical composition comprising the same, in which the humanized		
PT	monoclonal polypeptide is used as autoimmune disease treating drug or		
PT	immune-suppressive.		
XX	Example 2; SEQ ID NO 38; 42pp; Korean.		
PS	The invention relates to a humanized monoclonal antibody (based on mouse		
XX	4785 monoclonal antibody) specific for human 4-lbb molecule (tumor		
CC	necrosis factor receptor superfamily, member 9) and a pharmaceutical		
CC	composition comprising the same. The humanized monoclonal antibody has a		
CC	high affinity to human 4-lbb molecule and similar amino acid sequence to		
CC	a human antibody, and is thus useful as an autoimmune disease (especially		
CC	systemic lupus erythematosus) treating drug or immune-suppressive drug		
CC	without adverse side effects. The present sequence is the wild-type mouse		
CC	4785 heavy chain.		
XX	Sequence 466 AA;		
SQ	Query Match 29.1%; Score 1025.5; DB 9; Length 466;		
	Best Local Similarity 36.6%; Pred. No. 1e-52;		
	Matches 245; Conservative 61; Mismatches 112; Indels 251; Gaps 14;		
QY	1	EVQLQSGDPLVKPGASVKISCKASGYSTGYMHVWVKQSPGKGLEWIGRIINPNNGVTLY	60
DB	20	QVQLQPGAEILVRPGASVKLSCKASGYTFTSYWINWVKRPGQGLEWIGNIYPSDSVTNY	79
QY	61	NQKFKDKATLTVDKSSNTTAYMELRSLTSEDSAVYYCARSTM---ITNYVMDYWGQGSVT	117
DB	80	NQKFKDKATLTVDKSSNTVMYQLNSPTSEDSAVYYCTRNGVEGYPHYAYMEYWGQGSVT	139
QY	118	VSSAKTTTPSVYPLAPGSAQAOTNSMTVLGCLVKGYFPEPVTVTWNSGSLSSGVHTTFAVL	177
DB	140	VSSAKTTTPSVYPLAPGSAQAOTNSMTVLGCLVKGYFPEPVTVTWNSGSLSSGVHTTFAVL	199
QY	178	QSDLYTLSSSVTPSSSTWPSSETVTCNVAHPASSTKVDKIVPRDSCGPSEKSEINEKDL	237
DB	200	QSDLYTLSSSVTPSSSTWPSSETVTCNVAHPASSTKVDKIVPRDCG-----	245
QY	238	RKKSLEQGTALGNLKQIYYNYSKAITSEKSAQDQFLNTLLFKGFTTGHVNDLLVDLG	297
DB	246	---CKPCICTVPEVSSVFIFPPK-----PKDVLITL-----	274
QY	298	STAATSEYEGSSVDLYGAYGYQCAGGTENKTCACMYGGVTLHDNNRLTBEKKVPINLWID	357
DB	275	-----TP-KVTCVVVDIS-----KDDPEVQFSWFVD	299
QY	358	GKQTTVPIDKVKTSKKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVGQRLG	408
DB	300	---DVEVHTAQTQPREEQFNSTFRSVSELPIMHQDLNGKEPKCRVNSAAPPAPTEK--	353
QY	409	IVFHSSEGSTVSYDLFDAQGYDPTLLRIYRDNNTTISLTSLSLYLYTTSIVMTQTPTS	468
DB	354	-----TIKST-----	358
QY	469	LLVSAGDRVTITCKASQSVNDVAWYQKPGQSPKLLISVTSRYAGVDRFSGSGYGT	528
DB	359	-----	358
QY	529	FTLTISVQAEADAAYVFCQDYNPSPTFGGKTKLEIKRADAAPTIVFPSSSQLTSGGA	588
DB	359	-----KGRPKASQVYTIIPPKQMAKDKV	382
QY	589	SVVCFLNFPYKIDINVKWKIDGSEKONGVLSWTDQSDKSDTYSMSSTLTITKDEYERHN	648
DB	383	SLTCMITDFPEDITVEWQNGQPAEN-YKNTQPIMDT-DGSYFVYKLVQKSNWEAGN	440
QY	649	SVTCEATHK	657
DB	441	TFTCVSLHE	449
RESULT 42			
ADX39137			
ID	ADX39137	standard; protein; 466 AA.	
AC	ADX39137;		
DT	21-APR-2005	(first entry)	
DE	Mouse monoclonal antibody 4785 heavy chain	SEQ ID 38.	
XX	Monoclonal antibody; heavy chain; autoimmune disease; immunosuppressive;		
KW	immune disorder; systemic lupus erythematosus; antiinflammatory;		
KW	dermatological; dermatological disease; metabolic disorder;		
KW	musculoskeletal disease; tumor necrosis factor receptor.		
XX	Mus sp.		
OS			
XX	KR2004083918-A.		
PN			
XX	06-OCT-2004.		
PD			

XX	25-MAR-2003;	2003KR-00018621.			
PF	25-MAR-2003;	2003KR-00018621.			
XX	(IMMU-)	IMMUNOMICS CO LTD.			
PA	(KWON/)	KWON B S.			
XX	Kim JY,	Kwon BS, Kwon MH, Lee UH;			
PI	WPI;	2005-108831/12.			
XX	Humanized monoclonal polypeptide specific for human 4-lbb molecule and pharmaceutical composition comprising the same, in which the humanized monoclonal polypeptide is used as autoimmune disease treating drug or immune-suppressive.				
PT	Example 2; SEQ ID NO 38; 42pp; Korean.				
XX	The invention relates to a humanized monoclonal antibody (based on mouse 4785 monoclonal antibody) specific for human 4-lbb molecule (tumor necrosis factor receptor superfamily, member 9) and a pharmaceutical composition comprising the same. The humanized monoclonal antibody has high affinity to human 4-lbb molecule and similar amino acid sequence to a human antibody, and is thus useful as an autoimmune disease (especially systemic lupus erythematosus) treating drug or immune-suppressive drug without adverse side effects. The present sequence is the wild-type mouse 4785 heavy chain.				
CC	Sequence 466 AA;				
XX	Query Match				
XX	Best Local Similarity				
XX	Matches				
QY	1	EVQLQSGDPLVKPGASVKISCKASGYFTGYMHVWVKSPGKGLEWIGRIINPNNGVTLV	60		
DB	20	QVQLQPGAEVLRPGASVKLSCKASGYFTSYWVNWVKRPGGLEWIGNIYPSDSVTNY	79		
QY	61	NQKFKDKATLTVDKSGSTTAYMEIRLSLTSDESAVYYCARSTM----	117		
DB	80	NQKFKDKATLTVDKSSNTVMQLNSPTSEDSAVYYCTRNGVEGPHYAYMEYQGQTSVT	139		
QY	118	VSAKTTTPSVPLAPGSAQTNSMTLGLVKGYFPEPVTVTWNSGSLSSGVHTTFAVL	177		
DB	140	VSAKTTTPSVPLAPGSAQTNSMTLGLVKGYFPEPVTVTWNSGSLSSGVHTTFAVL	199		
QY	178	QSDLYTLSSSVTPSSSTWPSSETVTCNVAHPASSTKYDKKIVPRDSCGPSEKSEINEKDL	237		
DB	200	QSDLYTLSSSVTPSSSTWPSSETVTCNVAHPASSTKYDKKIVPRDCG-----	245		
QY	238	RKXSELOQTALGNLKOIYYNYSKATISSEKSAQDQFLNTLLFKGFTTGHVNDLLVDLG	297		
DB	246	---CKPCICTVPEVSSVFIFPPK-----PKDVLITL-----	274		
QY	298	STAATSEYEGSSVDLYGAYGYQCAGGTENKTCACMYGGVTLHDNNRLTBEKKVPINLWID	357		
DB	275	-----TP-KVTCVVVDIS-----KDDPEVQFSWFVD	299		
QY	358	GKQTTVPIDKVKTSKKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVGQRLG	408		
DB	300	---DVEVHTAQTQPREEQFNSTFRSVSELPIMHQDLNGKEPKCRVNSAAPPAPTEK--	353		
QY	409	IVFHSSEGSTVSYDLFDAQGYDPTLLRIYRDNNTTISLTSLSLYLYTTSIVMTQTPTS	468		
DB	354	-----TIKST-----	358		
QY	469	LLVSGDRVTITCKASQSVNDVAWYQKPGQSPKLLISVTSRYAGVDRFSGSGYGTD	528		
DB	359	-----	358		
QY	529	FTLTISVQAEADAAYVFCQDYNPSPTFGGKTKLEIKRADAAPTIVFPSSSQLTSGGA	588		

Db 359 -----KGRPKASQVYTIPTPPKEQMAKDKV 382

Qy 589 SVVCELNNFVKPDINVKWKIDGSEKQNGVLNSWTDODSKDSTYSMSSTLTTLTKDEYERHN 648

Db 383 SLTFCMTDFFPEDITVEMQWNGQPAEN-YKNTQPIMDT-DGSYFVYSKLVNQKSNWEAGN 440

Qy 649 SYTCEATHK 657

Db 441 TPTCSVLHE 449

RESULT 43

AAE18380

ID AAE18380 standard; protein; 613 AA.

XX

AC AAE18380;

DT 07-MAY-2002 (first entry)

XX Human N-terminal DAV-1 heavy chain-mature SCF fusion protein.

XX Human; bifunctional molecule; monoclonal antibody; gene therapy; cancer;

KW vascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder;

KW hyperproliferative disorder; hormonal disorder; DAV-1 heavy chain;

KW cytostatic; vasotropic; ophthalmological; stem cell factor; SCF;

XX fusion protein.

OS Homo sapiens.

OS Synthetic.

OS Chimeric.

XX

XX Key Location/Qualifiers

FT Region 1..438

FT /note= "N-terminal portion of DAV-1 heavy chain"

FT Region 439..449

FT /note= "Linker peptide"

FT Region 450..613

FT /note= "Human mature SCF"

XX

PN WO200204522-A2.

XX

PD 17-JAN-2002.

XX

PF 09-JUL-2001; 2001WO-EP007878.

XX

PR 10-JUL-2000; 2000US-00613017.

XX

PA (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

PA (SCRI) SCRIPPS RES INST.

XX

PI Nemerow GR, Li E;

XX

XX WPI; 2002-171707/22.

XX

PT New bifunctional molecules comprising an antibody or its antigen-binding

PT portion, and a targeting agent, useful for e.g. gene therapy, or for

PT promoting Adenoviral vector-mediated gene delivery to cells lacking av

PT integrins.

XX

PS Claim 15; Page 102-103; 106pp; English.

XX

XX The present invention relates to a bifunctional molecule comprising an

CC antibody or its antigen-binding portion, and a targeting agent where the

CC antibody specifically binds to an antigen in a protein that binds to av

CC integrin, and the targeting agent specifically binds to a cell surface

CC protein that activates the phosphatidylinositol 3 (PI3K) signalling

CC pathway. The bifunctional molecules are useful for gene therapy, for

CC promoting Adenoviral (Ad) vector-mediated gene delivery to cells lacking

CC av integrins, for enhancing Ad binding and internalisation, and in gene

CC delivery of by fibreless adenovirus particles. The bifunctional molecules

CC permit targeting of viral and bacterial vectors to cells that express

CC targeted receptors. Diseases that can be targeted include cancers,

CC vascular disorders, diabetic retinopathies, restenosis, ophthalmic

CC disorders, hyperproliferative disorders, and hormonal disorders. The

CC present sequence is human N-terminal DAV-1 heavy chain-mature stem cell

CC factor (SCF) fusion protein which is used in the invention

XX

Qy Sequence 613 AA;

Query Match 29.1%; Score 1024.5; DB 5; Length 613;

Best Local Similarity 37.3%; Pred. No. 1.6e-52;

Matches 250; Conservative 51; Mismatches 115; Indels 255; Gaps 14;

Qy 1 EVOLQSGPDLVKPGASVKISKASGYSTFGYNNHVKQSPGKLEWIGHINPNNGVTLY 60

Db 20 EVOLQSGPELVKPGASVKISKASGYTFDYNNHVKQSHGKSLWIGYIYYPKGGTGY 79

Qy 61 NQKFKDKATLTVDKSSSTTAYMELSLTSDSVAIYCARSTMTIYNNVMDYVQGGTSVTVSS 120

Db 80 NQKFKSKATLTDTSSNTAYMELSLTSDASAIYICARG-----IAYVQGGTLTVSA 132

Qy 121 AKTTPPSVYPLAPGSAATNSMVTGLGVKGYPEPVTVTWNSGSLSSGVTHTPPAVLQSD 180

Db 133 AKTTPPSVYPLAPGSAATNSMVTGLGVKGYPEPVTVTWNSGSLSSGVTHTPPAVLQSD 192

Qy 181 LYTLSSSVTPSPSTWSETVTCNVNAPASSTKVDKIVPRDSDGSPSEKSEINEKDLRKK 240

Db 193 LYTLSSSVTPSPSTWSETVTCNVNAPASSTKVDKIVPRDCG----- 235

Qy 241 SELQGTALGNLKOIYYNNSKAITSSSEKADQFLNTLLPKGFTGHPWYNLLVDLGSTA 300

Db 236 CRPCICTVPEVSSVFIPTPK-----PKDVLTITL----- 264

Qy 301 ATSEYEGSSVDLYGAYYGYQCAGGTNKTACMYGGVTLHDNNRLTBKKVPINLWIDGKQ 360

Db 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD--- 289

Qy 361 TTVPIDKVTSKKEV-----TVQELDLQARHLYHGK-FGL-YNSDSFGKVGQRLIVF 411

Db 290 -DVEVHTAQTPREQFNSTFRSVSELPIMHQDLNGKEPKCRVNSAAPAPIEK----- 343

Qy 412 HSSEGSTVSYDLFDQAQGYPDTLRIYRDNLTSTLSLSISLYLYTTSIVMTQPTSLLV 471

Db 344 -----TISKT----- 348

Qy 472 SAGDRVITITCKASQSVNDVAMVYQKPGOSPKLLISYTSRSRYAGVDPDRFSGSGYGTDTL 531

Db 349 ----- 348

Qy 532 TISSVQAEADAVYFCQDYNSPPTFGGTYKLEIKRADAAPTIFPPSSQLTSGGASVV 591

Db 349 -----KGRPKAPQVYTIPTPPKEQMAKDKVSLT 375

Qy 592 CFLNNEFVKPDINVKWKIDGSEKQNGVLNSWTDODSKDSTYSMSSTLTTLTKDEYERHNSY 651

Db 376 CMITDFFPEDITVEMQWNGQPAEN-YKNTQPIMDT-DGSYFVYSKLVNQKSNWEAGNFTFI 433

Qy 652 CEATHKTSTSP 662

Db 434 CSVLHEFCRYP 444

RESULT 44

ABG76355

ID ABG76355 standard; protein; 613 AA.

XX

AC ABG76355;

XX

DT 23-OCT-2003 (revised)

DT 10-MAY-2003 (first entry)

XX

DE Mouse DAV-1 heavy chain-mature human SCF fusion protein.

XX

XX Human; bifunctional molecule; antigen-binding portion; alpha integrin;

KW cell surface protein; phosphatidylinositol-3-OH kinase; PI3K;

XX	PS	Example 10; SEQ ID NO 10; 269pp; English.	XX	Db	334	-----KGRPKAPQVYTIPTPPKQMAKDVSLSLT	360
XX	CC	The invention describes a non-murine antibody (I) that competes with	XX	Qy	592	CFLNNEVPKDIINVKWIKDGSERGVNSWTDODSDSTYSMSSTLTLTDEYERHNSYT	651
XX	CC	monoclonal antibody RX1 for binding to macrophage colony stimulating	XX	Db	361	CMITDFPDDITVEMQWNGQPAEN-YKNTQPIMDT-DGSYFVYKLVNQSKEAGNTFT	418
XX	CC	factor (M-CSF) by more than 75%, where the monoclonal antibody RX1 has	XX	Qy	652	CSRATHK 657	
XX	CC	the heavy chain and light chain amino acid sequences having a fully	XX	Db	419	CSVLHE 424	
XX	CC	defined 447 amino acids (SEQ ID No. 2) and 214 amino acids (SEQ ID No. 4)					
XX	CC	sequences given in the specification, respectively. (I) is useful for					
XX	CC	preventing a subject afflicted with a disease that causes or contributes					
XX	CC	to osteolysis, where the antibody effectively reduces the severity of					
XX	CC	bone loss associated with the disease. The disease is chosen from					
XX	CC	metabolic bone diseases associated with relatively increased osteoclast					
XX	CC	activity, including endocrinopathies, hypercalcemia, deficiency states,					
XX	CC	chronic diseases, and hereditary diseases, cancer, osteoporosis,					
XX	CC	osteopetrosis, inflammation of bone associated with arthritis and					
XX	CC	rheumatoid arthritis, periodontal disease, fibrous dysplasia, and/or					
XX	CC	Paget's disease. (I) is useful for preventing or treating metastatic					
XX	CC	cancer. Antibodies of the invention are useful for preventing or reducing					
XX	CC	bone loss; osteolysis; metastatic cancer to bone and cancer. (I) is					
XX	CC	useful for manufacturing a medicament for preventing or reducing bone					
XX	CC	loss in a patient exhibiting osteolysis, manufacturing a medicament for					
XX	CC	treating a patient afflicted with a disease that causes or contributes to					
XX	CC	osteolysis, and metastatic cancer to bone in a patient suffering from					
XX	CC	metastatic cancer, for manufacturing a medicament for treating a patient					
XX	CC	having cancer. (I) in synergistic combination, is useful for preparing a					
XX	CC	medicament for treating a patient exhibiting osteolysis. This is the					
XX	CC	amino acid sequence of macrophage colony stimulating factor (M-CSF)					
XX	CC	specific murine antibody 5H4 heavy chain.					
XX	Qy	Sequence 441 AA;					
XX	Qy	Query Match					
XX	Qy	Best Local Similarity 29.1%; Score 1023.5; DB 9; Length 441;					
XX	Qy	Mismatches 249; Conservative 53; Mismatches 113; Indels 251; Gaps 15;					
XX	Qy	1 EVLOQSGDPLVKPGASVKISCKASGYSTFTGYMHVYKQSPGKLEWIGRINPNNGVTLY 60					
XX	Qy	1 EIQLQSGDPLVKPGASVKISCKASGYSTFTGYMHVYKQSPGKLEWIGRINPNNGVTLY 60					
XX	Qy	61 NQFKDKATLTVDKSTTAYMEIRSLTSDSAYYCARSTMTITNYMDYVNGQSTVTSS 120					
XX	Qy	61 NONFKGATFTVDTSSSTAYMQNSTSDSAYYCARSTMTITNYMDYVNGQSTVTSS 117					
XX	Qy	121 AKTTTPSVPLAPGSAQAQNSMTVLGCLVKGYFPEPTVTWNSGSLSSGVHTPPAVLQSD 180					
XX	Qy	118 AKTTTPSVPLAPGSAQAQNSMTVLGCLVKGYFPEPTVTWNSGSLSSGVHTPPAVLQSD 177					
XX	Qy	181 LYTSSSVTPSPSTWSPSETVTCNVHPASSTKVDKIVPRDSGGPSEKSEINEKDLRKK 240					
XX	Qy	178 LYTSSSVTPSPSTWSPSETVTCNVHPASSTKVDKIVPRDSGGPSEKSEINEKDLRKK 220					
XX	Qy	241 SELQGTALGNLKIYYNYSKAITSSSEKADQFTNTLLPKGFTGHPWYNLLAVDLGSA 300					
XX	Qy	221 CKPCICTVPEVSVVFIPPK-----PKDVLITL----- 249					
XX	Qy	301 ATSEYEGSSVDLYGAYYQCAGTGNKTAACMTGVTLDHNNRLTBKKVPINLWIDGKQ 360					
XX	Qy	250 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD--- 274					
XX	Qy	361 TTVPIDKVTSKKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVGQRLVLP 411					
XX	Qy	275 -DVEVHTAQTPREEQFNSTFRSVELPIMHODWLNKGEFKCRVNSAAPPAPTEK----- 328					
XX	Qy	412 HSEGSSTVSLFDQAQGPDTLLRIYRDNNTTSSLSLSLSLYTTSIVMTQTPSLLV 471					
XX	Qy	329 -----TISKT----- 333					
XX	Qy	472 SAGDRVITTCASQSVNDVAVYQKPGQPKLLISVTSRYAGVDPFRFSGSGYGTDFTL 531					
XX	Qy	334 ----- 333					
XX	Qy	532 TISSVOAEDAAVYFCQDYNSPPTFGGKLEIKRADAAPTYSIFPPSEQLTSGGASVV 591					

XX	PS	Example 10; SEQ ID NO 10; 269pp; English.	XX	Db	334	-----KGRPKAPQVYTIPTPPKQMAKDVSLSLT	360
XX	CC	The invention describes a non-murine antibody (I) that competes with	XX	Qy	592	CFLNNEVPKDIINVKWIKDGSERGVNSWTDODSDSTYSMSSTLTLTDEYERHNSYT	651
XX	CC	monoclonal antibody RX1 for binding to macrophage colony stimulating	XX	Db	361	CMITDFPDDITVEMQWNGQPAEN-YKNTQPIMDT-DGSYFVYKLVNQSKEAGNTFT	418
XX	CC	factor (M-CSF) by more than 75%, where the monoclonal antibody RX1 has	XX	Qy	652	CSRATHK 657	
XX	CC	the heavy chain and light chain amino acid sequences having a fully	XX	Db	419	CSVLHE 424	
XX	CC	defined 447 amino acids (SEQ ID No. 2) and 214 amino acids (SEQ ID No. 4)					
XX	CC	sequences given in the specification, respectively. (I) is useful for					
XX	CC	preventing a subject afflicted with a disease that causes or contributes					
XX	CC	to osteolysis, where the antibody effectively reduces the severity of					
XX	CC	bone loss associated with the disease. The disease is chosen from					
XX	CC	metabolic bone diseases associated with relatively increased osteoclast					
XX	CC	activity, including endocrinopathies, hypercalcemia, deficiency states,					
XX	CC	chronic diseases, and hereditary diseases, cancer, osteoporosis,					
XX	CC	osteopetrosis, inflammation of bone associated with arthritis and					
XX	CC	rheumatoid arthritis, periodontal disease, fibrous dysplasia, and/or					
XX	CC	Paget's disease. (I) is useful for preventing or treating metastatic					
XX	CC	cancer. Antibodies of the invention are useful for preventing or reducing					
XX	CC	bone loss; osteolysis; metastatic cancer to bone and cancer. (I) is					
XX	CC	useful for manufacturing a medicament for preventing or reducing bone					
XX	CC	loss in a patient exhibiting osteolysis, manufacturing a medicament for					
XX	CC	treating a patient afflicted with a disease that causes or contributes to					
XX	CC	osteolysis, and metastatic cancer to bone in a patient suffering from					
XX	CC	metastatic cancer, for manufacturing a medicament for treating a patient					
XX	CC	having cancer. (I) in synergistic combination, is useful for preparing a					
XX	CC	medicament for treating a patient exhibiting osteolysis. This is the					
XX	CC	amino acid sequence of macrophage colony stimulating factor (M-CSF)					
XX	CC	specific murine antibody 5H4 heavy chain.					
XX	Qy	Sequence 441 AA;					
XX	Qy	Query Match					
XX	Qy	Best Local Similarity 29.1%; Score 1023.5; DB 9; Length 441;					
XX	Qy	Mismatches 249; Conservative 53; Mismatches 113; Indels 251; Gaps 15;					
XX	Qy	1 EVLOQSGDPLVKPGASVKISCKASGYSTFTGYMHVYKQSPGKLEWIGRINPNNGVTLY 60					
XX	Qy	1 EIQLQSGDPLVKPGASVKISCKASGYSTFTGYMHVYKQSPGKLEWIGRINPNNGVTLY 60					
XX	Qy	61 NQFKDKATLTVDKSTTAYMEIRSLTSDSAYYCARSTMTITNYMDYVNGQSTVTSS 120					
XX	Qy	61 NONFKGATFTVDTSSSTAYMQNSTSDSAYYCARSTMTITNYMDYVNGQSTVTSS 117					
XX	Qy	121 AKTTTPSVPLAPGSAQAQNSMTVLGCLVKGYFPEPTVTWNSGSLSSGVHTPPAVLQSD 180					
XX	Qy	118 AKTTTPSVPLAPGSAQAQNSMTVLGCLVKGYFPEPTVTWNSGSLSSGVHTPPAVLQSD 177					
XX	Qy	181 LYTSSSVTPSPSTWSPSETVTCNVHPASSTKVDKIVPRDSGGPSEKSEINEKDLRKK 240					
XX	Qy	178 LYTSSSVTPSPSTWSPSETVTCNVHPASSTKVDKIVPRDSGGPSEKSEINEKDLRKK 220					
XX	Qy	241 SELQGTALGNLKIYYNYSKAITSSSEKADQFTNTLLPKGFTGHPWYNLLAVDLGSA 300					
XX	Qy	221 CKPCICTVPEVSVVFIPPK-----PKDVLITL----- 249					
XX	Qy	301 ATSEYEGSSVDLYGAYYQCAGTGNKTAACMTGVTLDHNNRLTBKKVPINLWIDGKQ 360					
XX	Qy	250 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD--- 274					
XX	Qy	361 TTVPIDKVTSKKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVGQRLVLP 411					
XX	Qy	275 -DVEVHTAQTPREEQFNSTFRSVELPIMHODWLNKGEFKCRVNSAAPPAPTEK----- 328					
XX	Qy	412 HSEGSSTVSLFDQAQGPDTLLRIYRDNNTTSSLSLSLSLYTTSIVMTQTPSLLV 471					
XX	Qy	329 -----TISKT----- 333					
XX	Qy	472 SAGDRVITTCASQSVNDVAVYQKPGQPKLLISVTSRYAGVDPFRFSGSGYGTDFTL 531					
XX	Qy	334 ----- 333					
XX	Qy	532 TISSVOAEDAAVYFCQDYNSPPTFGGKLEIKRADAAPTYSIFPPSEQLTSGGASVV 591					

SQ	Sequence 456 AA;	
	Query Match 29.1%; Score 1023.5; DB 5; Length 456; Best Local Similarity 37.4%; Pred. No. 1.3e-52; Matches 249; Conservative 51; Mismatches 111; Indels 255; Gaps 14;	
QY	1 EVOLQSGPDLVKPGASVKISKASGYFTGYMHVVKSPGKLEWIGRINPNNGVTLY 60	QY 1 EVOLQSGPDLVKPGASVKISKASGYFTGYMHVVKSPGKLEWIGRINPNNGVTLY 60
Db	20 EVOLQSGPDLVKPGASVKISKASGYFTGYMHVVKSHGKSLWIGIYIPYKGGTY 79	Db 20 EVOLQSGPELVKPGASVKISKASGYTFTDYNMHVVKSHGKSLWIGIYIPYKGGTY 79
QY	61 NQKFKDKATLTVDKSTTAYMELRSLTSDSAVYYCARSTMTITNYVMDYMGQTSVTSS 120	QY 61 NQKFKDKATLTVDKSTTAYMELRSLTSDSAVYYCARSTMTITNYVMDYMGQTSVTSS 120
Db	80 NQKFKSKATLTDDSSNTAYMELRSLTSDSAVYYCARG-----IAYWQGQTLVTVSA 132	Db 80 NQKFKSKATLTDDSSNTAYMELRSLTSDASAVYYCARG-----IAYWQGQTLVTVSA 132
QY	121 AKTTPPSVYPLAPGSAQAQNSMVTLCGLVKGYFPEPVTVTWNSGSLSSGVHPTPAVLQSD 180	QY 121 AKTTPPSVYPLAPGSAQAQNSMVTLCGLVKGYFPEPVTVTWNSGSLSSGVHPTPAVLQSD 180
Db	133 AKTTPPSVYPLAPGSAQAQNSMVTLCGLVKGYFPEPVTVTWNSGSLSSGVHPTPAVLQSD 192	Db 133 AKTTPPSVYPLAPGSAQAQNSMVTLCGLVKGYFPEPVTVTWNSGSLSSGVHPTPAVLQSD 192
QY	181 LYTLSSTVTPSSTWPSSETVTCNVAHPASSTKVDDKIIVPRDSDGSPSEKSEINEKDLRKK 240	QY 181 LYTLSSTVTPSSTWPSSETVTCNVAHPASSTKVDDKIIVPRDSDGSPSEKSEINEKDLRKK 240
Db	193 LYTLSSTVTPSSTWPSSETVTCNVAHPASSTKVDDKIIVPRDCG----- 235	Db 193 LYTLSSTVTPSSTWPSSETVTCNVAHPASSTKVDDKIIVPRDCG----- 235
QY	241 SELOQTALGNLQIYYNNSKAITSSSEKSAQDFLTNTLLFKGFTTGHFWYNDLLVDLGSTA 300	QY 241 SELOQTALGNLQIYYNNSKAITSSSEKSAQDFLTNTLLFKGFTTGHFWYNDLLVDLGSTA 300
Db	236 CKPCTVPEVSSVFIPPK-----PKDVLITL----- 264	Db 236 CKPCTVPEVSSVFIPPK-----PKDVLITL----- 264
QY	301 ATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTEBEKVPINLWIDGKQ 360	QY 301 ATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTEBEKVPINLWIDGKQ 360
Db	265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFDV--- 289	Db 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFDV--- 289
QY	361 TTVPIDKVTSSKEV-----TVQLDLQARHYLHGK-FGL-YNDSDFGGKVQORGLIVF 411	QY 361 TTVPIDKVTSSKEV-----TVQLDLQARHYLHGK-FGL-YNDSDFGGKVQORGLIVF 411
Db	290 -DVEVHTAQTPREEQFNSTFRSVSELPIHQDLWLGKEFKCRVNSAAPAPIEK----- 343	Db 290 -DVEVHTAQTPREEQFNSTFRSVSELPIHQDLWLGKEFKCRVNSAAPAPIEK----- 343
QY	412 HSSEGSTVSYDLFDAQGQVPTLLRIYRDNNTTISSTLSISLYLYTTSIVMTQTPTSLLV 471	QY 412 HSSEGSTVSYDLFDAQGQVPTLLRIYRDNNTTISSTLSISLYLYTTSIVMTQTPTSLLV 471
Db	344 -----TISK----- 348	Db 344 -----TISK----- 348
QY	472 SAGDRVTITCKASQSVNDVAVYQQPGQSKLLISYTSRYAGVDPDRSGSGYGTDFTL 531	QY 472 SAGDRVTITCKASQSVNDVAVYQQPGQSKLLISYTSRYAGVDPDRSGSGYGTDFTL 531
Db	349 ----- 348	Db 349 ----- 348
QY	532 TISSVQAEAAVYFCQDYNPPFTFGGTTKLEIKRADAAPTYSIFPPSSEQLTSGGASVV 591	QY 532 TISSVQAEAAVYFCQDYNPPFTFGGTTKLEIKRADAAPTYSIFPPSSEQLTSGGASVV 591
Db	349 -----KGRPKAPQVYIIPPKQAKDKVSLT 375	Db 349 -----KGRPKAPQVYIIPPKQAKDKVSLT 375
QY	592 CFLNFPYPKDINVKWKIDGSEKQGVNSWTDQSDKSTYSMSSTLTLTDEYERHNSYT 651	QY 592 CFLNFPYPKDINVKWKIDGSEKQGVNSWTDQSDKSTYSMSSTLTLTDEYERHNSYT 651
Db	376 CMITDFFPEDITVEWQWNGQPAEN-YKNTQPIMDT-DGSYFVYSKLVNOKSNWEAGNTFI 433	Db 376 CMITDFFPEDITVEWQWNGQPAEN-YKNTQPIMDT-DGSYFVYSKLVNOKSNWEAGNTFI 433
QY	652 CEATHK 657	QY 652 CEATHK 657
Db	434 CSVLHE 439	Db 434 CSVLHE 439
RESULT 47		
ABG76345		
ID	ABG76345 standard; protein; 456 AA.	
XX		
AC	ABG76345;	
XX		
DT	10-MAY-2003 (first entry)	
XX		
DE	Mouse DAV-1 heavy chain monoclonal antibody.	
XX		
KW	Mouse; bifunctional molecule; antigen-binding portion; alpha integrin;	
KW	cell surface protein; phosphatidylinositol-3-OH kinase, PI3K;	
KW	signalling pathway; targeted gene therapy; delivery vector;	
KW	adenoviral gene delivery particle; viral infection; cancer;	
KW	rheumatoid arthritis; cardiovascular disorder; diabetic retinopathy;	
KW	restenosis; ophthalmic disorder; hyperproliferative disorder;	
KW	hormonal disorder; virucide; antiinflammatory; antirheumatic;	
KW	antiarthritic; ophthalmologic; DAV-1 heavy chain;	

KW	penton base monoclonal antibody.	
XX		
OS	Mus sp.	
XX		
PN	US2002164333-A1.	
XX		
PD	07-NOV-2002.	
XX		
PF	10-JUL-2001; 2001US-00903327.	
XX		
PR	10-JUL-2000; 2000US-00613017.	
PR	10-JUL-2000; 2000US-0325781P.	
XX		
PA	(SCRI) SCRIPPS RES INST.	
XX		
PI	Nemerow GR, Li E;	
XX		
DR	WPI; 2002-171707/22.	
DR	N-PSDB; ABX12744.	
XX		
PT	New bifunctional molecules comprising an antibody or its antigen-binding	
PT	portion, and a targeting agent, useful for e.g. gene therapy, or for	
PT	promoting Adenoviral vector-mediated gene delivery to cells lacking av	
PT	integrins.	
XX		
PS	Claim 10; Page 30-31; 49pp; English.	
XX		
CC	The present invention relates to a bifunctional molecule comprising an	
CC	antibody or its antigen-binding portion, and a targeting agent. The	
CC	antibody specifically binds to an antigen in a protein that binds to	
CC	alpha integrin, and the targeting agent specifically binds to a cell	
CC	surface protein that activates the phosphatidylinositol-3-OH kinase	
CC	(PI3K) signalling pathway. The bifunctional molecules are useful for	
CC	targeted gene therapy using targeting delivery vectors, such as	
CC	adenoviral gene delivery particles. The bifunctional molecules are useful	
CC	for treating viral infections, rheumatoid arthritis, cancers,	
CC	cardiovascular disorders, diabetic retinopathies, restenosis, ophthalmic	
CC	disorders, hyperproliferative disorders, and hormonal disorders. The	
CC	present sequence represents mouse DAV-1 heavy chain, penton base	
CC	monoclonal antibody	
XX		
SQ	Sequence 456 AA;	
	Query Match 29.1%; Score 1023.5; DB 5; Length 456; Best Local Similarity 37.4%; Pred. No. 1.3e-52; Matches 249; Conservative 51; Mismatches 111; Indels 255; Gaps 14;	
QY	1 EVOLQSGPDLVKPGASVKISKASGYFTGYMHVVKSPGKLEWIGRINPNNGVTLY 60	QY 1 EVOLQSGPDLVKPGASVKISKASGYFTGYMHVVKSPGKLEWIGRINPNNGVTLY 60
Db	20 EVOLQSGPELVKPGASVKISKASGYTFTDYNMHVVKSHGKSLWIGIYIPYKGGTY 79	Db 20 EVOLQSGPELVKPGASVKISKASGYTFTDYNMHVVKSHGKSLWIGIYIPYKGGTY 79
QY	61 NQKFKDKATLTVDKSTTAYMELRSLTSDSAVYYCARSTMTITNYVMDYMGQTSVTSS 120	QY 61 NQKFKDKATLTVDKSTTAYMELRSLTSDSAVYYCARSTMTITNYVMDYMGQTSVTSS 120
Db	80 NQKFKSKATLTDDSSNTAYMELRSLTSDASAVYYCARG-----IAYWQGQTLVTVSA 132	Db 80 NQKFKSKATLTDDSSNTAYMELRSLTSDASAVYYCARG-----IAYWQGQTLVTVSA 132
QY	121 AKTTPPSVYPLAPGSAQAQNSMVTLCGLVKGYFPEPVTVTWNSGSLSSGVHPTPAVLQSD 180	QY 121 AKTTPPSVYPLAPGSAQAQNSMVTLCGLVKGYFPEPVTVTWNSGSLSSGVHPTPAVLQSD 180
Db	133 AKTTPPSVYPLAPGSAQAQNSMVTLCGLVKGYFPEPVTVTWNSGSLSSGVHPTPAVLQSD 192	Db 133 AKTTPPSVYPLAPGSAQAQNSMVTLCGLVKGYFPEPVTVTWNSGSLSSGVHPTPAVLQSD 192
QY	181 LYTLSSTVTPSSTWPSSETVTCNVAHPASSTKVDDKIIVPRDSDGSPSEKSEINEKDLRKK 240	QY 181 LYTLSSTVTPSSTWPSSETVTCNVAHPASSTKVDDKIIVPRDSDGSPSEKSEINEKDLRKK 240
Db	193 LYTLSSTVTPSSTWPSSETVTCNVAHPASSTKVDDKIIVPRDCG----- 235	Db 193 LYTLSSTVTPSSTWPSSETVTCNVAHPASSTKVDDKIIVPRDCG----- 235
QY	241 SELOQTALGNLQIYYNNSKAITSSSEKSAQDFLTNTLLFKGFTTGHFWYNDLLVDLGSTA 300	QY 241 SELOQTALGNLQIYYNNSKAITSSSEKSAQDFLTNTLLFKGFTTGHFWYNDLLVDLGSTA 300
Db	236 CKPCTVPEVSSVFIPPK-----PKDVLITL----- 264	Db 236 CKPCTVPEVSSVFIPPK-----PKDVLITL----- 264
QY	301 ATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTEBEKVPINLWIDGKQ 360	QY 301 ATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTEBEKVPINLWIDGKQ 360
Db	265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFDV--- 289	Db 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFDV--- 289
QY	361 TTVPIDKVTSSKEV-----TVQLDLQARHYLHGK-FGL-YNDSDFGGKVQORGLIVF 411	QY 361 TTVPIDKVTSSKEV-----TVQLDLQARHYLHGK-FGL-YNDSDFGGKVQORGLIVF 411
Db	290 -DVEVHTAQTPREEQFNSTFRSVSELPIHQDLWLGKEFKCRVNSAAPAPIEK----- 343	Db 290 -DVEVHTAQTPREEQFNSTFRSVSELPIHQDLWLGKEFKCRVNSAAPAPIEK----- 343
QY	412 HSSEGSTVSYDLFDAQGQVPTLLRIYRDNNTTISSTLSISLYLYTTSIVMTQTPTSLLV 471	QY 412 HSSEGSTVSYDLFDAQGQVPTLLRIYRDNNTTISSTLSISLYLYTTSIVMTQTPTSLLV 471
Db	344 -----TISK----- 348	Db 344 -----TISK----- 348
QY	472 SAGDRVTITCKASQSVNDVAVYQQPGQSKLLISYTSRYAGVDPDRSGSGYGTDFTL 531	QY 472 SAGDRVTITCKASQSVNDVAVYQQPGQSKLLISYTSRYAGVDPDRSGSGYGTDFTL 531
Db	349 ----- 348	Db 349 ----- 348
QY	532 TISSVQAEAAVYFCQDYNPPFTFGGTTKLEIKRADAAPTYSIFPPSSEQLTSGGASVV 591	QY 532 TISSVQAEAAVYFCQDYNPPFTFGGTTKLEIKRADAAPTYSIFPPSSEQLTSGGASVV 591
Db	349 -----KGRPKAPQVYIIPPKQAKDKVSLT 375	Db 349 -----KGRPKAPQVYIIPPKQAKDKVSLT 375
QY	592 CFLNFPYPKDINVKWKIDGSEKQGVNSWTDQSDKSTYSMSSTLTLTDEYERHNSYT 651	QY 592 CFLNFPYPKDINVKWKIDGSEKQGVNSWTDQSDKSTYSMSSTLTLTDEYERHNSYT 651
Db	376 CMITDFFPEDITVEWQWNGQPAEN-YKNTQPIMDT-DGSYFVYSKLVNOKSNWEAGNTFI 433	Db 376 CMITDFFPEDITVEWQWNGQPAEN-YKNTQPIMDT-DGSYFVYSKLVNOKSNWEAGNTFI 433
QY	652 CEATHK 657	QY 652 CEATHK 657
Db	434 CSVLHE 439	Db 434 CSVLHE 439

Db 290 -DVEVHTAQTPREQFNSTFRSVSELPIMHQDLNGKEFKCRVNGAAPPAPIEK----- 343
QY 412 HSSEGSTSVSYDLFDAQGGYPTLLRIYRDNNTTISSTLSLSLYLYTTSIVMTQPTSLIV 471
Db 344 -----TISK----- 348
QY 472 SAGDRVITCKASQSVSNDAVYQKPGQSPKLLISYTSRYAGVDPDRFGSGGYGDTFTL 531
Db 349 ----- 348
QY 532 TISSVQAEADAAYFCQDQYNSPPTFGGGTKLEIKRADAAPTIFPPSSBQLTSGGASVV 591
Db 349 -----KGRPKAPQVYTIPTPPKEQMAKDKVSLT 375
QY 592 CFLNFPYKPDINVKWKIDGSRQNGVNSWTDQSKDSTYSMSSTLTLTDEYERHNSYT 651
Db 376 CMITDFPDDITVEWQNGQPAEN-YKNTQPIMDT-DGSYFVYVKLVNQSNEAGNFTFI 433
QY 652 CEATHK 657
Db 434 CSVLHE 439
RESULT 48
AEB96754
ID AEB96754 standard; protein; 456 AA.
AC AEB96754;
DT 20-OCT-2005 (first entry)
XX DAV-1 antibody heavy chain.
DE Gene therapy; cancer; vascular disease; diabetic retinopathy; restenosis;
KW ocular disease; hyperproliferation; hormone metabolism disorder;
KW cytostatic; vasotropic; antidiabetic; ophthalmological; metabolic-gen.;
KW DAV-1; heavy chain; antibody.
XX Synthetic.
OS WO2005075506-A1.
PN 18-AUG-2005.
XX 29-DEC-2004; 2004WO-1B004324.
XX 09-JAN-2004; 2004US-0535199P.
XX (SCRI) SCRIPPS RES INST.
XX Nemerow GR, Li E;
XX WPI; 2005-555928/56.
XX New modified adenovirus fiber protein comprising a fiber shaft and a
PT modified knob, useful for treating cancer, vascular disorders, diabetic
PT retinopathies, restenosis and vascular, ophthalmic, hyperproliferative or
PT hormonal disorders.
XX Example 1; SEQ ID NO 28; 250pp; English.
XX The invention relates to a modified adenovirus fiber protein comprising a
CC fiber shaft that contains a sufficient number of shaft repeats to permit
CC trimerization in the absence of a fiber knob or in the absence of an
CC extrinsic trimerization domain, and optionally a modified knob, where, if
CC the knob is included, it is modified to remove or disable the
CC trimerization domain of the knob. The invention also relates to a
CC modified adenovirus fiber protein comprising a modified knob, where the
CC modification of the knob removes or disables a trimerization domain of
CC the knob, and the modified fiber trimerizes a nucleic acid molecule
CC comprising a sequence of nucleotides that encodes the modified adenovirus
CC fiber protein, a cell comprising the nucleic acid, an adenovirus particle
CC comprising the modified fiber, a composition formulated for

CC administration to a subject, comprising the adenovirus particle,
CC detargeting an adenoviral vector particle comprising producing the
CC adenoviral particle, where the binding of the particle to a native
CC receptor is reduced or eliminated as compared to binding of a particle
CC containing the unmodified fiber, introducing the adenoviral particle into
CC cells, introducing the cells into a subject and administering the
CC composition to the subject. The modified adenovirus fiber protein is
CC useful for treating cancer, vascular disease, diabetic retinopathy,
CC restenosis, ocular diseases, hyperproliferative disorders and hormonal
CC disorders. This sequence represents a DAV-1 antibody heavy chain used in
CC the scope of the invention.
XX
SQ Sequence 456 AA;
Query Match 29.1%; Score 1023.5; DB 9; Length 456;
Best Local Similarity 37.4%; Pred. No. 1.3e-52;
Matches 249; Conservative 51; Mismatches 111; Indels 255; Gaps 14;
QY 1 EVLOQSGDPLVKPGASVKISKASGYSTFYGMHVKQSPGKLEWIGRINPNNGVTLY 60
Db 20 EVLOQSGDPLVKPGASVKISKASGYSTFYGMHVKQSPGKLEWIGRINPNNGVTLY 79
QY 61 NOKFKDKATLTVDKSSSTTAYMELRSITSDSAVYCYCARSTMTITNYVMDYMGQGSTVTVSS 120
Db 80 NOKFKSKATLTDDSSNTAYMELRSITSDSAVYCYCARSTMTITNYVMDYMGQGSTVTVSS 132
QY 121 AKTTPPSVYPLAPGSAQTNSMVTGLGCLVKGYFPEPTVTWNSGSLSSGVTHTPAVLQSD 180
Db 133 AKTTPPSVYPLAPGSAQTNSMVTGLGCLVKGYFPEPTVTWNSGSLSSGVTHTPAVLQSD 192
QY 181 LYTLSSTVTPSTWSPSETVTCNVAHPASSTKVKKIVPRDSCGSGPSEKSEINEKDLRKK 240
Db 193 LYTLSSTVTPSTWSPSETVTCNVAHPASSTKVKKIVPRDSCGSGPSEKSEINEKDLRKK 235
QY 241 SELQGTALGNLQIYVYNSKAITSSSEKADQFLNTLLFKGPTFGHPWYNLLDLGSTA 300
Db 236 CKPCITCTVESSSVFIPTPK-----PKDVLITFL----- 264
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLTBEKKVPINLWIDGKQ 360
Db 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD--- 289
QY 361 TTVPIDKVTSKKEV-----TVQELDLQARHYLHGK-FGL-YNSDSGGKVGQGLIVF 411
Db 290 -DVEVHTAQTPREQFNSTFRSVSELPIMHQDLNGKEFKCRVNGAAPPAPIEK----- 343
QY 412 HSSEGSTSVSYDLFDAQGGYPTLLRIYRDNNTTISSTLSLSLYLYTTSIVMTQPTSLIV 471
Db 344 -----TISK----- 348
QY 472 SAGDRVITCKASQSVSNDAVYQKPGQSPKLLISYTSRYAGVDPDRFGSGGYGDTFTL 531
Db 349 ----- 348
QY 532 TISSVQAEADAAYFCQDQYNSPPTFGGGTKLEIKRADAAPTIFPPSSBQLTSGGASVV 591
Db 349 -----KGRPKAPQVYTIPTPPKEQMAKDKVSLT 375
QY 592 CFLNFPYKPDINVKWKIDGSRQNGVNSWTDQSKDSTYSMSSTLTLTDEYERHNSYT 651
Db 376 CMITDFPDDITVEWQNGQPAEN-YKNTQPIMDT-DGSYFVYVKLVNQSNEAGNFTFI 433
QY 652 CEATHK 657
Db 434 CSVLHE 439
RESULT 49
AAE18379
ID AAE18379 standard; protein; 493 AA.
XX AAE18379;
XX

Db 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD--- 289
Qy 361 TTVPIDKVTSKKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVORGLIVF 411
Db 290 -DVEVHTAQTPREEQFNSTFRSVSELPIMHQDLNGKEFKCRVNSAAPPAPIEK----- 343
Qy 412 HSSEGSTVSVDLPDAQGQYPTLLRIYRDNTTISSTLSLSISLYLYTTSIVMTQTPTSLLV 471
Db 344 -----TISK----- 348
Qy 472 SAGDRVITICKASQSVSNVAVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTFTL 531
Db 349 ----- 348
Qy 532 TISSVQAEAAVYFCQDYNSPPTFGGKLEIKRADAAPTYSIFPPSSEQLTSGGASVV 591
Db 349 -----KGRPKAPQVYTIIPPKEQMAKDKVSLT 375
Qy 592 CFLNNFPYKIDINVKWKIDGSRQGVNSWTDQSDSTYSMSSTLTLTKDEYERHNSYT 651
Db 376 CMITDFPEDITVEMQWQPAEN-YKNTQPIMDT-DGSFYFVYSKLVNOKSNWEAGNTFI 433
Qy 652 CEATHK 657
Db 434 CSVLHE 439
RESULT 53
AAE18372
ID AAE18372 standard; protein; 438 AA.
AC AAE18372;
DT 07-MAY-2002 (first entry)
DE Human penton base monoclonal antibody, DAV-1 heavy chain fragment.
KW Human; bifunctional molecule; monoclonal antibody; gene therapy; cancer;
KW vascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder;
KW hyperproliferative disorder; hormonal disorder; DAV-1 heavy chain;
KW cytostatic; vasotropic; ophthalmological.
OS Homo sapiens.
PN WO200204522-A2.
XX 17-JAN-2002.
XX 09-JUL-2001; 2001WO-EP007878.
XX 10-JUL-2000; 2000US-00613017.
XX (NOVS) NOVARTIS AG.
XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX (SCRI) SCRIPPS RES INST.
XX Nemerow GR, Li E;
XX WPI; 2002-171707/22.
XX N-PSDB; AAE18372.
XX New bifunctional molecules comprising an antibody or its antigen-binding
XX portion, and a targeting agent, useful for e.g. gene therapy, or for
XX promoting adenoviral vector-mediated gene delivery to cells lacking av
XX integrins.
PS Claim 10; Page 96; 106pp; English.
XX The present invention relates to a bifunctional molecule comprising an
XX antibody or its antigen-binding portion, and a targeting agent where the
XX antibody specifically binds to an antigen in a protein that binds to av
XX integrin, and the targeting agent specifically binds to a cell surface

CC protein that activates the phosphatidylinositol 3 (PI3K) signalling
CC pathway. The bifunctional molecules are useful for gene therapy, for
CC promoting Adenoviral (Ad) vector-mediated gene delivery to cells lacking
CC av integrins, for enhancing Ad binding and internalisation, and in gene
CC delivery of by fibreless adenovirus particles. The bifunctional molecules
CC permit targeting of viral and bacterial vectors to cells that express
CC targeted receptors. Diseases that can be targeted include cancers,
CC vascular disorders, diabetic retinopathies, restenosis, ophthalmic
CC disorders, hyperproliferative disorders, and hormonal disorders. The
CC present sequence is human penton base monoclonal antibody, DAV-1 heavy
CC chain fragment
XX
SQ Sequence 438 AA;
Query Match 29.0%; Score 1022.5; DB 5; Length 438;
Best Local Similarity 37.4%; Pred. No. 1.4e-52;
Matches 249; Conservative 50; Mismatches 111; Indels 255; Gaps 14;
Qy 1 EVLOQSGDPLVKPGASVKISKASGYSTGYMHVVKSPGKLEWIGRINPNNGVTLY 60
Db 20 EVLOQSGDPLVKPGASVKISKASGYSTGYMHVVKSPGKLEWIGRINPNNGVTLY 79
Qy 61 NQKFKDQKATLTVDKSTTAYMELRSLTSEDSAVYVCARSTMITNYMDYMGQGSTVTSS 120
Db 80 NQKFKDQKATLTVDKSTTAYMELRSLTSEDSAVYVCARSTMITNYMDYMGQGSTVTSS 132
Qy 121 AKTTPSPVYPLAPGSAAGTNSMVTGLCLVKGYFPEPTVTWNSGSLSSGVHTTFAVLQSD 180
Db 133 AKTTPSPVYPLAPGSAAGTNSMVTGLCLVKGYFPEPTVTWNSGSLSSGVHTTFAVLQSD 192
Qy 181 LYTLSSVTVPSTWSPSETVTCNVAHPASSTKVDKIVPRDSGGSPGSEKSENEKDLRKK 240
Db 193 LYTLSSVTVPSTWSPSETVTCNVAHPASSTKVDKIVPRDSGGSPGSEKSENEKDLRKK 235
Qy 241 SELQGTALGNLQIYYNSKAITSSSEKSDAQELTNTLLFKGPTGHPWYNLDLVLGSTA 300
Db 236 CRPKICTVPEVSSVFIPPK-----PKDVLITL----- 264
Qy 301 ATSEYEGSSVDLYGAYGYQCAGGTPTKACMGVTVLHNNRLTEKKVPINLWIDGKQ 360
Db 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD--- 289
Qy 361 TTVPIDKVTSKKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVORGLIVF 411
Db 290 -DVEVHTAQTPREEQFNSTFRSVSELPIMHQDLNGKEFKCRVNSAAPPAPIEK----- 343
Qy 412 HSSEGSTVSVDLPDAQGQYPTLLRIYRDNTTISSTLSLSISLYLYTTSIVMTQTPTSLLV 471
Db 344 -----TISK----- 348
Qy 472 SAGDRVITICKASQSVSNVAVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTFTL 531
Db 349 ----- 348
Qy 532 TISSVQAEAAVYFCQDYNSPPTFGGKLEIKRADAAPTYSIFPPSSEQLTSGGASVV 591
Db 349 -----KGRPKAPQVYTIIPPKEQMAKDKVSLT 375
Qy 592 CFLNNFPYKIDINVKWKIDGSRQGVNSWTDQSDSTYSMSSTLTLTKDEYERHNSYT 651
Db 376 CMITDFPEDITVEMQWQPAEN-YKNTQPIMDT-DGSFYFVYSKLVNOKSNWEAGNTFI 433
Qy 652 CEATHK 656
Db 434 CSVLH 438
RESULT 54
ABG76347
ID ABG76347 standard; protein; 438 AA.
XX
AC ABG76347;
XX

DT 10-MAY-2003 (first entry)
XX
DE Portion of mouse DAV-1 heavy chain monoclonal antibody.
XX
KW Mouse; bifunctional molecule; antigen-binding portion; alpha integrin;
KW cell surface protein; phosphatidylinositol-3-OH kinase; p13k;
KW signalling pathway; targeted gene therapy; delivery vector;
KW adenoviral gene delivery particle; viral infection; cancer;
KW rheumatoid arthritis; cardiovascular disorder; diabetic retinopathy;
KW restenosis; ophthalmic disorder; hyperproliferative disorder;
KW hormonal disorder; virucide; antiinflammatory; antirheumatic;
KW antilarthritic; ophthalmological; DAV-1 heavy chain;
KW penton base monoclonal antibody.
XX
OS Mus sp.
XX
PN US2002164333-A1.
XX
PD 07-NOV-2002.
XX
PF 10-JUL-2001; 2001US-00903327.
XX
PR 10-JUL-2000; 2000US-00613017.
PR 10-JUL-2000; 2000US-0325781P.
XX
PA (SCRI) SCRIPPS RES INST.
XX
XX Nemerow GR, Li E;
DR WPI; 2002-171707/22.
DR N-PSDB; ABX12746.
XX
XX New bifunctional molecules comprising an antibody or its antigen-binding
PT portion, and a targeting agent, useful for e.g. gene therapy, or for
PT promoting Adenoviral vector-mediated gene delivery to cells lacking av
PT integrins.
XX
PS Claim 10; Page 35-36; 49pp; English.
XX
CC The present invention relates to a bifunctional molecule comprising an
CC antibody or its antigen-binding portion, and a targeting agent. The
CC antibody specifically binds to an antigen in a protein that binds to
CC alpha integrin, and the targeting agent specifically binds to a cell
CC surface protein that activates the phosphatidylinositol-3-OH kinase
CC (p13k) signalling pathway. The bifunctional molecules are useful for
CC targeted gene therapy using targeting delivery vectors, such as
CC adenoviral gene delivery particles. The bifunctional molecules are useful
CC for treating viral infections, rheumatoid arthritis, cancers,
CC cardiovascular disorders, diabetic retinopathies, restenosis, ophthalmic
CC disorders, hyperproliferative disorders, and hormonal disorders. The
CC present sequence represents a portion of the mouse DAV-1 heavy chain that
CC is used for a fusion protein bifunctional antibody
XX
SQ Sequence 438 AA;
Query Match 29.0%; Score 1022.5; DB 5; Length 438;
Best Local Similarity 37.4%; Pred. No. 1.4e-52;
Matches 249; Conservative 50; Mismatches 111; Indels 255; Gaps 14;
QY 1 EVQLQSGDPLVKPGASVKISCKASGYFTGYMHVVKQSPGKLEWIGRINPNNGVTLLY 60
DB 20 EVQLQSGDPLVKPGASVKISCKASGYFTDYNMHVVKQSHGKSLDWIGIYIPYKGTGY 79
QY 61 NQKPKDKATLTVDKSTTAYMELRSLSLSDSAVYICARSTMTNVMYWGQSTVTVSS 120
DB 80 NQKFKSKATLTDDSSNTAYMELRSLSLSDSAVYICARG-----IAYWGQSTLTVTSA 132
QY 121 AKTTPSVVPLAPGSAQNTSMVTLGLVKGYFPEPTVTWNSGSLSSGVHTFPFVLQSD 180
DB 133 AKTTPSVVPLAPGSAQNTSMVTLGLVKGYFPEPTVTWNSGSLSSGVHTFPFVLQSD 192
QY 181 LYTLSSTVTPSPSTWSPSETVTCNVAHPASSTKVDDKIVPRDCG----- 235
XX

DB 193 LYTLSSTVTPSPSTWSPSETVTCNVAHPASSTKVDDKIVPRDCG----- 235
QY 241 SELOQTALGNLKQIYYNYSKAITSSSEKSDAQELFTWLLFKGFFTGHPWNLDLLVGSTA 300
DB 236 CKPCICTVPEVSSVFIFPK-----PKVLTTTL----- 264
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQ 360
DB 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFDV----- 289
QY 361 TTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVGQRLIVF 411
DB 290 -DVEVHTAQTPREBQFNSTFRSVSELPIMHQDLWLGKEFKCRVNSAAFPAIEK----- 343
QY 412 HSSEGSTSVSYDLFDAAGQYPTDLLRIYRDNRTIISSTLSISLYLYTTSIVMTQTPTSLLV 471
DB 344 -----TISKT----- 348
QY 472 SAGDRVTITCKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDFTL 531
DB 349 ----- 348
QY 532 TISSVQAEDAAYVFCQDYNSPPTFGGTKLEIKRADAAPTVSIFFPSSEQLTSGGASVV 591
DB 349 -----KGRPKAPQVVVTIPPKKEQNAKDKVSLT 375
QY 592 CFLNNPYKDIVNWKIDGSEKQNGVLNSWTDQSDKDYSSMSTLTLTCKDEVERHNSYT 651
DB 376 CMITDFPEDITVEQWNGQPAEN-YKNTQPIMDT-DGSFYFVYSLNVOKSNWEAGNTFI 433
QY 652 CEATH 656
DB 434 CSVLH 438
RESULT 55
ADQ07403
ID ADQ07403 standard; protein; 697 AA.
XX
AC ADQ07403;
XX
DT 07-OCT-2004 (first entry)
XX
DE hCBEl1/hBHA10 bispecific-1 antibody construct mature heavy chain.
XX
KW tumour volume; lymphotoxin-beta receptor; LT-beta-R; agonist; antibody;
KW chemotherapeutic; supra-additive; inhibition; cytostatic; gene therapy;
KW cancer; mature heavy chain; hCBEl1/hBHA10 bispecific-1.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO2004058183-A2.
XX
XX 15-JUL-2004.
XX
XX 22-DEC-2003; 2003WO-US041243.
XX
XX 20-DEC-2002; 2002US-0435185P.
XX
XX (BIOG-) BIOGEN IDEC MA INC.
XX
XX Lepage D, Gill A;
XX
XX WPI; 2004-525785/50.
DR N-PSDB; ADQ07402.
XX
XX Inhibiting tumor volume comprising administering an amount of a
PT lymphotoxin-beta receptor agonist or antibody and a chemotherapeutic
PT agent (e.g. gemcitabine or adriamycin).
XX
PS Disclosure; SEQ ID NO 2; 161pp; English.
XX

Db 301 STYRVSVLTVLHODWLNGKEYCKYKSNKALPAPIEKTISKAKGQPREQVYTLPPSRDE 360
QY 272 FITN-----TLLFKGPTGHPWNLDLVLGSTR-ATSEYEGSS--VDLYGAYVGYQCAGG 324
Db 361 LTKNQVSLTCLVKGFYP-----SDIAVEWESNGQPNKYKTTTPVLDSDGSFFLYSKL-- 413
QY 325 TPNKTACMYGGV-----TLHD--NNRLTEEK-----KVPINLWIDGKQTTVP 364
Db 414 TVDKSRWQGNQVFCSCVMHEALHNHYTKQSLSPGCGGGGGGGGQVQLVQSGAEVKRP 473
QY 365 IDKVKTSK-----EVTQELDQARHYLHGKFLGFLYNSDSFGCKVQVGLI 409
Db 474 GSSVKVSCKASGYFTFTYYLHWVRQPGQGLEWGMWYIFGNVHAQYN-EKFKGRV----- 527
QY 410 VFHSSEGSTVVDLFDQAQGYPTLRIYRDNTTISSTLSLSLYL-----TT----- 458
Db 528 -----TITADKSTAYMELSLR--SEDTAVYYCARSMWEGFFYWGQGITVTIVSSGG 577
QY 459 -----SIVMTQTPSLVLSAGDRVITITCKASQSVNDVAVYQCKPGQSPKLL 505
Db 578 GSGSGGGGGGSDIQMTQSPSLASVGDVRVTITCKASQNGVINAVYQCKPGKAPKSL 637
QY 506 ISYTSRYAGVPRFSGSGYGTDTLTITISSVQAEADAAYFCQDYNPSPTFGGQTKLEIK 565
Db 638 ISSASYRSGVPRFSGSGYGTDTLTITISSLOPEDFATYFCQYDYPTFTFGQTKVEIK 697

RESULT 57
AAY39452
ID AAY39452 standard; protein; 206 AA.
XX AAY39452;
AC AAY39452;
XX
DT 19-NOV-1999 (first entry)
XX
DE Antibody ABX-CBL light chain sequence.
XX
DE Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.
XX
OS Homo sapiens.
XX
PN WO9945031-A2.
XX
PD 10-SEP-1999.
XX
PF 03-MAR-1999; 99WO-US0004583.
XX
PR 03-MAR-1998; 98US-00034607.
PR 03-FEB-1999; 99US-00244253.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
XX
DR WPI; 1999-540816/45.
XX
PT New monoclonal antibody, used for treating e.g. graft versus host
PT disease, cancers, autoimmune diseases and inflammatory diseases.
XX
PS Disclosure; Page 58; 245pp; English.
XX
CC This sequence represents the light chain of the antibody ABX-CXL. The
CC invention relates to a monoclonal antibody (mAb) with an isotype that
CC fixes complement and a variable region that binds to the epitope on CD147
CC bound by the IgM mAb ABX-CBL, providing that the antibody is not CBL1.
CC The mAb can selectively kill activated T-cells, activated B-cells or
CC resting or activated monocytes. The products and methods can be used for
CC treating diseases involving activated T-cells or B-cells or monocytes,
CC e.g. graft versus host disease (GVHD), organ transplant rejection

CC diseases (e.g. renal transplant, ocular transplant), cancers (e.g.
CC cancers of the blood (e.g. leukaemia's and lymphomas) and pancreatic),
CC autoimmune diseases (e.g. lupus), and inflammatory diseases (e.g.
CC arthritis)
XX
SQ Sequence 206 AA;
Query Match 28.9%; Score 1018; DB 2; Length 206;
Best Local Similarity 95.1%; Pred. No. 1.1e-52; Indels 0; Gaps 0;
Matches 193; Conservative 4; Mismatches 6;
QY 469 LLVSAGDRVITITCKASQSVNDVAVYQCKPGQSPKLLISYTSRYAGVPRFSGSGYGT 528
Db 3 LLVSAGDRVITITCKASQSVNDVAVYQCKPGQSPKLLIYASNRYTGVDRFTGSGVGT 62
QY 529 FTLTISVQAEADAAYFCQDYNPSPTFGGQTKLEIKRADAAPTIVSIFPPSSQLTSGGA 588
Db 63 FTLTISVQAEADLAVYFCQDYSSPYTFGGQTKLEIKRADAAPTIVSIFPPSSQLTSGGA 122
QY 589 SVVCFLNFPYKIDINVKWIKDGSERQNGVLNSWTDQDSKDYTSMSSTLTLTCKDEYERHN 648
Db 123 SVVCFLNFPYKIDINVKWIKDGSERQNGVLNSWTDQDSKDYTSMSSTLTLTCKDEYERHN 182
QY 649 SYTCETHAKTSPIVKSFNRNE 671
Db 183 SYTCETHAKTSPIVKSFNRNE 205
RESULT 58
AAR66758
ID AAR66758 standard; protein; 465 AA.
XX AAR66758;
AC AAR66758;
XX
DT 01-SEP-1995 (first entry)
XX
DE Anti-tobacco mosaic virus monoclonal Ab heavy chain.
XX
KW Tobacco mosaic virus; TMV; monoclonal antibody; heavy chain;
KW virus-resistant plants; biofarming.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT Peptide /label= leader
FT Peptide 20..465
FT Domain /label= mat_peptide
FT Domain 20..128
FT Domain /note= "variable heavy domain"
FT Domain 129..141
FT Domain /note= "J heavy 4 domain"
FT Domain 142..465
FT Domain /note= "constant heavy domain"
XX
PN JP06319396-A.
XX
PD 22-NOV-1994.
XX
XX 07-MAY-1993; 93JP-00131208.
XX
PR 07-MAY-1993; 93JP-00131208.
XX
PA (NISB) JAPAN TOBACCO INC.
PA (KURS) KURARAY CO LTD.
XX
XX WPI; 1995-040220/06.
DR N-PSDB; AAQ79930.
XX
PT Transformed plant producing animal-derived anti-virus antibody - esp.
XX tobacco plants producing anti-tobacco mosaic virus monoclonal antibody.
XX Example 2; Page 14-15; 26pp; Japanese.
PS

Db	355	-----KGRPKAPQVYTIPTPKQMAKDVKSL	380
QY	591	VFPLNNFYPKDINVKKIDGSEKQGVLSWTDQSDKSTYSMSSTLTUTKDEYERHSY	650
Db	381	TCMITDFPDDITVEQWQGAEN-YKNTQPIMDT-DGSYFYSLKYNQKSNWEAGNTF	438
QY	651	TCEATHK	657
Db	439	TCSVLHE	445
RESULT 60			
ADQ07409			
ID	ADQ07409	standard; protein; 701 AA.	
AC	ADQ07409;		
XX			
XX	07-OCT-2004	(first entry)	
DE	hCBEl1	monospecific-1 antibody construct mature heavy chain.	
XX			
KW	tumour volume; lymphotoxin-beta receptor; LT-beta-R; agonist; antibody;		
KW	chemotherapeutic; supra-additive; inhibition; cytostatic; gene therapy;		
KW	cancer; mature heavy chain; hCBEl1	monospecific-1.	
OS	Homo sapiens.		
OS	Synthetic.		
XX			
PN	WO2004058183-A2.		
PD	15-JUL-2004.		
XX			
PF	22-DEC-2003;	2003WO-US041243.	
XX			
PR	20-DEC-2002;	2002US-0435185P.	
XX			
PA	(BIOG-) BIOGEN IDSC MA INC.		
XX			
PI	Lepage D, Gill A;		
XX			
DR	WPI; 2004-525785/50.		
DR	N-PSDB; ADQ07408.		
XX			
PT	Inhibiting tumor volume comprising administering an amount of a		
PT	lymphotoxin-beta receptor agonist or antibody and a chemotherapeutic		
PT	agent (e.g. gemcitabine or adriamycin).		
XX			
PS	Disclosure; SEQ ID NO 8; 161pp; English.		
XX			
CC	The invention relates to a novel method for inhibiting tumour volume. The		
CC	method comprises administering an amount of a lymphotoxin-beta receptor		
CC	(LT-beta-R) agonist or antibody and an amount of at least one		
CC	chemotherapeutic agent, where the administration of the LT-beta-R agonist		
CC	or antibody and the chemotherapeutic agent results in supra-additive		
CC	inhibition of the tumour. The invention further relates to: a		
CC	pharmaceutical composition comprising an amount of an LT-beta-R agonist		
CC	and at least one chemotherapeutic agent, and a pharmaceutical carrier,		
CC	which upon administration to a subject results in supra-additive		
CC	inhibition of a tumour. The lymphotoxin-beta receptor agents have		
CC	cytostatic activity. Gene therapy may be used in the tumour inhibition		
CC	method. The method is useful for inhibiting tumour volume or for treating		
CC	cancer. The lymphotoxin-beta receptor agonist and the chemotherapeutic		
CC	agent are useful for preparing a medicament for the treatment of cancer,		
CC	which upon administration to a subject results in supra-additive		
CC	inhibition of a tumour. This sequence represents the mature heavy chain		
CC	of the hCBEl1 monospecific-1 antibody construct for use in the tumour		
CC	volume inhibition method of the invention.		
XX			
SQ	Sequence 701 AA;		
Query Match 28.6%; Score 1006; DB 8; Length 701;			
Best Local Similarity 34.9%; Pred. No. 2.4e-51;			
Matches 256; Conservative 94; Mismatches 183; Indels 200; Gaps 21;			

QY	1	EVQLQSGPDLVKGASVKISKASGYFTGYMHWVKOSPGKLEWIGRINPNNGVTLY	60
Db	1	EVQLVESGGGLVPGGSKURLSCAASGFTFDYIMWFROAPGKRGLEWATISDGGSYTY	60
QY	61	NQKFQDKATLTVDKSTTAYMELRLSITSDSAVYVCARSTMITNYVMDYWGQTSYTVSS	120
Db	61	PDSVKGRFTISRDNAKNSLYLQWSSLRADETAVYICAREENGNYFYFDYWGQTTVTSS	120
QY	121	AKTTPPSVYPLAPGAAQNSMVTGLGVKGFPEPPTVTVNSGSLSSGVHFPVAVLQSD	180
Db	121	ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTFPAVLQSS	180
QY	181	-LYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKVDKKIIPRDS-----GG	224
Db	181	GLYSLSVVTVPSSSLGIQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCTPCPAPPELLGG	240
QY	225	PS-----EKSEEI-----NEKDLRKSEIQGTALGNLK---QIYYYN	258
Db	241	PSVFLFPPPKDITLMSRTPETVCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN	300
QY	259	S-----KATISSE-----KSADQ	271
Db	301	STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE	360
QY	272	FLTN-----TLLPKGFPTGHPWYNDLLDLGSTA-ATSEYEGSS--VDLYGAYVYQCAGG	324
Db	361	LTQNQVSLTCLVKGFYP-----SDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSKL--	413
QY	325	TPNKTACMYGGV---TLHD--NNRLTEEK-----KVPINLWIDGKQTTVP	364
Db	414	TVDKSRWQGNVFCSCVMHEALHNHYTKLSLSPGGGGSGGGSEVQLVESGGGLVKP	473
QY	365	IDKVTSKKEVTVQELDLQARHYLHGKFLGYNDSFGGKVGQRL-IVFHSSEGSTVSYDL	423
Db	474	GGSLR-----LSCAASGFTFDYIMWFROAPGK---GLEWATISDGGSYTY--	518
QY	424	FDAQGYPTDLLRIYRDNTTISSTLSISLYLVTS-----	459
Db	519	-----YDPSV---KGRFTISRDNAKNSLYLQWSSLRADETAVYICAREENGNYFYFDY	568
QY	460	-----IVMTQTPTSLLVSAGDRVTITCKASQSVSNDA	492
Db	569	WQGGTTVTTVSSGGGGSGGGGGSDIQMTQSPSSLSASVGRVTITCKAGQDIKSYLS	628
QY	493	WYQQRPGQSPKLLISYTSRYAGVDRPSGSGYGTDTLTITSSVQAEADAIVFCQDYNS	552
Db	629	WYQQRPGKAPKLLIYYATRLADGVPSRFSFGSGSGTDYTLTISLSQPEDFATYYCLOHGES	688
QY	553	PPTFGGSGTKLEIK	565
Db	689	PWTFGGSGTKLEIK	701
RESULT 61			
ID	ADQ12186	standard; protein; 701 AA.	
AC	ADQ12186;		
XX			
XX	07-OCT-2004	(first entry)	
DE	Heavy chain of hucBE11	monospecific-1 antibody.	
XX			
KW	lymphotoxin-beta receptor; LT-abgr-R; Cytostatic; cancer; tumour;		
KW	hucBE11; hUBHA10.		
XX			
OS	Homo sapiens.		
XX			
PN	WO2004058191-A2.		
PD	15-JUL-2004.		
XX			

QY 1 EVLOQSGPDLVKPGASVKISCKASGYSTGYMHVWKSPGKGLWIGRINPNNGVTLY 60
Db 21 EVLOQSGAALMRPGSVKISKSGSYTDTYTMHWKQSHAKSLEWIGLITFFYGDALY 80
QY 61 NOKFKDKATLTVDKSTTAYMELRLSTSDSAVYCARSTMITNYVMDYWGQTSVTSS 120
Db 81 NOKFKGKATLTVDKSSSTAYMELARLTSDSAIYYCTRGRLRGPFPAYWGQTLVTUSA 140
QY 121 AKTTPSVVPLAPGSAQTNSMVTLCGLVKGYFPEPVTVTWNSGSLSSGVHFFPAVLQSD 180
Db 141 AKTTPSVVPLAPGSAQTNSMVTLCGLVKGYFPEPVTVTWNSGSLSSGVHFFPAVLQSD 200
QY 181 LYTSSSVTPSPSTWSPSETVTCNVAHPASSTKVKKIIPRDSGGPSEKSENEKDLRKK 240
Db 201 LYTSSSVTPSPSTWSPSETVTCNVAHPASSTKVKKIIPRDCG----- 243
QY 241 SELQGTALGNLQIYYVNSKAITSEKSAQDLTNTLLFKGFTGHPWYNDLLVDLGSTA 300
Db 244 CKPICTVPEVSSVFPPK-----PKDVLITL----- 272
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTBEKKVPLNLMIDGKQ 360
Db 273 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD--- 297
QY 361 TTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVQRCGLIYF 411
Db 298 -DVEVHTAQTPREEQFNSTFRSVSELPIMHQDLNGKEFKCRVNSAAPPIEK----- 351
QY 412 HSSEGSTSVYDLFDAQGQVPTLLRIYRDNNTTISSTLSLSISLYLTTSIVMTQTPTSLIV 471
Db 352 -----TISK----- 356
QY 472 SAGDRVITITCKASQSVNSDVAMVYQKPGQSKLLISYTSRYAGVDRFSGSGYGTDFTL 531
Db 357 ----- 356
QY 532 TISSVQAEADAAYFCODYNSPTFGGKLEIKRADAAPTVSIIPPSSEQLTSGGASVV 591
Db 357 -----KGRPKAPQVYTIPTPPKEQWAKOKVSLT 383
QY 592 CFLNFPYKIDINVKWKIDGSRQNGVLNWSWTDQSDKSTYSMSSTLTLTCKDEYERHNSYT 651
Db 384 CMITDFPEDITVEQWQNGQPAEN-YKNTQPIMDT-DGSYFYVYSKLVQKSNWEAGNTFT 441
QY 652 CEATHK 657
Db 442 CSVLHE 447

RESULT 63
ADN97521
ID ADN97521 standard; protein; 700 AA.

XX AC ADN97521;
XX DT 01-JUL-2004 (first entry)
XX DE Artificial protein construction protein #19.
XX DE artificial proporotein; propeptide; protein engineering; antibody.
XX KW Unidentified.
XX OS WO2004031362-A2.
XX PN 15-APR-2004.
XX PD 03-OCT-2003; 2003WO-US031420.
XX PF 03-OCT-2002; 2002US-0415940P.
XX PR (LARG-) LARGE SCALE BIOLOGY CORP.
XX PA

XX Reini SJ, Edwards P;
XX WPI; 2004-330170/30.
XX N-PSDB; ADN97520.
XX New artificial proprotein comprises three peptide sequences, useful for
XX artificial multimeric protein engineering in eukaryotes.
XX Example 14; SEQ ID NO 94; 244pp; English.
XX The invention relates to an artificial proprotein comprising three
XX peptide sequences: a first peptide sequence of interest, a propeptide
XX sequence attached to the C-terminus of the first peptide sequence of
XX interest, and a second peptide of interest attached to the C-terminus of
XX the propeptide sequence. The artificial proprotein and polynucleotides
XX are useful for artificial multimeric protein engineering, e.g. antibodies
XX and antibody fragments in eukaryotes. This sequence corresponds to a
XX protein used in the generation of the protein of the invention.
XX Sequence 700 AA;
Query Match 28.4%; Score 1000; DB 8; Length 700;
Best Local Similarity 36.8%; Pred. No. 5.5e-51;
Matches 242; Conservative 54; Mismatches 131; Indels 230; Gaps 11;
QY 1 EVLOQSGPDLVKPGASVKISCKASGYSTGYMHVWKSPGKGLWIGRINPNNGVTLY 60
Db 257 QVLOQSGPELVKPGASLKLCTASGFNIKDTYIHWKORPEQGLEWIGRIYPTNYTRY 316
QY 61 NOKFKDKATLTVDKSTTAYMELRLSTSDSAVYCARSTMITNYVMDYWGQTSVTSS 120
Db 317 DKFQDKATITADTSNTAYLQVSLTSDTAVYCSRGGDGFYAMDYWGQASVTSS 376
QY 121 AKTTPSVVPLAPGSAQTNSMVTLCGLVKGYFPEPVTVTWNSGSLSSGVHFFPAVLQSD 180
Db 377 AKTTPSVVPLAPGSAQTNSMVTLCGLVKGYFPEPVTVTWNSGSLSSGVHFFPAVLQSD 436
QY 181 LYTSSSVTPSPSTWSPSETVTCNVAHPASSTKVKKIIPRDSGGPSEKSENEKDLRKK 240
Db 437 LYTSSSVTPSPSTWSPSETVTCNVAHPASSTKVKKIIPRDCG----- 479
QY 241 SELQGTALGNLQIYYVNSKAITSEKSAQDLTNTLLFKGFTGHPWYNDLLVDLGSTA 300
Db 480 -----CKPC 483
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTBEKKVPLNLMIDGKQ 360
Db 484 ICTVPEVSSVFIF-----PPK-----PKDVLITLTPKV 512
QY 361 TTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRLIVFHSSEGSTVS 420
Db 513 TCVVD-----ISKDDPEVQ-----FS 529
QY 421 YDLFDAQGOYPTLLRIYRDNNTTISSTLSLSISLYLTTSIVMTQTPTSLLSAGDRVIT 480
Db 530 WFDVDEVHTAQTPREEQFNSTFRSV-----ELPIHQD----- 565
QY 481 CKASQSVNSDVAMVYQKPGQSKLLISYTSRYAGVDRFSGSGYGTDFTLTSSVQAE 540
Db 566 -----WLNDKEFK-----RVNSAAPPAPIEKTIS----- 590
QY 541 AAVYFCQDYNPPTFGGKLEIKRADAAPTVSIIPPSSEQLTSGGASVCFNNFPYK 600
Db 591 -----KTGRPKAPQVYTIPTPPKEQWAKOKVSLTCTMITDFPE 628
QY 601 DINVKWKIDGSRQNGVLNWSWTDQSDKSTYSMSSTLTLTCKDEYERHNSYTCEATHK 657
Db 629 DITVEQWQNGQPAEN-YKNTQPIMDT-DGSYFYVYSKLVQKSNWEAGNTFTCSVLHE 683
RESULT 64
AAW85692

08-APR-2003; 2003WO-US010856.
09-APR-2002; 2002US-0371610P.
(SCRI) SCRIPPS RES INST.
Burton DR, Williamson RA, Moroncini G;
WPI; 2003-877028/81.
N-PSDB; ADE06765.
New motif-grafted hybrid polypeptides binding to the infectious form of a prion, useful for diagnosing or treating diseases of protein aggregation or conformation, e.g. amyloidosis, Alzheimer's disease, renal failure or diabetes.
Disclosure; SEQ ID NO 36; 115pp; English.
The present invention describes a hybrid polypeptide (I) comprising: (a) a polypeptide motif containing a sufficient number of contiguous amino acid residues from a polypeptide associated with a disease of protein aggregation or conformation to bind an aggregating form of the polypeptide or to a disease-associate conformer of the polypeptide; and (b) an additional amino acids from a polypeptide other than the polypeptide from which the motif is derived, where the resulting hybrid polypeptide binds with greater affinity to a disease causing or infectious conformer of the polypeptide than is the source of the polypeptide motif compared to a benign form of the polypeptide. Also described: (1) a nucleic acid molecule encoding (I); (2) a vector comprising the nucleic acid molecule; (3) a cell comprising the vector; (4) detecting an isoform or a PrPsc form of a prion polypeptide or a polypeptide associated with a disease of protein aggregation, in a sample; (5) a solid support comprising a plurality of polypeptides described above; (6) detecting cells that contain a protein conformer associated with a disease of protein aggregation; (7) preparing a hybrid molecule that specifically interacts with one conformer of a protein involved in the disease mentioned above; and (8) an anti-idiotype antibody that specifically binds to an infectious form of a prion protein. (I) has neuroprotective, neurotropic, antidiabetic, anticonvulsant, cerebroprotective, antiparkinsonian, cytostatic, nephrotropic, cardiant, antiinflammatory and antiarteriosclerotic activities, and can be used in gene therapy. The composition and methods of the present invention can be used in diagnosing or treating diseases of protein aggregation or conformation, such as Creutzfeldt-Jakob disease, scrapie and bovine spongiform encephalopathy, Alzheimer's disease, Type II diabetes, Huntington's disease, immunoglobulin amyloidosis, reactive amyloidosis associated with chronic inflammatory disease, hereditary systemic amyloidosis associated with autosomal dominant inheritance of variant transthyretin gene, amyotrophic lateral sclerosis, Pick's disease, Parkinson's disease, Frontotemporal dementia, multiple myeloma, plasma cell dyscrasias, familial amyloidotic polyneuropathy, medullary carcinoma of thyroid, chronic renal failure, congestive heart failure, senile cardiac and systemic amyloidosis, chronic inflammation, atherosclerosis or familial amyloidosis. The present sequence is used in the exemplification of the present invention.

Query Match 27.8%; Score 979.5; DB 7; Length 223;
Best Local Similarity 87.4%; Pred. No. 2.3e-50;
Matches 194; Conservative 7; Mismatches 16; Indels 5; Gaps 2;
QY 1 EVQLQSGDPLVKPGASVKISKAGSYFTGYMHVWVQSPKGLIEWIGRINPNNGVTL 59
DB 3 EVQLQSGDPLVKPGSSVKISKAGSYRTFTDYNMDWKQSHKGLIEWIGYIPNTGVG 62
QY 60 YNOKFKDKATLTVDKSTTAYMELSLTSDSAVYYCARSTMTITNVMDYWGOGTSVTVS 119
DB 63 YNORFGKATLTVDKSSSTAYMELSLTSDSAVYYCAG-----FYGMVWGOGTSVTVS 118
QY 120 SAKTTPPSVYPLAPGSAQAQNSMVTGLCGLVKGYFPEPVTVMNSGSLSGVHTFPVQLQS 179
DB 119 SAKTTPPSVYPLAPGSAQAQNSMVTGLCGLVKGYFPEPVTVMNSGSLSGVHTFPVQLQY 178

QY 180 DLYTLSSSVTPSPSTWPSSTVTCNVAHPASSTKVDKIVPRD 221
DB 179 DLYTSSSVTPSPSTWPSSTVTCNVAHPASSTKVDKIVPRD 220

RESULT 66
AAV55081
ID AAY55081 standard; protein; 626 AA.
XX
AC AAY55081;
DT 25-FEB-2000 (first entry)
XX
DE Single chain Fv protein sequence shPM1-kappa-BvGS3.
XX

Gene isolation; membrane-bound protein; fusion protein; drug production;
antigen-binding cell; secretable functional protein; antigenic protein;
protein isolation; diagnosis; ScFv.

Synthetic.

WO9960113-A1.

25-NOV-1999.

30-APR-1999; 99WO-JP002341.

20-MAY-1998; 98JP-00138652.

01-OCT-1998; 98JP-00279876.

(CHUS) CHUGAI SEIYAKU KK.

Tsuchiya M, Saito M, Ohtomo T;

WPI; 2000-039382/03.

N-PSDB; AA240316.

Efficient and selective isolation of a gene encoding membrane protein

with low or no antigenic binding activity, for diagnosis, study of, and

production of drugs treating abnormal functions of the protein.

Example 7; Page 103-109; 120pp; Japanese.

This sequence represents a single chain Fv (ScFv) sequence. The invention relates to a method for isolating a gene encoding a membrane-bound protein, comprising introducing a vector into a cell, contacting an antigen with the cell expressing the fused protein encoded by the vector on its surface to select an antigen-binding cell, and isolating the cDNA. The vector contains DNA encoding a secretable functional protein with antigenicity and binding affinity, and a cDNA ligated to DNA downstream of the 3' end of the coding sequence. The method can be used to isolate a membrane-bound protein for diagnosis and study. It can also be used for producing drugs treating abnormal functions of the protein. Such a technique is efficient and selective, which is different from the prior-art transmembrane trap (TMT) method wherein an epitope recognised by an antibody is carried in a fused protein

Sequence 626 AA;

Query Match 27.8%; Score 977.5; DB 3; Length 626;

Best Local Similarity 35.2%; Pred. No. 1e-49;

Matches 253; Conservative 92; Mismatches 216; Indels 157; Gaps 22;

QY 1 EVQLQSGDPLVKPGASVKISKAGSYFTG-YMHVWVQSPKGLIEWIGRINPNNGVTL 59

DB 20 QVQLQESGGLVRPQSLTCTVSGYSITSDHAWSWVRQPPGRLIEWIGYIS-YSGIT 78

QY 60 YNOKFKDKATLTVDKSTTAYMELSLTSDSAVYYCARSTMTITNVMDYWGOGTSVTVS 119

DB 79 YNPSLSRVTLMDLRSKNQFSLRLSVTAADTAVYYCARSLARTT-AMYYWGOGSLTVS 137

QY 120 SA-----KTTTPPSVYPLAPGSAQAQNSMVTGLCL-----VKGYF----- 153

RESULT 68
AA42294
ID AA42294 standard; protein; 243 AA.
AC AA42294;
DT 06-DEC-1999 (first entry)
XX
DE Anti-5T4 secreted single chain antibody Fv fragment.
XX
KW Cytochrome; targeting; localisation; cancer; tumour; prodrug; reduction;
nucleus.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9945127-A2.
XX
PD 10-SEP-1999.
PF 05-MAR-1999; 99WO-GB000674.
XX
PR 06-MAR-1998; 98GB-00004841.
PR 19-AUG-1998; 98GB-00018103.
PR 29-JAN-1999; 99GB-00002081.
XX
(OXFO-) OXFORD BIOMEDICA UK LTD.
PA Stratford IJ, Patterson AV, Kingman SM, Kan O, Griffiths L;
PI Mitrophanous K;
XX
DR WPI; 1999-551046/46.
DR N-PSDB; AA219786.
XX
PT New prodrug activating agent targeted to selected cells or tissues,
particularly hypoxic cells, for treating e.g. tumors.
XX
PS Example 9; Fig 3; 187pp; English.
XX
CC This sequence represents an example of a secreted single chain antibody
Fv fragment (in this case, directed against the 5T4 antigen), which is
involved in transcellular localisation. A secreted single chain antibody
Fv fragment can be fused to cytochrome P450 reductase (P450R) derivatives
such as anchorless P450R (AA42287) or FN fragment (AA42288). This
enables the fusion protein to be delivered to other cells where it is
then transported to the nucleus. Many drugs' sites of action are in the
nucleus, rather than the cytoplasm, where P450R normally functions. P450R
or its derivatives can be used to activate prodrugs to their active form
via reduction. Administration of a prodrug is useful where the active
drug may be metabolised before it reaches its site of action or where the
active drug is cytotoxic, e.g., anticancer drugs. Targeted delivery of
such prodrug activators allows a reduction in dose of the prodrug, and
thus of systemic side-effects. P450R derivative fusion proteins, or
vectors that express them, are specifically used to treat tumours, or
inflammation, atherosclerosis and muscular dystrophy, but may also be
used to treat many other conditions, e.g., cerebral malaria, rheumatoid
arthritis, or conditions associated with hypoxia, ischaemia or
hypoglycemia, or to deliver antibiotics, antiviral agents, analgesics,
anaesthetics, anti-inflammatories, antineoplastic agents and diagnostic
agents
XX
SQ Sequence 243 AA;
Query Match 27.6%; Score 972.5; DB 2; Length 243;
Best Local Similarity 40.1%; Pred. No. 6.6e-50;
Matches 227; Conservative 3; Mismatches 13; Indels 323; Gaps 5;
QY 1 EVQLQSGDPLVKPGASVKISKASGYSFTGYIMHWVKQSPGKLEWIGRINPNNGVTLY 60
DB 1 EVQLQSGDPLVKPGASVKISKASGYSFTGYIMHWVKQSHGKSLIEWIGRINPNNGVTLY 60

QY 61 NOKEKDKATLTVDKSSSTTAYMELRSITSEDSAVYYCARSTMTINYYMDYWGQGTSTVTS 120
DB 61 NOKFKDKAILTVDKSSSTTAYMELRSITSEDSAVYYCARSTMTINYYMDYWGQGTSTVTS- 119
QY 121 AKTTPSPVYFLAPGSAQAQTNMVTLLGCLVKGYFPEPVTVTVNSGSLSSGVHTPAPVLQSD 180
DB 120 ----- 119
QY 181 LYTSSSVTVSPSTWPSPTVTCNVAHPASSTKVVDKIVPRDSGGPSEKSEINEKDLRKK 240
DB 120 -----SGG----- 122
QY 241 SELQGTALGNLQIYYYNKAITSSSEKADQFLTNTLLFKGPTGHPWYNDLLVLDLSTA 300
DB 123 ----- 122
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTBEKVPINLWDGKQ 360
DB 123 -----GGSGGGT----- 132
QY 361 TTVPIDKVKTSKKEVTYQELDLQARHYLHGKFGLYNSDSFGKVKQRLIVFHSSEGSTVS 420
DB 133 -----GG----- 134
QY 421 YDLFDAQGOYPTDLLRIYRDNTTISSTSLISLYLTTSIVMTQTPTSLLSVSGDRVIT 480
DB 135 -----SSIVMTQTPTFLLSVSGDRVIT 157
QY 481 CKASQSVSNDAVYQOKPQSPKLLISYTSRYAGVDPDRFSGSGYGTDTFTLTSSVOAED 540
DB 158 CKASQSVSNDAVYQOKPQSPKLLISYTSRYAGVDPDRFSGSGYGTDTFTLTSSVOAED 217
QY 541 AAVYFCQDYNSPPTFGGSKLEIKR 566
DB 218 LAVYFCQDYNSPPTFGGSKLEIKR 243
RESULT 69
AA427407
ID AA427407 standard; protein; 243 AA.
XX
AC AA427407;
XX
DT 23-NOV-1999 (first entry)
XX
DE 5T4 scFv antibody signal peptide.
XX
KW Prodrug; localization domain; tumor-selective antibody; cytochrome P450;
prodrug activating domain; modified hematopoietic stem cell; MHSC; tumor;
inflammation; atherosclerosis; muscular dystrophy; cerebral malaria;
rheumatoid arthritis; hypoxia; ischemia; hypoglycemia; tumor antigen;
5T4 scFv.
XX
OS Unidentified.
XX
PN WO9945126-A2.
XX
PD 10-SEP-1999.
XX
PF 05-MAR-1999; 99WO-GB000672.
PR 06-MAR-1998; 98GB-00004841.
PR 19-AUG-1998; 98GB-00018103.
PR 29-JAN-1999; 99GB-00002081.
XX
(OXFO-) OXFORD BIOMEDICA UK LTD.
PA Stratford IJ, Patterson AV, Kingman SM, Kan O, Griffiths L;
PI Mitrophanous K;
XX
DR WPI; 1999-540852/45.
DR N-PSDB; AA207810.
XX

PT New produg activating agent targeted to selected cells or tissues,
PT particularly hypoxic cells, for treating e.g. tumors or inflammation.
XX
PS
XX Example 9; Fig 3F; 149pp; English.
XX
CC The invention provides a new produg activating agent that comprises: (i)
CC a localization domain (LD; other than a tumor-selective antibody) and a
CC produg activating domain (PAD); (ii) at least one nucleic acid encoding
CC a cytochrome P450 and under control of at least one constitutive or
CC inducible expression control sequence or (iii) a modified hematopoietic
CC stem cell (MHSC) containing at least one nucleic acid encoding a PAD and
CC under control of elements as in (ii). The produg activating agent or
CC vectors that express them, are specifically used to treat tumors,
CC inflammation, atherosclerosis and muscular dystrophy, but may also be
CC used to treat many other conditions, e.g. cerebral malaria, rheumatoid
CC arthritis, or conditions associated with hypoxia, hypoglycemia or
CC ischemia, or to deliver antibiotics, antiviral agents, analgesics,
CC anesthetics, anti-inflammatories, antineoplastic agents and diagnostic
CC agents. LD optimize activity of PAD, e.g. by delivering it to selected
CC locations or by delivering it to neighboring cells (bystander effect),
CC and allow a reduction in dose of produg, and thus of systemic side-
CC effects. Nucleic acids encoding the agent may be expressed selectively in
CC hypoxic cells. The present sequence represents the single chain variable
CC antibody fragment against the tumor antigen 5T4 (5T4 scFv). 5T4 scFv is
CC used in the construction of a fusion protein comprising 5T4 scFv and a
CC human P450 reductase derivative alp450R
XX
SQ Sequence 243 AA;

Query Match 27.6%; Score 972.5; DB 2; Length 243;
Best Local Similarity 40.1%; Pred. No. 6.6e-50;
Matches 227; Conservative 3; Mismatches 13; Indels 323; Gaps 5;

QY 1 EVOLQSGDPLVKPGASVKISCKASGYFTGYMHVWKQSPGKGLWIGRINPNNVTLY 60
DB 1 EVOLQSGDPLVKPGASVKISCKASGYFTGYMHVWKQSPGKGLWIGRINPNNVTLY 60
QY 61 NQKFKDKATLVDRKSTTAYMELSLTSDSAVYICARSTMTITNYVMDYQGQTSVTSS 120
DB 61 NQKFKDKAIIIVDKSSTTAYMELSLTSDSAVYICARSTMTITNYVMDYQGQTSVTSS 119
QY 121 AKTTPSVYPLAGSAAQNTSMVTLGLVKGYFPEPVTVTWNSGSLSSGVHTPAVLQSD 180
DB 120 ----- 119
QY 181 LYTSSSVTVPSSTWPTSETVCNVAHPASSTKVDKIVPRDSDGSPSEKSEINEKDLRKK 240
DB 120 -----SGG----- 122
QY 241 SELQGTALGNLKIYYNSKAITSEKSAQDQPLTLLFKGFTGHPWYNDLLVLDGSTA 300
DB 123 ----- 122
QY 301 ATSEYEGSSVDLYGAYGYQCAGTGNKTAQMGVTLHDNNRLTEBKVPINLWIDGKQ 360
DB 123 -----GGSGGGT----- 132
QY 361 TTVPIDKVTSKKEVTQVQLDQARHVLHCKFGLYNSDSFGKVGQRLIVPHSSEGSTVS 420
DB 133 -----GG----- 134
QY 421 YDLFDAQGQVPTLLRIYRDNNTTISSTLSISLYLTYTTSIVMTQTPTSLVSAAGRVIT 480
DB 135 -----SSIVMTQTPTFLVSAAGRVIT 157
QY 481 CKASQSVNSDVAVYQKPGSPKLLISYTSRAGVDPDRFGSGGYGHDFTLTLSVQAE 540
DB 158 CKASQSVNSDVAVYQKPGSPKLLISYTSRAGVDPDRFGSGGYGHDFTLTLSVQAE 217
QY 541 AAVYFCODYNSPPTFGGKLEIKR 566
DB 218 LAVYFCODYNSPPTFGGKLEIKR 243

RESULT 70
AAB83835

ID AAB83835 standard; protein; 243 AA.

XX AAB83835;

AC AAB83835;

DT 23-JUL-2001 (first entry)

XX Amino acid sequence of a 5T4 ScFv designated 5T4ScFv.1.

XX Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
XX hypersensitivity; autoimmune disease; central nervous system disorder;
XX Parkinson's disease; periodontal disease; cardiopulmonary disease;
XX cardiovascular disease; gastrointestinal disorder; infection; diabetes;
XX Helicobacter-related disease; immune disorder.

OS Synthetic.

OS Mus sp.

XX Key Location/Qualifiers

FT Misc-difference 169

FT /note= "Ala encoded by GDT"

XX WO200136486-A2.

XX 25-MAY-2001.

XX 13-NOV-2000; 2000WO-GB004317.

XX 18-NOV-1999; 99WO-GB003859.

XX 15-FEB-2000; 2000GB-00003527.

XX 02-MAR-2000; 2000GB-00005071.

XX (OXFO-) OXFORD BIOMEDICA UK LTD.

XX Kingman A, Kingman SM, Bebbington CR, Carroll MW, Ellard FM;

XX Myers KA;

XX WPI; 2001-343805/36.

XX N-PSDB; AAF69729.

XX Use of single chain antibody capable of recognizing a disease associated

XX molecule for manufacturing a medicament for preventing and/or treating a

XX disease condition associated with disease associated molecule.

XX Claim 3; Fig 1; 118pp; English.

XX The specification describes the use of a single chain antibody (ScFv),
XX which is capable of recognizing a disease associated molecule in the
XX manufacture of a medicament for the prevention and treatment of a disease
XX condition. The ScFv antibody is useful in the manufacture of a
XX medicament, for affecting a disease in vivo, for preparing a
XX pharmaceutical composition, for in vivo imaging and/or for adjuvant
XX treatment of a disease. The ScFv antibody is also useful for treating
XX inflammatory diseases including arthritis, hypersensitivity, autoimmune
XX diseases, cancers, central nervous system disorders including Parkinson's
XX disease, periodontal diseases, cardiopulmonary diseases, cardiovascular
XX diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
XX related diseases, and other immune disorders. The present sequence the VH and
XX VL regions from murine 5T4 monoclonal antibody, joined by a linker
XX sequence

SQ Sequence 243 AA;

Query Match 27.6%; Score 972.5; DB 4; Length 243;

Best Local Similarity 40.1%; Pred. No. 6.6e-50;

Matches 227; Conservative 3; Mismatches 13; Indels 323; Gaps 5;

QY 1 EVOLQSGDPLVKPGASVKISCKASGYFTGYMHVWKQSPGKGLWIGRINPNNVTLY 60

DB 1 EVOLQSGDPLVKPGASVKISCKASGYFTGYMHVWKQSPGKGLWIGRINPNNVTLY 60

PT New vector encoding a tumour interacting protein for treating cancer -
PT contains a desired nucleotide sequence and/or protein which recognises
tumours, and is used as a gene delivery system to treat cancer.

PS Example 5; Fig 2; 82pp; English.

XX This is the amino acid sequence of B7-1.5T4.1, a fusion protein
CC comprising the extracellular domain (amino acids 1-215) of human co-
stimulatory molecule B7-1 joined via a flexible peptide linker to an scFv
CC (see AAW86002) derived from murine 5T4 monoclonal antibody. B7-1.5T4.1
CC cDNA (see AAV80292) can be inserted into vector pCI to allow expression
CC of the fusion protein in mammalian cells. The trophoblast cell surface
CC antigen defined by 5T4 is expressed at high levels on the cells of a wide
CC variety of human tumours. The invention relates to a vector comprising a
CC nucleotide sequence coding for a tumour interacting protein (TIP) and
CC optionally a nucleotide sequence of interest (NOI) which encodes a
CC protein of interest (POI), the vector being capable of delivering the NOI
CC and/or POI to the tumour recognised by the TIP. Delivery can be in vivo
CC or ex vivo. The vector is used to treat cancer, and may also be used as a
CC gene delivery system for introducing at least 1 gene encoding a TIP
CC (preferably a tumour binding protein) into a haematopoietic cell lineage.
CC B7-1 is expected to bind specifically to CD28 and CTLA-4 present on human
CC T-cells

XX Sequence 488 AA;

Query Match 27.5%; Score 967.5; DB 2; Length 488;
Best Local Similarity 40.0%; Pred. No. 3e-49;
Matches 226; Conservative 3; Mismatches 13; Indels 323; Gaps 5;

QY 1 EVLOQSGDPLVKPGASVKISKASGYFTGYNMHWKSPGKLEWIGRINPNNGVTL 60
DB 247 EVLOQSGDPLVKPGASVKISKASGYFTGYNMHWKSPGKLEWIGRINPNNGVTL 306
QY 61 NQKFKDKATLTVDKSTTAYMELRLTSDSAVYCARSTMTITNYMDYWGQTSVTSS 120
DB 307 NQKFKDKATLTVDKSTTAYMELRLTSDSAVYCARSTMTITNYMDYWGQTSVTSS - 365
QY 121 AKTTPPSVYPLAPGSAQTNSMVTGLVKGPPEPVTWTNSGSLSSGVHTFPAVLQSD 180
DB 366 ----- 365
QY 181 LYTLSSVTPSPSTWSEVTCNVHPASTKVKIVPRDGGPSEKSEINEKDLRKK 240
DB 366 ----- 368
QY 241 SELQGTALGNLKIYYNSKAITSEKSADQFLTNLLPKGFTGHPWYNDLLVDLGSTA 300
DB 369 ----- 368
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTNKTACMYGGVTLHDNNRLTBEKKVPINLWDGKQ 360
DB 369 ----- 378
QY 361 TTVPIDKVTSKKEVTVQELDLQARHYLHGKFLGYNLSDSPGKQVGRGLIVFHSSESTVS 420
DB 379 ----- 380
QY 421 YDLFDAQGYPTDLLRIYRDNNTTISLSLSISLYLTTSIVMTQTPTSLVSGDRVTIT 480
DB 381 ----- 403
QY 481 CKASQSVNDVAVYQKPGSKLLISYTSRVRAGVDFRPSGSGYGTDFTLTSSVQAE 540
DB 404 CKASQSVNDVAVYQKPGSKLLISYTSRVRAGVDFRFIGSGYGTDFTLTSSVQAE 463
QY 541 AAVYFCQDYNSPPTFGGKLEIK 565
DB 464 LAVYFCQDYNSPPTFGGKLEIK 488

RESULT 73
AAB83836

ID AAB83836 standard; protein; 488 AA.
XX AC AAB83836;
XX DT 23-JUL-2001 (first entry)

XX Amino acid sequence of a B7-1.5T4.1 fusion protein.

DE Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
XX hypersensitivity; autoimmune disease; central nervous system disorder;
KW Parkinson's disease; periodontal disease; cardiopulmonary disease;
KW cardiovascular disease; gastrointestinal disorder; infection; diabetes;
KW Helicobacter-related disease; immune disorder.

XX Synthetic.

OS Mus sp.

OS Homo sapiens.

XX WO200136486-A2.

XX 25-MAY-2001.

XX 13-NOV-2000; 2000WO-GB0004317.

XX 18-NOV-1999; 99WO-GB003859.

PR 15-FEB-2000; 2000GB-00003527.

PR 02-MAR-2000; 2000GB-00005071.

XX (OXFO-) OXFORD BIOMEDICA UK LTD.

XX Kingman A, Kingman SM, Bebbington CR, Carroll MW, Ellard FM;

PI Myers KA;

XX WPI; 2001-343805/36.

DR N-PSDB; AAF89730.

XX Use of single chain antibody capable of recognizing a disease associated
PT molecule for manufacturing a medicament for preventing and/or treating a
PT disease condition associated with disease associated molecule.

XX Claim 3; Fig 2; 118pp; English.

XX The specification describes the use of a single chain antibody (ScFv),
CC which is capable of recognizing a disease associated molecule in the
CC manufacture of a medicament for the prevention and treatment of a disease
CC condition. The ScFv antibody is useful in the manufacture of a
CC medicament for affecting a disease in vivo, for preparing a
CC pharmaceutical composition, for in vivo imaging and/or for adjuvant
CC treatment of a disease. The ScFv antibody is also useful for treating
CC inflammatory diseases including arthritis, hypersensitivity, autoimmune
CC diseases, cancers, central nervous system disorders including Parkinson's
CC disease, periodontal diseases, cardiopulmonary diseases, cardiovascular
CC diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
CC related diseases, and other immune disorders. The present sequence
CC represents a B7-1.5T4.1 fusion protein. This comprises the N-terminus of
CC the 5T4 ScFv is fused after amino acid 215 of human B7-1

XX Sequence 488 AA;

Query Match 27.5%; Score 967.5; DB 4; Length 488;
Best Local Similarity 40.0%; Pred. No. 3e-49;
Matches 226; Conservative 3; Mismatches 13; Indels 323; Gaps 5;

QY 1 EVLOQSGDPLVKPGASVKISKASGYFTGYNMHWKSPGKLEWIGRINPNNGVTL 60
DB 247 EVLOQSGDPLVKPGASVKISKASGYFTGYNMHWKSPGKLEWIGRINPNNGVTL 306
QY 61 NQKFKDKATLTVDKSTTAYMELRLTSDSAVYCARSTMTITNYMDYWGQTSVTSS 120
DB 307 NQKFKDKATLTVDKSTTAYMELRLTSDSAVYCARSTMTITNYMDYWGQTSVTSS - 365
QY 121 AKTTPPSVYPLAPGSAQTNSMVTGLVKGPPEPVTWTNSGSLSSGVHTFPAVLQSD 180

Db 366 ----- 365
QY 181 LYTSSSVTPSPSTWPTSETVTCNVAHPASSTKVDDKIVPRDGGPSEKSEINEKDLRKK 240
Db 366 ----- 368
QY 241 SELQGTALGNLKQIYYYNKAITSSSEKADQFLTNTLLFKGFTGHPWYNDLLVDLGSTA 300
Db 369 ----- 368
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTBEKKVPINLWIDGKQ 360
Db 369 ----- 378
QY 361 TTVPIDKVKTSKEVTVQBLDQARHLHGKFGLYNSDSFGKVGKQRLIVFHSSEGSTVS 420
Db 379 ----- 380
QY 421 YDLFDAQQGYPDTLRLRIYRDNTTISSTLSISLYLTTSIVMTQTPTSLLSAGDRVTIT 480
Db 381 ----- 403
QY 481 CKASQSVNDVAVYQKPGQSPKLLISYTSRRYAGVDPDRFSGSGYGTDFTLTSSVQAD 540
Db 404 CKASQSVNDVAVYQKPGQSPKLLISYTSRRYAGVDPDRFSGSGYGTDFTLTSSVQAD 463
QY 541 AAVYFCQDYNSPPTFGGKTLEIK 565
Db 464 LAVYFCQDYNSPPTFGGKTLEIK 488

RESULT 74
ABU07262
ID ABU07262 standard; protein; 488 AA.
XX AC ABU07262;
XX DT 29-JAN-2003 (first entry)
XX DE Human expressed protein tag (EPT) #1963.
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX (ZYCO-) ZYCOS INC.
XX PI Chicx RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.

PS XX Example 2; SEQ ID NO 1963; 134pp; English.
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 488 AA;
Query Match 27.5%; Score 967.5; DB 6; Length 488;
Best Local Similarity 40.0%; Pred. No. 3e-49;
Matches 226; Conservative 3; Mismatches 13; Indels 323; Gaps 5;
QY 1 EVQLQSGPDLVKPGASVKISCKASGYSTGYMHVWVKQSPCKGLEWIGRINPNNGVTILY 60
Db 247 EVQLQSGPDLVKPGASVKISCKASGYSTGYMHVWVKQSHGKSLIEWIGRINPNNGVTILY 306
QY 61 NOKFKDKATLTVDKSTTAYMELRLTSDSDSAVYVCARSTMTITNYVMDYWGQTSVTVS 120
Db 307 NOKFKDKAILTVDKSTTAYMELRLTSDSDSAVYVCARSTMTITNYVMDYWGQTSVTVS- 365
QY 121 AKTTPPSVYPLAPGSAAGTNSMTVLGCLVKGYFPEPTVTWNSGSLSSGVHTFPAVLQSD 180
Db 366 ----- 365
QY 181 LYTSSSVTPSPSTWPTSETVTCNVAHPASSTKVDDKIVPRDGGPSEKSEINEKDLRKK 240
Db 366 ----- 368
QY 241 SELQGTALGNLKQIYYYNKAITSSSEKADQFLTNTLLFKGFTGHPWYNDLLVDLGSTA 300
Db 369 ----- 368
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTBEKKVPINLWIDGKQ 360
Db 369 ----- 378
QY 361 TTVPIDKVKTSKEVTVQBLDQARHLHGKFGLYNSDSFGKVGKQRLIVFHSSEGSTVS 420
Db 379 ----- 380
QY 421 YDLFDAQQGYPDTLRLRIYRDNTTISSTLSISLYLTTSIVMTQTPTSLLSAGDRVTIT 480
Db 381 ----- 403
QY 481 CKASQSVNDVAVYQKPGQSPKLLISYTSRRYAGVDPDRFSGSGYGTDFTLTSSVQAD 540
Db 404 CKASQSVNDVAVYQKPGQSPKLLISYTSRRYAGVDPDRFSGSGYGTDFTLTSSVQAD 463
QY 541 AAVYFCQDYNSPPTFGGKTLEIK 565
Db 464 LAVYFCQDYNSPPTFGGKTLEIK 488
RESULT 75
ABU07253
ID ABU07253 standard; protein; 488 AA.
XX AC ABU07253;
XX XX

DT 29-JAN-2003 (first entry)
XX Human expressed protein tag (EPT) #1954.
DE
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX Homo sapiens.
XX WO200278524-A2.
PN 10-OCT-2002.
XX 28-MAR-2002; 2002WO-US009671.
XX 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX (ZYCO-) ZYCOS INC.
XX Chicx RM, Tomlinson AJ, Urban RG;
PI WPI; 2003-040607/03.
DR
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX Example 2; SEQ ID NO 1954; 134pp; English.

Search completed: February 15, 2006, 20:13:13
Job time : 225.229 secs

Query Match 27.5%; Score 967.5; DB 6; Length 488;
Best Local Similarity 40.0%; Pred. No. 3e-49;
Matches 226; Conservative 3; Mismatches 13; Indels 323; Gaps 5;

QY 1 EVLOQSGDPLVKGASVKISCKASGYFTGYMHWVKQSPGKLEWIGRINPNNGVTL 60
DB 247 EVLOQSGDPLVKGASVKISCKASGYFTGYMHWVKQSPGKLEWIGRINPNNGVTL 306
QY 61 NQKFKDKAILTVDKSSTAYMELRLSTSDSAVYCARSTMTNYNDYMGQTSVTSS 120
DB 307 NQKFKDKAILTVDKSSTAYMELRLSTSDSAVYCARSTMTNYNDYMGQTSVTSS- 365
QY 121 AKTPSPSVPLAPGSAQAQNSMTLGLCKLVKGYFPEPTVTWNSGSLSSGVHTFPVLQSD 180
DB 366 ----- 365

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103	472.5	13.4	120	2	S25175	Ig heavy chain V r	176	442.5	12.6	123	2	G48677	Ig heavy chain V-D
104	472	13.4	106	1	X1RTA	Ig kappa chain C r	177	442	12.5	111	2	S25024	Ig heavy chain V r
105	471	13.4	120	2	B22769	Ig heavy chain V r	178	442	12.5	111	2	S25032	Ig heavy chain V r
106	469	13.3	107	2	S26320	Ig heavy chain V r	179	442	12.5	112	2	A30502	Ig heavy chain V-D
107	468.5	13.3	123	2	S20646	Ig heavy chain V r	180	441.5	12.5	117	2	S01822	Ig heavy chain V r
108	468	13.3	117	2	PL0234	Ig heavy chain V r	181	441	12.5	111	2	S25033	Ig heavy chain V r
109	468	13.3	120	2	E45722	anti-glycoprotein	182	441	12.5	111	2	S25047	Ig heavy chain V r
110	468	13.3	144	2	B30502	Ig heavy chain V r	183	440.5	12.5	136	2	PL0208	Ig heavy chain pre
111	467.5	13.3	121	2	H37266	Ig heavy chain V r	184	440.5	12.5	140	2	PH1484	Ig heavy chain V r
112	467	13.3	335	1	G2MSAB	Ig gamma-2a chain	185	440	12.5	120	2	S09956	Ig heavy chain V-D
113	466	13.2	120	2	F45722	anti-glycoprotein	186	439.5	12.5	135	2	PH1493	Ig heavy chain V-D
114	465	13.2	118	2	S38717	Ig heavy chain V r	187	439.5	12.5	136	2	B47159	Ig heavy chain V r
115	465	13.2	233	2	S29577	Ig light chain - r	188	439.5	12.5	140	2	PH1488	Ig heavy chain V r
116	464.5	13.2	121	2	F37266	Ig heavy chain V r	189	439.5	12.5	231	2	S25738	Ig heavy chain V r
117	464.5	13.2	592	2	S25705	Ig mu chain - shee	190	439.5	12.5	235	2	S25750	Ig lambda chain -
118	464	13.2	136	2	JL0077	Ig heavy chain pre	191	439	12.5	111	2	S25045	Ig heavy chain V r
119	464	13.2	572	2	B46529	Ig Y heavy chain (192	439	12.5	123	2	S60067	Ig heavy chain V r
120	463.5	13.2	140	2	PH1482	Ig heavy chain V r	193	438.5	12.5	121	2	A30551	Ig heavy chain V r
121	463	13.1	509	2	S17597	Ig delta chain (WI	194	438.5	12.5	233	2	S25752	Ig lambda chain -
122	462	13.1	113	2	S55535	Ig heavy chain V r	195	438	12.4	115	2	B25924	Ig kappa chain pre
123	461.5	13.1	121	2	A26405	Ig heavy chain V r	196	437.5	12.4	119	2	PH1521	Ig heavy chain V r
124	461.5	13.1	123	2	F48677	Ig heavy chain V-D	197	437.5	12.4	138	1	HVMS17	Ig heavy chain pre
125	461	13.1	113	2	S55534	Ig heavy chain V r	198	437.5	12.4	216	2	S29258	Ig lambda chain V
126	461	13.1	171	2	S23623	Ig heavy chain V r	199	437.5	12.4	329	2	S00847	Ig gamma-2c chain
127	460.5	13.1	138	2	PH0105	anti-digoxin trans	200	437	12.4	109	2	S25038	Ig heavy chain V r
128	460	13.1	127	2	S04577	Ig kappa chain pre	201	437	12.4	111	2	S25034	Ig heavy chain V r
129	459.5	13.0	117	2	S03305	Ig heavy chain V r	202	437	12.4	118	2	S36265	Ig heavy chain V r
130	459.5	13.0	122	2	S20643	Ig heavy chain V r	203	437	12.4	249	2	S69340	Ig heavy chain VHI
131	459.5	13.0	138	2	S21810	Ig heavy chain V r	204	436.5	12.4	140	2	S26318	Ig heavy chain V r
132	459	13.0	119	2	A24672	Ig heavy chain pre	205	436.5	12.4	140	2	S04575	Ig heavy chain pre
133	458.5	13.0	111	2	PH0990	Ig heavy chain V r	206	436.5	12.4	233	2	S25747	Ig lambda chain -
134	458.5	13.0	138	2	S35513	Ig heavy chain pre	207	436	12.4	107	2	D53285	Ig kappa chain V a
135	458	13.0	115	2	A54378	Ig heavy chain V r	208	436	12.4	110	2	PH0995	Ig heavy chain V r
136	458	13.0	117	2	S25176	Ig heavy chain V r	209	436	12.4	120	2	F28195	Ig heavy chain V r
137	458	13.0	122	2	S24287	Ig heavy chain V r	210	436	12.4	213	2	S21066	Ig lambda chain V
138	457.5	13.0	123	2	E48677	Ig heavy chain V-D	211	435.5	12.4	121	2	PL0281	Ig heavy chain V r
139	457	13.0	106	1	K1RTB	Ig kappa chain C r	212	434	12.3	116	2	S26309	Ig heavy chain V r
140	455	12.9	110	2	PH1000	Ig heavy chain V r	213	434	12.3	217	2	JE0246	Ig lambda chain NI
141	454.5	12.9	118	2	S38565	Ig heavy chain V r	214	433.5	12.3	119	2	PH1520	Ig heavy chain V r
142	454.5	12.9	118	2	PL0200	anti-DNA autoantib	215	433.5	12.3	120	2	S03471	Ig heavy chain V-D
143	454.5	12.9	119	2	S03077	Ig heavy chain V r	216	433	12.3	102	2	S42176	Ig gamma chain V r
144	454.5	12.9	138	2	S45249	Ig heavy chain pre	217	433	12.3	111	2	S25051	Ig heavy chain V r
145	454	12.9	113	2	S25041	Ig heavy chain V r	218	433	12.3	113	2	S55533	Ig heavy chain V r
146	454	12.9	137	1	G2MS43	Ig heavy chain pre	219	433	12.3	115	2	PL0238	Ig heavy chain V r
147	453.5	12.9	113	2	PH0974	Ig heavy chain V r	220	433	12.3	120	1	MHMS15	Ig heavy chain V r
148	453.5	12.9	140	2	PH1489	Ig heavy chain V r	221	432.5	12.3	118	2	PL0231	Ig heavy chain V r
149	453	12.9	116	2	S53751	antibody Fab Jel 1	222	432.5	12.3	118	2	A24754	Ig heavy chain V r
150	452.5	12.8	119	2	S20640	Ig heavy chain V r	223	432.5	12.3	135	2	PH1492	Ig lambda chain -
151	452	12.8	111	2	S25048	Ig heavy chain V r	224	432.5	12.3	231	2	S25753	Ig heavy chain V r
152	452	12.8	235	2	S20000	Ig light chain pre	225	432	12.3	113	2	S55528	Ig heavy chain V r
153	450.5	12.8	140	1	HVMSG7	Ig heavy chain pre	226	431.5	12.3	111	2	PH0994	Ig heavy chain V r
154	450	12.8	115	2	C27563	Ig heavy chain V r	227	431.5	12.3	114	2	S20707	Ig heavy chain V r
155	450	12.8	118	2	S37201	Ig heavy chain V r	228	431.5	12.3	119	2	PH1502	Ig heavy chain V r
156	450	12.8	232	2	S25756	Ig heavy chain V r	229	431	12.2	111	2	S25054	Ig heavy chain V r
157	449.5	12.8	233	2	S25744	Ig lambda chain -	230	431	12.2	111	2	S25031	Ig heavy chain V r
158	448.5	12.7	111	2	PH0992	Ig heavy chain V r	231	431	12.2	145	2	PL0014	Ig kappa chain pre
159	447	12.7	108	2	PH0975	Ig heavy chain V r	232	430.5	12.2	140	2	PH1483	Ig heavy chain V r
160	447	12.7	113	2	S25044	Ig heavy chain V r	233	430	12.2	113	2	S55532	Ig heavy chain V r
161	446	12.7	118	2	C30560	Ig heavy chain V r	234	429.5	12.2	140	2	PH1486	Ig heavy chain V r
162	446	12.7	120	2	G28195	Ig heavy chain V r	235	429.5	12.2	140	2	PH1498	Ig heavy chain V r
163	446	12.7	333	2	PS0018	Ig gamma-2b chain	236	429.5	12.2	231	2	S25751	Ig lambda chain -
164	445.5	12.6	105	2	PH0978	Ig heavy chain V r	237	429	12.2	111	2	S25030	Ig heavy chain V r
165	445.5	12.6	121	2	A21854	Ig heavy chain V r	238	429	12.2	113	2	S55531	Ig heavy chain pre
166	445.5	12.6	131	2	A24742	Ig heavy chain pre	239	429	12.2	135	2	A30577	Ig heavy chain V r
167	445	12.6	111	2	S25052	Ig heavy chain V r	240	428.5	12.2	110	2	S26317	Ig lambda chain (B
168	444.5	12.6	109	2	PH0973	Ig heavy chain V r	241	428.5	12.2	216	2	A42193	Ig heavy chain V r
169	444.5	12.6	111	2	PH0993	Ig heavy chain V r	242	428	12.2	97	2	PH1137	Ig heavy chain V r
170	444.5	12.6	117	2	JC3269	PL7-6 antibody hea	243	427.5	12.1	114	2	A27563	Ig heavy chain V r
171	444.5	12.6	228	2	S25575	Ig light chain - r	244	427.5	12.1	119	2	PH1504	Ig heavy chain V r
172	444	12.6	111	2	S25055	Ig heavy chain V r	245	427.5	12.1	119	2	PH1512	Ig heavy chain V r
173	444	12.6	1005	2	T18537	Ig heavy chain - c	246	427.5	12.1	235	2	S05270	Ig lambda chain pr
174	443	12.6	107	2	S09964	Ig kappa chain V-J	247	427	12.1	111	2	S25040	Ig heavy chain V r
175	443	12.6	108	2	PH0977	Ig heavy chain V r	248	427	12.1	118	2	PL0084	Ig heavy chain V r

249	426.5	12.1	124	2	S06824	Ig heavy chain V r
250	426	12.1	98	2	PH1149	Ig heavy chain V r
251	426	12.1	109	2	PH0989	Ig heavy chain V r
252	426	12.1	109	2	PH1094	Ig heavy chain V r
253	426	12.1	113	2	S55530	Ig heavy chain V r
254	426	12.1	117	2	S55541	Ig heavy chain V r
255	426	12.1	144	2	FL0106	Ig heavy chain pre
256	426	12.1	235	2	S25754	Ig lambda chain -
257	425.5	12.1	106	2	S26315	Ig heavy chain V r
258	425.5	12.1	119	2	S45714	Ig heavy chain V r
259	425.5	12.1	577	2	S50731	Ig heavy chain - n
260	425	12.1	98	2	PH1138	Ig heavy chain V r
261	425	12.1	98	2	PH1106	Ig heavy chain V r
262	425	12.1	106	2	PH1005	Ig heavy chain V r
263	425	12.1	117	1	HVMS61	Ig heavy chain pre
264	425	12.1	233	2	S25741	Ig lambda chain -
265	424.5	12.1	119	2	PH1518	Ig heavy chain V r
266	424.5	12.1	119	2	PH1500	Ig heavy chain V r
267	424.5	12.1	234	2	S25757	Ig lambda chain -
268	424	12.0	106	2	S25036	Ig heavy chain V r
269	424	12.0	120	2	A54256	Ig heavy chain V r
270	424	12.0	140	2	S09216	Ig heavy chain pre
271	423.5	12.0	109	2	PH1001	Ig heavy chain V r
272	423.5	12.0	111	2	PH0998	Ig heavy chain V r
273	423.5	12.0	117	2	S03960	Ig heavy chain V-D
274	423.5	12.0	117	2	G45722	anti-glycoprotein
275	423.5	12.0	232	2	S25742	Ig lambda chain -
276	423	12.0	98	2	PH1154	Ig heavy chain V r
277	423	12.0	98	2	PH1156	Ig heavy chain V r
278	423	12.0	98	2	I28833	Ig kappa chain V r
279	423	12.0	112	2	S26473	Ig heavy chain V r
280	423	12.0	149	1	KVMS11	Ig kappa chain pre
281	422.5	12.0	114	2	PH1522	Ig heavy chain V r
282	422.5	12.0	117	2	S03961	Ig heavy chain V-D
283	422.5	12.0	119	2	FL0089	Ig heavy chain V r
284	422.5	12.0	129	2	S46393	Ig heavy chain V r
285	422	12.0	98	2	PH1119	Ig heavy chain V r
286	422	12.0	109	2	PH1096	Ig heavy chain V r
287	422	12.0	114	2	FL0247	Ig heavy chain V r
288	422	12.0	117	1	HVMS8A	Ig heavy chain pre
289	421	12.0	98	2	PH1118	Ig heavy chain V r
290	421	12.0	98	2	PH1105	Ig heavy chain V r
291	420.5	11.9	136	1	HVMSB1	Ig heavy chain pre
292	420.5	11.9	142	2	A32483	Ig heavy chain V r
293	420.5	11.9	258	2	H89968	enterotoxin SeN [i
294	420	11.9	98	2	PH1134	Ig heavy chain V r
295	420	11.9	98	2	PH1151	Ig heavy chain V r
296	420	11.9	135	2	S49530	anti-Sm antibody V
297	419.5	11.9	112	2	FL0232	Ig heavy chain V r
298	419.5	11.9	115	2	A56700	Ig heavy chain (an
299	419.5	11.9	235	2	S25749	Ig lambda chain -
300	419	11.9	98	2	PH1126	Ig heavy chain V r

ALIGNMENTS

RESULT 1
A28179
enterotoxin E precursor - Staphylococcus aureus
C/Species: Staphylococcus aureus
C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C/Accession: A28179
R/Couch, J.L.; Soltis, M.T.; Betley, M.J.
J. Bacteriol. 170, 2954-2960, 1988
A/Title: Cloning and nucleotide sequence of the type E staphylococcal enterotoxin gene.
A/Reference number: A28179; PMID:88257005; PMID:3384800
A/Accession: A28179
A/Molecule type: DNA
A/Residues: 1-257 <COL>
A/Cross-references: UNIPROT:P12993; UNIPARC:UPI000012A275; GB:M21319; NID:gl53001; PDB:
C/Superfamily: enterotoxin B

	Query Match	31.4%;	Score 1107;	DB 2;	Length 257;
	Best Local Similarity	89.7%;	Pred. No. 7.9e-51;		
	Matches 209;	Conservative 9;	Mismatches 15;	Indels 0;	Gaps 0
Qy	226	SEKSEEEINEXDLRKKSELQGTALGNLQIYYYNKSKAITSSSEKSDAQLTNTLLFKGFFTG	285		
Db	25	SEKSEEEINEXDLRKKSELQNALSNLQIYYYNKSKAITENKESDDOFLNTLLFKGFFTG	84		
Qy	286	HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTVLTHDNNRLT	345		
Db	85	HPWYNDLLVDLGSKDANTKYGGKVDLYGAYGYQCAGGTENKTACMYGGVTVLTHDNNRLT	144		
Qy	346	EEKVPIPNLWIDGKQTTVPIDKVKTSKEVTVQBELDQARHYLHGKFGCLYNSDSFGGKVQ	405		
Db	145	EEKVPIPNLWIDGKQTTVPIDKVKTSKEVTVQBELDQARHYLHGKFGCLYNSDSFGGKVQ	204		
Qy	406	RLIVFHSSSGSTVSYDLFDAQGYPTPLRLIYRDNTTISSTISLSISLYLTTT	458		
Db	205	RLIVFHSSSGSTVSYDLFDAQGYPTPLRLIYRDNKTINSENLHIDLYLTT	257		

RESULT 2

S37484
Ig kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C;Accession: S37484
R;Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A;Reference number: S37483
A;Accession: S37484
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-235 <DUC>
A;Cross-references: UNIPARC:UPI0000116118; EMBL:X70424; NID:g406254; PIDN:C
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin

	Query Match	29.48;	Score 1036.5;	DB 2;	Length 225;
	Best Local Similarity	93.94;	Pred. No. 3.le-47;		
	Matches 200;	Conservative 4;	Mismatches 8;	Indels 1;	Gaps 1
Qy	459	SIVMTQPTGILLVSAGDRVITTCASOSVNDVAWYQQKPGQSPKLLISYSSRRTAGVPD	518		
Db	13	SIVMTQPKELLLSAGDRVITTCASOSVNDVAWYQQKPGQSPKLLIYYASSRTGTGVPD	72		
Qy	519	RFGSGYGTDFTLTISVQAEDAAVFCCQDYNPPTFGGGTKLEIKRAADAAPTYSIPPP	578		
Db	73	RFTGSYGTDFTFTISTVQAEDLAVIFCQDYSS-YTFGGGTKLEIKRAADAAPTYSIPFP	131		
Qy	579	SSEQLTSGGASVVCFLNFPKDINVKWKIDGSRQRGVLSNWTDDQSKDSTYSMSSTLT	638		
Db	132	SSEQLTSGGASVVCFLNFPKDINVKWKIDGSRQRGVLSNWTDDQSKDSTYSMSSTLT	191		
Qy	639	LTKDEYERHNSYTCEATHKTSTSPIVKSFNRRNE	671		
Db	192	LTKDEYERHNSYTCEATHKTSTSPIVKSFNRRNE	224		

RESULT 3

S40295
Ig gamma-2a chain (mAb735) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C;Accession: S40295
R;Kiebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Froesch, M.; Weisgerber, F.
submitted to the EMBL Data Library, January 1993
A;Description: Primary structure of the murine monoclonal IgG2a antibody mAb735
A;Reference number: S40295
A;Accession: S40295
A;Molecule type: protein
A;Residues: 1-446 <KLE>
A;Cross-references: UNIPROT:099125; UNIPARC:UPI0000176F38

Db 200 LYTSSSVTVTSWPSQSTICNVNHPASSTKVDKIEPR---GPTIKPCP----- 247

QY 241 SELQGTALGNLKOIYYNSKAITSSSEKADQFLTNLLFKGFTGHPWYNLDLVLGSTA 300

Db 248 ----- 247

QY 301 ATSEYEGSSVDLYGAYGYQCAGTGNKTCMVGTVLHNNRLTEBKKVPINLWIDGKQ 360

Db 248 -----PCKCPAPN-----LLGGPSVF----- 263

QY 361 TTVPIDKVKTSKKEVTVQELDLQARHVLHGKFGLYNSDSFGGKVORGLIIVFHSSEGSTVS 420

Db 264 -----IPPKIKOVLMI-----SLSPVIT 282

QY 421 YDLFDAQQGYPDTLRLRIYRDNTTISSTLSISLYLTTISVMQTPTSTLLVASGDRVTIT 480

Db 283 CVVDVSEDDPD-----VQISFWFVNNVEHTAQTI----- 313

QY 481 CKASQSVSNDAVWYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDTFLTITSSVOAED 540

Db 314 -----HREDYNSTLRV----- 325

QY 541 AAVYFCQDYNSPPTFGGKLEIKRAD-----AAPTVISIFPPSSEQLT 584

Db 326 SALPIOHQDMSKEF-----KCVNNKDLPAPIERTISKPGSVRAPQVTVLPPPEEMT 381

QY 585 SGGASVVCFLNNFPKIDNVKIDGSEKQ-----GVLSNMTDQDSKDSYMSSTLTL 639

Db 382 KKQVTLTCMTDMPEDIVYEWNTNGKTELNYKTEPVLDS-----DGSYFWYKLRV 434

QY 640 TKDEYERHNSYTCETHK-TSTSPIVKSFNR 669

Db 435 EKKNWVERNSYSCSVVHEGLNHHHTTKFSR 465

RESULT 6

A28664

enterotoxin A precursor - Staphylococcus aureus

C;Species: Staphylococcus aureus

C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004

C;Accession: A28664; A29566

R;Betley, M.J.; Mekalanos, J.J.

J. Bacteriol. 170, 34-41, 1988

A;Title: Nucleotide sequence of the type A staphylococcal enterotoxin gene.

A;Reference number: A28664; MUID:88086892; PMID:3335483

A;Accession: A28664

A;Molecule type: DNA

A;Residues: 1-257 <BET>

A;Cross-references: UNIPROT:P13163; UNIPARC:UPI000012A273; GB:M18970; NID:g153120; PIDN:

A;Experimental source: strain FRI337

R;Huang, I.Y.; Hughes, J.L.; Bergdoll, M.S.; Schantz, E.J.

J. Biol. Chem. 262, 7006-7013, 1987

A;Title: Complete amino acid sequence of staphylococcal enterotoxin A.

A;Reference number: A29566; MUID:87222293; PMID:3584106

A;Accession: A29566

A;Molecule type: protein

A;Residues: 25-241,'S',243-257 <HUA>

A;Cross-references: UNIPARC:UPI00001766F5

C;Genetics:

A;Gene: entA

A;Map position: 6

C;Superfamily: enterotoxin B

Query Match 26.9%; Score 948; DB 2; Length 257;

Best Local Similarity 76.4%; Pred. No. 1.5e-42;

Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSSSEKADQFLTNLLFKGFTG 285

Db 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESHQFLQHTILFKGFTD 84

QY 286 HPWYNLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGTGNKTCMVGTVLHNNRLT 345

Db 85 HSWYNLLVDFPSKOTIVDKYKGGKVDLYGAYGYQCAGTGNKTCMVGTVLHNNRLT 144

QY 346 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHVLHGKFGLYNSDSFGGKVQ 405

Db 145 EEKKVPINLWIDGKQNTVPLETVKTKNKNVTYQELDLQARRYLOEKYNLYNSDVFQKVQ 204

QY 406 RGLIVFHSSEGSTVSVDLFDAGQYDPDTLLRIYRDNTTISSTLSISLYLTT 458

Db 205 RGLIVFTSTEPSVNYDLFCAQGYQSYNTLLRIYRDNTKNTINSENMHIDILYTS 257

RESULT 7

S38864

Ig epsilon chain C region - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-May-2001

C;Accession: S38864

R;Kipp, B.; Becker, W.; Schlaak, M.

submitted to the EMBL Data Library, November 1993

A;Description: Combination of a defined specificity and desired isotype by cloning of an

A;Reference number: S38864

A;Accession: S38864

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-548 <KIP>

A;Cross-references: UNIPARC:UPI00001165CC; EMBL:Z27397; NID:g416537; PIDN:CAA81788.1; PI:

C;Superfamily: immunoglobulin C region; immunoglobulin homology

F;353-421/Domain: immunoglobulin homology <IMM>

Query Match 26.4%; Score 931; DB 2; Length 548;

Best Local Similarity 35.0%; Pred. No. 2.9e-41;

Matches 241; Conservative 83; Mismatches 186; Indels 178; Gaps 19;

QY 1 EVOLQOQSGDPLVKPGASVKISKASGYFTGYVMHWKQSPGKLEWIGRINPNNGVTLY 60

Db 1 QVKLSEGGDLVKPGSLKSLCAASGLTFSSYGMKSWRQIPDKLEWVATISSGGITYTY 60

QY 61 NQKFKDKATLVDSKSTTAYMELRSLTSEDSAVYCARSTMTITNYVMDYQGQTSVTSS 120

Db 61 PDSVKGRFTISRDNAKNTLYLQMSLSKSEDTAMYYCARQGVSTMIRFAYMGQGLTVTSA 120

QY 121 AKTTPSVVPLARGSAAQNTSMVTGLCKLVKGYFPEPVTWNSGSLSSGVHTTFAVLQSD 180

Db 121 GKTTPSVVPLAPGSAQNTSMVTGLCKLVKGYFPEPVTWNSGSLSSGVHTTFAVLQSD 180

QY 181 LYTSSSVTPSPSTWPSSETVTCNVNHPASSTKVDKIVPRDSG-----GPSEKSEET--- 232

Db 181 LYTSSSVTPSPSTWPSSETVTCNVNHPASSTKVDKIVPRDCGCKPCIVPEVSSVFIFPP 240

QY 233 NEKDLRKSELO-----GTALGNLKOIYYNSKAITSSSEKADQFLTNLLFKGFTG 286

Db 241 KPKDVLTRSTIQLCYFIYGHILNDVSVSWLMDREITDT-----LAQTVLIK----- 287

QY 287 PWYNLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGTGNKTCMVGTVLHNNRLTE 346

Db 288 -----EEKLASTCSKLNITEQQMMSESTFTCK-----VTSQGVLYLAH 326

QY 347 EKKVPINLWIDGKQTTV-----PIDKVKTSKKEVTVQELDLQARHVLHGKFGLYNSD 398

Db 327 TRCP-----DHEPRGVITYLPPSPDLIYQNGAPKLTCLVVDLESEKVN----- 372

QY 399 SFGKVQVRLIIVFHSSEGSTVSVDLFDAGQYDPDTLLRIYRDNTTISSTLSISLYLTT 458

Db 373 -----VTWNQEKTSVS-----ASQWYTK-----HNNNATTSITSI----- 403

QY 459 SIWMTQTPSLIIVSAGDRVTITCKASQSVSNDAVWYQKPGQSPKLLISYTSRYAGVDP 518

Db 404 -----LPVAKD-----WIE----- 413

QY 519 RFGSGYGTDTFLTITSSVOAEDAAVYFCQDYNSS--PPTFGGQTKLEIKRADAPTVSIF 576

Db 414 -----GYG-----YQCIVDHPDFPKPIVRSITKTPGQR--SAPEYVVF 449

QY 577 PPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQGVLSNSWTDQSDKST--YSMS 634
Db 450 PPEEBE-SDKRTLTLCLIONFFPEDISVQWLGKGLINSQHSSTTTPPLKSNSGNRRGFFIP 508
QY 635 STLTTLTKDEYERHNSYTCBATHKTSTSP 662
Db 509 SRLVAKTLWTQRKQFTCCVIHEALQKP 536

RESULT 8
S38950
Ig gamma chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C:Accession: S38950
R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Biol. Chem. Hoppe-Seyler 374, 993-1000, 1993
A:Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha
A:Reference number: S38950; MUID:94128242; PMID:8297501
A:Accession: S38950
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-246 <KLE>
A:Cross-references: UNIPARC:UPI0000176F3B
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:137-201/Domain: immunoglobulin homology <IMM>

Query Match 26.4%; Score 929; DB 2; Length 246;
Best Local Similarity 78.5%; Pred. No. 1.3e-41;
Matches 179; Conservative 18; Mismatches 25; Indels 6; Gaps 2;

QY 1 EVQLQSGDPLVKPGASVKISKASGYSTGYMHVWKQSPGKLEWIGRIINPNNGVTLY 60
Db 1 QIQLQSGPELVRPGASVKISKASGYTFTDYIHWVKQRPGEGLEWIGWIYPGSGNTKY 60

QY 61 NQKFKDKATLTVDKSTTAYMELRSITSDSAVYVCARSTMTNVMYMGOGTSVTGS 120
Db 61 NEKFKGKATLTVDTSSTAYMQLSSTSDSAVFCARG---GKFANDYMGOGTSVTGS 117

QY 121 AKTTPSPVPLAPGSAQNSMVTGLCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSD 180
Db 118 AKTAPSVPLAPVCGDTTGSSTGLCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSD 177

QY 181 LYTLSSTVTPSSTWSETVTCNVAHPASSTKVDKIIVRDSGGPSEK 228
Db 178 LYTLSSTVTPSSTWSPSQSITCNVAHPASSTKVDKKIEPR---GPTIK 222

RESULT 9
S68212
Ig kappa chain (Mab03-1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jan-2000
C:Accession: S68212
R:Takegi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T. FEBS Lett. 375, 273-276, 1995
A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A:Reference number: S68211; MUID:96085223; PMID:7498516
A:Accession: S68212
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-214 <TAK>
A:Cross-references: UNIPARC:UPI000017697E; EMBL:D29668
C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 26.3%; Score 926; DB 2; Length 214;
Best Local Similarity 83.1%; Pred. No. 1.6e-41;
Matches 177; Conservative 16; Mismatches 14; Indels 6; Gaps 1;

QY 460 IVMTQTPTSLVNSAGDRVITTCASQSVNSD-----VAMVQKQPGSPKLLISYTSRY 513
Db 2 IVMTQSPSSLAMSVGQKVMTMSCKSSQSLNSRNQKYLAWYQKPGSPKLLVYFPASTR 61

QY 514 AGVPRFSGSGYGTDFTLTISSVQAEADAAVYFCQDYNSPPTFGGTKLEIKRADAAPTV 573
Db 62 SGVPRFISGSGGTDFTLTISTVQAEADLADYFCQHQHSTPYTFGGTKLEIKRADAAPTV 121

QY 574 SIFPPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQGVLSNSWTDQSDKSTYSM 633
Db 122 SIFPPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQGVLSNSWTDQSDKSTYSM 181

QY 634 SSTLTTLTKDEYERHNSYTCBATHKTSTSPIVKS 666
Db 182 SSTLTTLTKDEYERHNSYTCBATHKTSTSPIVKS 214

RESULT 10
C89984
enterotoxin p [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: C89984
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogucima, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: C89984
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-260 <KUR>
A:Cross-references: UNIPROT:Q99SU3; UNIPARC:UPI00000C7F8A; GB:BA000018; PID:g13701743; P:J
A:Experimental source: strain N315
C:Genetics:
A:Gene: sep
C:Superfamily: enterotoxin B

Query Match 26.1%; Score 918; DB 2; Length 260;
Best Local Similarity 73.0%; Pred. No. 5.4e-41;
Matches 170; Conservative 21; Mismatches 42; Indels 0; Gaps 0;

QY 226 SKSSEINEKDLURKKSSELQGTALGNLQIYYNYSKAITSSSEKSAOQFLTNLLFKGFFTG 285
Db 28 SKSSEINGKDLQKKSELQGTALSNLRQTYHNGSAIIENKESNDQFLKNTILFNDFFTG 87

QY 286 HPWYNDLLVDLGLSTAATSEYEGSSVDLYGAVYGYOCAGGTGNKTACMYGSLVTHDNNRLT 345
Db 88 HQWYNDLLVDLGSKDTANIYKGGKVDLYGVYGYQCTGTPFKTACMYGGVTLHDNNQLE 147

QY 346 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFLGSLNSDSFGGRVQ 405
Db 148 EEKVPINLWIDGKQNTVPLGTVKTKKEVTVQELDLQSRHYLHETVNTYNTDAFNGKIQ 207

QY 406 RGLIVPHSSEGTSVSDLPDAQGQVPDTLLRIYRNTTISSTLSLSLYLYTT 458
Db 208 RGLIEFHPSSGSDGVYDLFGAQQVPTQLRIYRDNKTIKSNMHIDIYLYTT 260

RESULT 11
S52028
Ig kappa chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S52028
R:van Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkee, W.G.; Schots, A.; E submitted to the EMBL Data Library, August 1994
A:Description: Coordinate expression of antibody subunit genes yields high levels of function
A:Reference number: S52028
A:Accession: S52028
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-219 <VAN>
A:Cross-references: UNIPARC:UPI0000114B22; EMBL:L35138; NID:G522336; PIDN:AAA67525.1; PII
C:Superfamily: immunoglobulin V region; immunoglobulin homology

G2MS11
Ig gamma-2b chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1980 #sequence revision 01-Dec-2000 #text change 09-Jul-2004
C:Accession: S25057; A02157; A26235; A26232; A26233; A53598
R:Pisicher, R.; Voss, A.; Nierbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific m
A:Reference number: S25057
A:Accession: S25057
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-474 <FIS>
A:Cross-references: UNIPROT:P01866; UNIPARC:UPI0000116095; EMBL:X67210; NID:G54826; PIDN
R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from r
A:Reference number: A02157; MUID:80120716; PMID:6766534
A:Contents: a allele
A:Accession: A02157
A:Molecule type: DNA
A:Residues: 138-161, 'L', 163-189, 'FP', 193-376, 'T', 378-474 <YAM>
A:Cross-references: UNIPARC:UPI00000272D2; GB:J00461
A:Note: the sequence was determined from the germline gene
R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 206, 1299-1303, 1979
A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b hea
A:Reference number: A26235; MUID:80081501; PMID:117548
A:Contents: MPC 11
A:Accession: A26235
A:Molecule type: mRNA
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU1>
A:Cross-references: UNIPARC:UPI00001737AF
A:Note: Lys-474 is probably removed posttranslationally
R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immunogl
A:Reference number: A26232; MUID:80081502; PMID:117549
A:Accession: A26232
A:Molecule type: DNA
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU2>
A:Cross-references: UNIPARC:UPI00001737AF
R:Ollo, R.; Rougeon, F.
Nature 296, 761-763, 1982
A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamm
A:Reference number: A26233; MUID:82173203; PMID:6803173
A:Contents: b allele
A:Accession: A26233
A:Molecule type: DNA
A:Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLL>
A:Cross-references: UNIPARC:UPI00001737B0; GB:J00461
R:Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahash
J. Biol. Chem. 269, 12345-12350, 1994
A:Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
A:Reference number: A53598; MUID:94216359; PMID:7512967
A:Accession: A53598
A:Status: preliminary
A:Molecule type: protein
A:Residues: 234-251 <KIM>
A:Cross-references: UNIPARC:UPI00001737B1
C:Comment: The a allele sequence is shown.
C:Genetics: 138/1; 236/1; 258/1; 368/1
A:Introns: 138/1; 236/1; 258/1; 368/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: Immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobu
F:157-222/Domain: immunoglobulin homology <IM1>
F:236-257/Region: hinge
F:281-350/Domain: immunoglobulin homology <IM2>
F:387-454/Domain: immunoglobulin homology <IM3>
F:152/Disulfide bonds: interchain (to light chain) #status predicted
F:164-220,288-348,394-452/Disulfide bonds: #status predicted

F:247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted
F:324/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 25.6%; Score 900.5; DB 1; Length 474;
Best Local Similarity 35.4%; Pred. No. 9.2e-40;
Matches 238; Conservative 55; Mismatches 130; Indels 249; Gaps 17;
QY 1 EVQLQSGDPLVKPGASVKISKASGYSTGYGMHWKQSPGKLEWIGRIINPNNGVTLY 60
DB 20 EVQLQSGPELVNPGASVKMSCKASGYTFITVMHWKQSPGKLEWIGRIINPNKDGTRF 79
QY 61 NOKFKDKATLTVDKSGSTTAYMELSLTSDSAVYCARSTMTITNYMD---YKQGTSTVT 117
DB 80 NEKFKGKATLTSDKSSNTAYMELSLTSDSAVYCAR-----DYDYNFAWYWGQSTLVT 134
QY 118 VSAKTTTPSPVPLAPGSAQAQNSMYTLCLVKGYPPPEVTVTWNSGSLSSGVVHTF-PAV 176
DB 135 VSAAKTTTPSVPLAPGCGDTTSGSVTSGCLVKGYPPESVTVTWNSGSLSSSVHTLSQAL 194
QY 177 LOSDLTYLSSSVTPSSSTWPSSTVTCNVAHPASSTKVDKKIVPRDSGGSPSEKSEINE-- 234
DB 195 LOSGLYTMSSSVTPSSSTWPSQTVCVAHPASSITVDKKLEP---SGP---ISTINPCP 248
QY 235 --KDLRK--KSELQGTALGNLQIYYNSKAITTSEKSDAQFLTNTLLFKGFFTGHPWYN 290
DB 249 PCKECHCKCAPNLEG---GPSVFIPPPNIKDV-----TP----- 277
QY 291 DLLVDLGGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKV 350
DB 278 -LMISL-----TP----- 284
QY 351 PINLWIDGKQTTVPIDKVKTSKEVTQVELDLQARHYLHGKFLGYNDSFGGKVGQGLIV 410
DB 285 -----KVTGVVD-----VSEDDPDQVSWFVN-----VE 310
QY 411 FHSSEGSTVSYDLFDAQGYPTDLRIYRDNNTTSTSLTSLISLYLTTTIVMTQTPTSL 470
DB 311 VHTAQQTTHREDY-----NSTIRVVS----- 331
QY 471 VSAGDRVTITCKASQSVNDVAWYQKQPSQPKLLISYTSRYAGVDPDFSGSGYGTDF 530
DB 332 -----T 332
QY 531 LTISSVQAEDAAVYFCQDYNPPTFGGCTKLEIKRADAAPTVISIPPPSEQLTSGASV 590
DB 333 LPIQHODMWSGKEFKCKVNNKOLPSPIRTISKIKGLVRAPQVYILPPPAEQLSRKDVSL 392
QY 591 VCLNNFYPKDINVKWKIDGSRQN-----GVLNSWTDQDSKDSYTSMSSTLTLTDEYE 645
DB 393 TCLVVGFNFGDISVEWTSNGHTEENYKDTAPVLDS-----DGSFYIYKLNMTSKWE 445
QY 646 RNSVYTCETHK 657
DB 446 KTDSPFCNVRHE 457

RESULT 16

S38865
Ig kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 15-Jun-2001
C:Accession: S38865
R:Kipp, B.; Becker, W.; Schlaak, M.
submitted to the EMBL Data Library, November 1993
A:Description: Combination of a defined specificity and desired isotype by cloning of an
A:Reference number: S38864
A:Accession: S38865
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-219 <KIP>
A:Cross-references: UNIPARC:UPI00001165CB; EMBL:Z27396; NID:G416538; PIDN:CAA81787.1; PII
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyz
A:Reference number: JC5810; MUID:98063277; PMID:9398605
A:Accession: PC4436
A:Molecule type: protein
A:Residues: 1-444 <AKA>
A:Cross-references: UNIPARC:UPI0000176P41
C:Comment: This catalytic antibody has peroxidase oxidase activity. It is directed again
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:251-320/Domain: immunoglobulin homology <IMM>
F:22/Disulfide bonds: interchain (to 98) #status predicted
F:99/Disulfide bonds: interchain (to 109) #status predicted

Query Match 24.7%; Score 870; DB 2; Length 444;
Best Local Similarity 32.0%; Pred. No. 3.3e-38;
Matches 214; Conservative 71; Mismatches 131; Indels 252; Gaps 15;

QY 1 EVQLQSGDPLVKPGASVKISKASGYFTGYMHVVKQSPGKLEWIG--RINPNNVT 58
Db 1 EVQXVETGGGLVRPGNSLKLSCLTSGFTFSNRMHLRQPPGKLEWIAVITVKSNDYGA 60
QY 59 LYNQKPKDKATLTVDKSSSTAYMELSLTSEDSAVVYCARSTMITNYVMNDYQGQGTSTV 118
Db 61 KYAESVRGRFTISRDDSKSVYLQMNRLREEDTATYYCCRTPMV--YAMDCWQGTSTV 118
QY 119 SSAKTTTPSPVYPLAPGSAQTNSMVTLCGLVKGYFPEPVTVTWNSGSLSSGVHTTPAVLQ 178
Db 119 SSAKTTTPSPVYPLAPGSAQTNSMVTLCGLVKGYFPEPVTVTWNSGSLSSGVHTTPAVLQ 178
QY 179 SDLYTLSSVTPSSVTPSETVTCNVAHPASSPKVDKIVPRDSGGPSEKSEINEKDLR 238
Db 179 SDLYTLSSVTPSSVTPSETVTCNVAHPASSPKVDKIVPRDCG----- 223
QY 239 KKSELGOTGALGNLKQIYYNSKAITSEKSAQDLNTLLFKGFFTHGPWYNDLLVDLGS 298
Db 224 --CKPICITVPEVSSVFIPPK-----PKDVLITL----- 252
QY 299 TAATSEYEGSSVDLYGAYGYQCAGGTPNKACMYGGVTLHDNNRLTEEKVPIINLWIDG 358
Db 253 -----TP-KVTCVVVDIS-----KDDPEVQVQSFVVD- 277
QY 359 KQTTVPIDKVTSKKEV-----TVQELDQARHYLHGK-FGL-YNSDSFGKVGQGLI 409
Db 278 ---DVEVHTAQTPREQFNSTFRSVELPIHQDWLNGKEFKCRVNSAAFPAPIEK--- 331
QY 410 VFHSSEGSTVYDLFDAQGYQPTLLRIYRDNNTISSTLSLSLYLYTTSIVMTQPTSL 469
Db 332 -----TISKT----- 336
QY 470 LVSAGDRVTITCKASQSVNDVAVYQQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDP 529
Db 337 ----- 336
QY 530 TLTISVQAEDAAYVFCQDYNSPPTFGGQTKLEIKRADAAPTVISIFPPSSEQLTSGGAS 589
Db 337 -----KGRPKAPQVYTIPTPKQMAKDVKY 361
QY 590 VVCFLLNFPYKIDINVKWKIDGSRQNGVLNSWTDQSKDSTYSMSSTLTTLTKDEYERHNS 649
Db 362 LTCMITDFFPEDITVEWQWNGQPAEN-YKNTQPIMDT-DGSFVYVKLVNPKNSWEAGNT 419
QY 650 YTCEATHK 657
Db 420 FTCSVLHE 427

RESULT 27
A56169
Ig kappa chain V region (clone 23.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 11-Jan-2000
C:Accession: A56169
R.Montardini, C.; Kleber-Emmons, T.; VonFelidt, J.M.; O'Malley, B.; Rosenbaum, H.; Godill

J. Biol. Chem. 270, 6628-6638, 1995
A:Title: Recombinant antibodies in bioactive peptide design.
A:Reference number: A56169; MUID:95204454; PMID:7896802
A:Accession: A56169
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-210 <MON>
A:Cross-references: UNIPARC:UPI0000114B4B
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 24.3%; Score 857; DB 2; Length 210;
Best Local Similarity 79.4%; Pred. No. 6.1e-38;
Matches 166; Conservative 13; Mismatches 26; Indels 4; Gaps 1;

QY 460 IVMOTPTSLVSGADRVITITCKASQSVND-----VAVYQQKPGQSPKLLISYTSRYAG 515
Db 2 IVLTQSPASLTVSLGORATISCRASKSVSSGYSYMHWTYQKPGQPKVLIYLASLNSG 61
QY 516 VPDREGSGYGTDFTLTISVQAEDAAYVFCQDYNSPPTFGGQTKLEIKRADAAPTISI 575
Db 62 VPPRFGSGSGYGTDFTLINHPVEEDAAATYICHSRELPTWTFGGTRELKRAADAAPTISI 121
QY 576 FPPSSEQLTSGGASVVCFLNFPYKIDINVKWKIDGSRQNGVLNSWTDQSKDSTYSMS 635
Db 122 FPPSSEQLTSGGASVVCFLNFPYKIDINVKWKIDGSRQNGVLNSWTDQSKDSTYSMS 181
QY 636 TLTLDKDEYERHNSYTCEATHKTSPIV 664
Db 182 TLTLDKDEYERHNSYTCEATHKTSPIV 210

RESULT 28
S06084
Ig kappa chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C:Accession: S06084
R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
A:Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA.
A:Reference number: S06084; MUID:90016888; PMID:2508067
A:Accession: S06084
A:Molecule type: mRNA
A:Residues: 1-240 <CRO>
A:Cross-references: UNIPARC:UPI0000113764; EMBL:X16129; NID:G56457; PIDN:CAA34256.1; PID:
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-240/Product: Ig kappa chain #status predicted <MAT>
F:153-222/Domain: immunoglobulin homology <IMM>

Query Match 24.2%; Score 853; DB 2; Length 240;
Best Local Similarity 69.6%; Pred. No. 1.2e-37;
Matches 165; Conservative 31; Mismatches 31; Indels 10; Gaps 2;

QY 445 SSTISISILYLYTT-----SIVMTQPTSLVSGADRVITITCKASQSV-----SNDVAVY 494
Db 3 SQTQVLSLLLSLWISGTCGDFVMTQSPSSLAVASAGETVITINCKSSQLSFYSGNOKNYLAWY 62
QY 495 QKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDFTLTISVQAEDAAYVFCQDYNSPP 554
Db 63 QKPGQSPKLLIYWASTRQSGVDPDRFIGSGSGTDFTLTISVQAEDLAIVYCLQYETPY 122
QY 555 TFGGQTKLEIKRADAAPTVISIFPPSSEQLTSGGASVVCFLNFPYKIDINVKWKIDGSRQ 614
Db 123 TFCAGTKLEIKRADAAPTVISIFPPSTEQLATGGASVVCFLMNFYPRDISYKWKIDGTER 182
QY 615 NGVLNSWTDQSKDSTYSMSSTLTTLTKDEYERHNSYTCEATHKTSPIVKSFNRE 671
Db 183 DGVLSVTDQSKDSTYSMSSTLSUSKADYESHNLTYCEVHKTSSPVPVKSFNRE 239

RESULT 29

S68211
IG heavy chain (Mab13-1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 20-Jun-2000
C:Accession: S68211
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A:Reference number: S68211; MUID:96085223; PMID:7498516
A:Accession: S68211
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-220 <TAK>
A:Cross-references: UNIPARC:UPI000011B261; EMBL:D29669; NID:g473956; PIDN:BA06140.1; PT
A>Note: the sequence of residues 1-4, 213-220 and the corresponding nucleotide sequence
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:136-200/Domain: immunoglobulin homology <IMM>

Query Match 22.9%; Score 808; DB 2; Length 220;
Best Local Similarity 70.2%; Pred. No. 2.3e-35;
Matches 153; Conservative 24; Mismatches 37; Indels 4; Gaps 2;

QY 6 QSGPDLVKPGASVKISKASGYFTGYMHVWKQSPKGLGWIG--RINPNNGVTLYNQK 63
DB 2 ESGGGLVRPNSLKISCLTSGFTFSNRYMRHLRQPPGKRLIEWIAVITKSDNYGAKYAES 61

QY 64 FKDKATLTVDKSSSTAYMELRSLTSDSAVYICARSTMTINVDYWGQGTSTVTSASAKT 123
DB 62 VRGRFTISRDDKSSVYLQNNRLREEDTAYYICRFPW--YAMDCWGQGTSTVIVSASAKT 119

QY 124 TPSPVYPLAPGSAQAQNSMTLGLVKGYPEPVTYTNWNSGSLSSGVHTTTPAVLQSDLYT 183
DB 120 TPSPVYPLAPGSAQAQNSMTLGLVKGYPEPVTYTNWNSGSLSSGVHTTTPAVLQSDLYT 179

QY 184 LSSSVTPSPSTWSPSETVTCNVAHPASSTKVDKIVPRD 221
DB 180 LSSSVTPSPSTWSPSETVTCNVAHPASSTKVDKIVPRD 217

RESULT 30

S68213
IG heavy chain (Mab03-1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 29-Jul-1997 #sequence_revision 17-Sep-1997 #text_change 31-Dec-2004
C:Accession: S68213
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A:Reference number: S68213; MUID:96085223; PMID:7498516
A:Accession: S68213
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-213 <TAK>
A:Cross-references: UNIPROT:Q91Z05; UNIPARC:UPI0000176F3F; EMBL:D29667
C:Superfamily: immunoglobulin homology
F:137-201/Domain: immunoglobulin homology <IMM>

Query Match 20.9%; Score 737.5; DB 2; Length 213;
Best Local Similarity 64.7%; Pred. No. 1e-31;
Matches 139; Conservative 29; Mismatches 44; Indels 3; Gaps 1;

QY 2 VQLQSQGPDLVKPGASVKISKASGYFTGYMHVWKQSPKGLGWIGRINPNNGVTLYN 61
DB 2 VOLVESGGGLVQPGSRKLSKCAASGFTFSFGMHVWRQAPKGLGWVAYISSGSSSIYA 61

QY 62 QKFKDKATLTVDKSSSTAYMELRSLTSDSAVYICARSTMTINVDYWGQGTSTVTSVA 121
DB 62 DTVKGRFTISRDRPNKNTFLQNTSLASEDTAMTYICARSWLLP---FDYWGQGTTLTVSSA 118

QY 122 KTTTPSVYPLAPGSAQAQNSMTLGLVKGYFPPEVTYTNWNSGSLSSGVHTTTPAVLQSD 191
DB 119 KTTTPSVYPLAPGCGDTTSGSVTLGLVKGYFPPEVTYTNWNSGSLSSGVHTTTPALLQSG 178

QY 182 YTLSSSVTPSPSTWSPSETVTCNVAHPASSTKVDK 216
DB 179 YTMSSSVTPSPSTWSPSQVTCTCSVAHPASSTVDK 213

RESULT 31

PC4155
IG gamma-2b chain V-C region Mab823 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 21-Jan-2000
C:Accession: PC4155
R:Kwak, J.W.; Choi, B.K.; Lee, D.I.; Kang, Y.K.; Seo, Y.G.; Cho, W.K.; Han, M.H.
Gene 169, 237-239, 1996
A:Title: Cloning and characterization of cDNAs coding for heavy and light chains of a mor
A:Reference number: PC4155; MUID:96194809; PMID:8647454
A:Accession: PC4155
A:Molecule type: mRNA
A:Residues: 1-231 <KWA>
A:Cross-references: UNIPARC:UPI00001157CB; GB:U28970; NID:g1262180; PIDN:AAC52489.1; PID
A>Note: This protein has unusual amino acid compared with the conserved sequences of mou
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:1-231/Product: heavy chain #status predicted <MAT>
F:98-102/Region: unique D sequence
F:103-119/Region: V region
F:139-203/Domain: immunoglobulin homology <IMM>

Query Match 20.3%; Score 715; DB 2; Length 231;
Best Local Similarity 60.9%; Pred. No. 1.6e-30;
Matches 137; Conservative 29; Mismatches 55; Indels 4; Gaps 2;

QY 1 EVQLVDSGPDLVKPGASVKISKASGYFTGYMHVWKQSPKGLGWIGRINPNNGVTLY 60
DB 1 EVQLVDSGPDLVKPGASVKISKASGYFTGYMHVWKQSPKGLGWIGRINPNNGVTLY 59

QY 61 NQFKDKATLTVDKSSSTAYMELRSLTSDSAVYICARSTMTINVDYWGQGTSTVTSV 120
DB 60 NSALKSRSLINKDNKSKSQVFLKMNLSLHDTDTANYCYKCHEDRYDYPVDMGAGTTVTSS 119

QY 121 AKTTTPSVYPLAPGSAQAQNSMTLGLVKGYPEPVTYTNWNSGSLSSGVHTTTPAVLQSD 180
DB 120 AKTTTPSVYPLAPGCGDTTSGSVTLGLVKGYFPPEVTYTNWNSGSLSSGVHTTTPALLQSG 179

QY 181 YTLSSSVTPSPSTWSPSETVTCNVAHPASSTKVDKIVPRDSGGP 225
DB 180 LYTMSSSVTPSPSTWSPSQVTCTCSVAHPASSTTVDKLEP---SGP 221

RESULT 32

JE0244
IG kappa chain NIG2 precursor - human
C:Species: Homo sapiens (man)
C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0244
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T
submitted to JIPID, November 1998
A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL amy
A:Reference number: JE0243
A:Accession: JE0244
A:Molecule type: protein
A:Residues: 1-215 <ALI>
A:Cross-references: UNIPARC:UPI0000176982
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 19.9%; Score 702.5; DB 2; Length 215;
Best Local Similarity 62.1%; Pred. No. 6.7e-30;
Matches 133; Conservative 36; Mismatches 42; Indels 3; Gaps 2;

QY 460 IVMTQPTSLVVSAGDRVTITCKASQSVNDVAWYQKQSPKLLISYTSRVSAGVPDR 519
DB 2 VLTQSPATLSVSPGERATLSCRASQSVHNSLAWYQKQCPQRLLIYRASTRATGIPAR 61

Db	139	VSSASTTAKVYPLSLSCCGDKSSVTTLGCLVSSYMPPEVPTVWNSGALKSGVHTPEAVL	198
Qy	178	QSD-LYTLSSSVTPSETVPTCNVAHPASSTKVDKKIIVPRDSGGPSEKSEINEKD	236
Db	199	QSSGLYSLSSVTPVPGST-SGQFTTCNVAHPASSTKVDKAVDPTCKPSPC-----D	248
Qy	237	LRKKSLOGTALGNLQIYYNSKAITSEKSDQFLTWTLFLPKGFTGHPWYNDLLVDL	296
Db	249	CCPPPELPGG-----PSVFIFPPKP-----KDTLT-----ISGTPEVTCVVVDV	287
Qy	297	GSTAATSEYEGSGVDLYGAYGYQCAGGTENKTACMYGVTLHDNNRLTEKKVPINLWI	356
Db	288	G-----HD-----DEVKFSWV	300
Qy	357	DGKQ-----TTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKRVQRLIVPH	412
Db	301	DVEVNTATTKPREEQFNSTYRV-VSALRIQHDMTGK-----EFCKVH-----	345
Qy	413	SSEGSTVSYDLFDAQOQYPTLLRIYRDNTTISSTLSLSLYLYTTSIVMTQTPTSLIYS	472
Db	346	-NEG-----LPAPIVR-----TISRT-----	360
Qy	473	AGDRVTTTCKASQSVNDVAWYQKPGQPKLLISYTSRKYAGVPDRFGSGYGTDFTLT	532
Db	361	-----KGPARBPQ-----	368
Qy	533	ISGVAEDAAYVFCQDYNSPPTFFGGTKLETKRADAAPTVSIFFPSSBOLTSGGASVVC	592
Db	369	-----VYVLAPPQBELSKSTVSLTC	388
Qy	593	FLNNFPKIDINVKKIDGSRQGVNLNSWTDQDSKDSYMSSTLTTLTKDEYERHNSYTC	652
Db	389	MVTSFYFDYIAVEWQRNGQPESGDKYGTTPQLQDADSSYFLYSLKLVDRNSWQEGDTYC	448
Qy	653	EATHK	657
Db	449	VNWE	453
RESULT 39			
S29593			
Ig kappa chain (WM65) - mouse (fragment)			
C:Species: Mus musculus (house mouse)			
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000			
A:Accession: S29593			
R:Seymour, R.			
submitted to the EMBL Data Library, February 1991			
A:Reference number: S29593			
A:Accession: S29593			
A:Status: preliminary			
A:Molecule type: mRNA			
A:Residues: 1-197 <SEY>			
A:Cross-references: UNIPARC:UPI0000115F08; EMBL:X57856; NID:G52588; PIDN:CAA40991.1; PID			
C:Superfamily: immunoglobulin V region; immunoglobulin homology			
C:Keywords: heterotetramer; immunoglobulin			
Query Match 18.8%; Score 663.5; DB 2; Length 197;			
Best Local Similarity 72.9%; Pred. No. 6.4e-28;			
Matches 132; Conservative 16; Mismatches 28; Indels 5; Gaps 2;			
Qy	460	IWVTOPTTSLIYSAGDRVITITCKASQSV--SND--VAWYQKPGQSPKLLISYTSRVA	514
Db	17	IWVTOAAPISVTPGSGASSTFLRLSRVEADVGFVFCQHLEYPYTFGGTKLEIKRADAPTYS	76
Qy	515	GVPDRFSGSGYGTDFLTITSSVQAEAAVYFCQDYNSPPTFGGTVKLEIKRADAPTYS	574
Db	77	GVPDRFSGSGSTSLRLSRVEADVGFVFCQHLEYPYTFGGTKLEIKRADAPTYS	136
Qy	575	IFPPSEQLTSGGASVVCFLNNFPKIDINVKKIDGSRQGVNLNSWTDQDSKDSYYSMS	634
Db	137	IFPPSEQLTSGGASVVCFLNNFPKIDINVKKIDGSRQGVNLNSWTDQDSKDSYYSMS	196

Qy	635	S	635
Db	197	S	197
RESULT 40			
S69131			
Ig heavy chain (DOT) - human (fragment)			
N:Alternate names: anti-riboflavin Igg Fd fragment			
C:Species: Homo sapiens (man)			
C:Date: 12-Feb-1998 #sequence_revision 22-May-1998 #text_change 21-Jan-2000			
A:Accession: S69131			
R:Stoppini, M.; Bellotti, V.; Negri, A.; Merlini, G.; Garver, F.; Ferri, G.			
Eur. J. Biochem. 228, 886-893, 1995			
A:Title: Characterization of the two unique human anti-flavin monoclonal immunoglobulins.			
A:Reference number: S69130; MUID:95255298; PMID:7737190			
A:Accession: S69131			
A:Molecule type: protein			
A:Residues: 1-241 <STO>			
A:Cross-references: UNIPARC:UPI0000176F40			
C:Superfamily: immunoglobulin C region; immunoglobulin homology			
C:Keywords: blocked amino end; heterotetramer; immunoglobulin; pyroglytamic acid			
F:1-241/Product: Ig heavy chain (DOT) {fragment} #status experimental <MAT>			
F:140-205/Domain: immunoglobulin homology <IMM>			
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental			
Query Match 18.8%; Score 661.5; DB 2; Length 241;			
Best Local Similarity 59.4%; Pred. No. 1e-27;			
Matches 130; Conservative 35; Mismatches 51; Indels 3; Gaps 3;			
Qy	1	EVLOQSGDLVKPGASVKISCKASYFTGYMHVVKQSPGKLEWIGRINPNNGVTLY	60
Db	1	QVQLVQSGVERKVPQASVRIKCAKAGYAFENYIHVRQAPGLGLEWMGIFNPVAG-AVS	59
Qy	61	NQKFDKATLTVDKSTTAYMELRSLTSDSAVYYCAR-STMITNYMDYWGQGTSTVYS	119
Db	60	SEKFRDLVMSSDTSANTVSMQLRSLRSDDTGRYFCARVSYDFSGYQMDVMWGQGTTVIS	119
Qy	120	SAKTPPSPVYPLAPGSAAGTNSMVLGCLVKCYFPEPTVTWNSGSLSSGVHTFPVLOS	179
Db	120	SASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLOS	179
Qy	180	D-LYTLSSSVTPSPSETVTCNVAHPASSTKVDKKI	217
Db	180	SGLYSLSSVTVFPSSNFGTQTTCNVDHKPSNTKVDKTV	218
RESULT 41			
A23746			
Ig kappa chain V-III (KAU cold agglutinin) - human			
C:Species: Homo sapiens (man)			
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000			
A:Accession: A23746			
R:Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.			
J. Biol. Chem. 266, 2836-2842, 1991			
A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglob			
A:Reference number: A23746; MUID:91131575; PMID:1993660			
A:Accession: A23746			
A:Status: preliminary			
A:Molecule type: protein			
A:Residues: 1-215 <LEO>			
A:Cross-references: UNIPARC:UPI0000176985			
C:Superfamily: immunoglobulin V region; immunoglobulin homology			
C:Keywords: heterotetramer; immunoglobulin			
F:16-91/Domain: immunoglobulin homology <IMM>			
Query Match 18.7%; Score 659.5; DB 2; Length 215;			
Best Local Similarity 62.0%; Pred. No. 1.1e-27;			
Matches 132; Conservative 31; Mismatches 49; Indels 1; Gaps 1;			
Qy	460	IWVTOPTTSLIYSAGDRVITITCKASQSV-SNDVAWYQKPGQSPKLLISYTSRVA	518
Db	2	IVLTQSPATLSLSPGERATLISGASQSVSNLYAWYQKPGQAPRLIIYDASSRATGIPD	61

C;Accession: B02159; A02160; B02158
R;Honjo, T.; Ohta, M.; Yamawaki-Kataoka, Y.; Kataoka, T.; Kawakami, T.; Takahashi, N.;
Cell 18, 559-568, 1979
A;Title: Cloning and complete nucleotide sequence of mouse immunoglobulin gamma1 chain c
A;Reference number: A02159; MUID:80045036; PMID:115593
A;Accession: B02159
A;Molecule type: DNA
A;Residues: 1-393 <HON>
A;Cross-references: UNIPROT:P01869; UNIPARC:UPI00000272D5; GB:J00453
A;Note: the sequence was determined from the germline gene
P;Tyler, B.M.; Cowman, A.F.; Gerondakis, S.D.; Adams, J.M.; Bernard, O.
Proc. Natl. Acad. Sci. U.S.A. 79, 2008-2012, 1982
A;Title: mRNA for surface immunoglobulin gamma chains encodes a highly conserved transme
A;Reference number: A02160; MUID:82197626; PMID:6804950
A;Accession: A02160
A;Molecule type: mRNA
A;Residues: 323-393 <TYL>
A;Cross-references: UNIPARC:UPI00001737A9
R;Rogers, J.; Choi, E.; Souza, L.; Carter, C.; Word, C.; Kuehl, M.; Eisenberg, D.; Wall,
Cell 26, 19-27, 1981
A;Title: Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma c
A;Reference number: A02158; MUID:82115295; PMID:6799207
A;Accession: B02158
A;Molecule type: DNA
A;Residues: 323-366 <ROG>
A;Cross-references: UNIPARC:UPI00001737AA
A;Note: this sequence is the translation of the first exon of the M segment
C;Comment: Cell lines producing IgG contain two mRNA species for Ig gamma chains. The ma
ncode membrane-bound chains in that it contains an alternative 3' end, encoded in separa
C;Genetics:
A;Introns: 1/1; 98/1; 111/1; 218/1; 323/1; 366/3
C;Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotrimer; immunoglobul
F;131-200/Domain: immunoglobulin homology <IMM>
F;340-357/Domain: transmembrane #status predicted <TM>
F;358-393/Domain: intracellular #status predicted <INT>
F;174,278/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.88; Score 557; DB 1; Length 393;
Best Local Similarity 28.34; Pred. No. 5.2e-22;
Matches 156; Conservative 48; Mismatches 89; Indels 258; Gaps 13;

QY 121 AKTTPSVYPLAGSAAQTNSMTGLCLVKGYPPEVTVTWNSGSLSSGVHTTTPAVLQSD 180
|||||
1 AKTTPSVYPLAGSAAQTNSMTGLCLVKGYPPEVTVTWNSGSLSSGVHTTTPAVLQSD 60
|||||

QY 181 LYTSSSVTVPSSTWSPSETVTCNVHPASSTKVDKIVPRDSGGPSEKSEINEKOLRKK 240
|||||
61 LYTSSSVTVPSSTWSPSETVTCNVHPASSTKVDKIVPRDCG----- 103
|||||

QY 241 SELQGTALGNLKIYYNSKATISSEKSAQDFLTNTLLFKGFTGHPYNDLLVDLGSTA 300
: : : : :
104 CKPCICTVPSVSVFIPPPK-----PKDVLITL----- 132
: : : : :
301 ATSEYEGSSVDLYGAYGYQCAGTGNKTCMVGTVTHDNNRLTEKVPINLWIDGKQ 360
||| : : : : :
133 -----TP-KVTCVVVDIS-----KDDPEVQFSWFDV--- 157
: : : : :
361 TTVPIDKVTSSKEV-----TVQELDLOARHYLHGK-FGL-YNSDSPGKGVORGLIVF 411
: : : : :
158 -DVEVHTAQTPREBQPNSTFRSVELPIMHQDLNGKEFKCRVNSAAPPAPTEK----- 211
: : : : :
412 HSSEGSTVSYDLDAQCOQYPTDLLRIYRDNVTTSISLSLSLYLYTTSIVMTQPTSLIV 471
||| : : : : :
212 -----TISKT----- 216
: : : : :
472 SAGDRVTTTCASQSVSNDVAVYQKPGQPKLLISYTSRYAGVDPDRFGSGVGDTFTL 531
: : : : :
217 ----- 216
: : : : :
532 TISSVQAEDAAVFCQDYNSPPTFGGKTKLEIKRADAAPTIVFPPSPBQLTSGGASVV 591

Db 217 -----KGRPKAPQVYTIPTPPKEQMAKDKVSLT 243
: : : : :
QY 592 CFLNNFYPKDIINVKWIDGSERON-----GVLNSWTDQDSKDYSGNSSTLTITLKDEYER 646
: : : : :
Db 244 CMITDFPEDITVEWQWNGQPAENYKNTQPIMT-----NGSYFYSKLVNPKVQSNWEA 296
: : : : :
QY 647 HNSYTCEATHK 657
: : : : :
Db 297 GNTFTCSVLHE 307
: : : : :
RESULT 54
KIMS
IG kappa chain C region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1980 #sequence revision 17-Dec-1982 #text change 09-Jul-2004
C;Accession: B90262; A90778; B93736; A92322; A93748; A02119
R;Svasti, J.; Milstein, C.
Biochem. J. 128, 427-444, 1972
A;Title: The complete amino acid sequence of a mouse kappa light chain.
A;Reference number: A90262; MUID:73053310; PMID:4638343
A;Contents: myeloma protein MOPC 21
A;Accession: B90262
A;Molecule type: protein
A;Residues: 1-52, 'BSBTZWB', 60-106 <SVA>
A;Cross-references: UNIPROT:P01837; UNIPARC:UPI0000173772
R;Svasti, J.; Milstein, C.
Biochem. J. 126, 837-850, 1972
A;Title: The disulphide bridges of a mouse immunoglobulin G1 protein.
A;Reference number: A90259; MUID:73008899; PMID:5073237
A;Contents: annotation; MOPC 21, disulfide bonds
A;Note: Cys-106 is involved in a light-heavy chain bond
R;Hamlyn, P.H.; Brownlee, G.G.; Cheng, C.C.; Gait, M.J.; Milstein, C.
Cell 15, 1067-1075, 1978
A;Title: Complete sequence of constant and 3' noncoding regions of an immunoglobulin mRNA
A;Reference number: A90778; MUID:79084137; PMID:103625
A;Accession: A90778
A;Molecule type: mRNA
A;Residues: 1-106 <HAM>
A;Cross-references: UNIPARC:UPI0000024D73
R;Hamlyn, P.H.; Gait, M.J.; Milstein, C.
Nucleic Acids Res. 9, 4485-4494, 1981
A;Title: Complete sequence of an immunoglobulin mRNA using specific priming and the dic
A;Reference number: A93736; MUID:82059477; PMID:6170937
A;Contents: MOPC 21
A;Accession: B93736
A;Molecule type: mRNA
A;Residues: 1-106 <HA2>
A;Cross-references: UNIPARC:UPI0000024D73
R;Max, E.E.; Maizel Jr., J.V.; Leder, P.
J. Biol. Chem. 256, 5116-5120, 1981
A;Title: The nucleotide sequence of a 5-kilobase DNA segment containing the mouse kappa
A;Reference number: A92322; MUID:81191915; PMID:6262318
A;Accession: A92322
A;Molecule type: DNA
A;Residues: 1-106 <MAX>
A;Cross-references: UNIPARC:UPI0000024D73
A;Note: the sequence was determined from the germline gene
R;Alteneburger, W.; Neumaier, P.S.; Steinmetz, M.; Zachau, H.G.
Nucleic Acids Res. 9, 971-981, 1981
A;Title: DNA sequence of the constant gene region of the mouse immunoglobulin kappa chain
A;Reference number: A93748; MUID:81198949; PMID:6785724
A;Accession: A93748
A;Molecule type: DNA
A;Residues: 1-106 <ALT>
A;Cross-references: UNIPARC:UPI0000024D73
A;Note: the sequence was determined from the germline gene
C;Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa)
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotrimer
F;26-86/Disulfide bonds: #status experimental

Query Match		15.8%;	Score 556;	DB 1;	Length 106;
Best Local Similarity		100.0%;	Pred. No. 1.1e-22;		
Matches 105;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	567	ADAAPTVSIFFPPSSEQLTSGGASVCFNNFYPKDINVKWKIDGSRQNGVLNSWTDQDS	626		
DB	1	ADAAPTVSIFFPPSSEQLTSGGASVCFNNFYPKDINVKWKIDGSRQNGVLNSWTDQDS	60		
QY	627	KDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTPIVKSFNNE	671		
DB	61	KDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTPIVKSFNNE	105		
RESULT 55					
A56446					
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)					
C:Species: Mus musculus (house mouse)					
C>Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996					
C:Accession: A56446					
R:Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.					
J. Biol. Chem. 270, 7829-7835, 1995					
A:Title: A high affinity digoxin-binding protein displayed on M13 is functionally identical					
A:Reference number: A56446; MUID:95229583; PMID:7713873					
A:Accession: A56446					
A>Status: preliminary					
A:Molecule type: mRNA					
A:Residues: 1-268 <TAN>					
A:Cross-references: UNIPARC:UPI000017C6D0; GB:U20617					
C:Keywords: heterotetramer; immunoglobulin					
Query Match		15.8%;	Score 556;	DB 2;	Length 268;
Best Local Similarity		26.7%;	Pred. No. 3.6e-22;		
Matches 152;		Conservative 36;	Mismatches 55;	Indels 326;	Gaps 9;
QY	1	EVQLQSGDPLVPGASVKISKASGVSFTGYVMHWKQSPGKLEWIGRIHPNNGVTLY	60		
DB	3	QVKLQSGAEVLKPGASVKLSCTSFNFKDTYMHVVKQRPQEGLEWIGRIAPANGITKY	62		
QY	61	NQKFKDKATLVVDKSTTAYMELRSITSDSAVYCARSTMIINYMDYWGQSTVTVSS	120		
DB	63	DPKFGKATIAADTSNTAYQLSSLTSEDATVYYCA-SYLLTRY-ENYWGQSTVTVS-	119		
QY	121	AKTTPSVVPLAPGSAQTNSMTVGLCVKGYPEPVTYTNWSGSLSSGVHIFPAVLQSD	180		
DB	120	-----	119		
QY	181	LYTLSSSVTPSPSTWTPSETVTCNVAHPASSTKVDDKIIVPRDSGGPSEKSEINEKDLRKK	240		
DB	120	-----	122		
QY	241	SELQGTALGNLKOIYYNKAITSSEKSDAQFLTNTLLFKGPTGHPWYNLLVDLGSTA	300		
DB	123	-----	122		
QY	301	ATSEYEGSSVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLTEKKVPINLWDGKQ	360		
DB	123	-----	127		
QY	361	TTVPIDKVKTSKEVTVQELDLQARHLYHGKFLGYNDSFGGKVQVGRGLIVFHSSGSTVS	420		
DB	128	-----	135		
QY	421	YDLFDAQQGYPDTLRIYRNTTISLSLSLYLTTISIVMTQTPTSLLSVAGDRVTIT	480		
DB	136	-----	157		
QY	481	CKASQSVNDVAVYQKPGSKLLSYTSRRYAGVDPDRFSGSGYGTDTLTLTSSVQAE	540		
DB	158	CRASSSV-NFIYVYQKQSDASPKLWYIYTHLPFGVPARFSGSGSGNSYSLTSSMEGD	216		
QY	541	AAVYFCQQDYNSPPTFGGGTKLEIKRADA	569		

DB	217	AATYYCQQTSSPFTFGSGTKLEIKRSAA				245
RESULT 56						
PS0017						
IG gamma-1 chain C region - rat						
C:Species: Rattus norvegicus (Norway rat)						
C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004						
C:Accession: PS0017; C25941						
R:Brueggemann, M.						
Gene 74, 473-482, 1988						
A:Title: Evolution of the rat immunoglobulin gamma heavy-chain gene family.						
A:Reference number: PS0017; MUID:89232738; PMID:3149946						
A:Accession: PS0017						
A:Molecule type: DNA						
A:Residues: 1-326 <BRU>						
A:Cross-references: UNIPROT:P20759; UNIPARC:UPI000012B27A						
R:Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, S.; Waldmann, H.						
Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986						
A:Title: Immunoglobulin heavy chain locus of the rat: striking homology to mouse antibody						
A:Reference number: A25941; MUID:86287397; PMID:3016742						
A:Accession: C25941						
A>Status: preliminary						
A:Molecule type: DNA						
A:Residues: 220-326 <BR2>						
A:Cross-references: UNIPARC:UPI0000176F06						
C:Genetics:						
A:Introns: 98/1; 113/1; 220/1						
C:Superfamily: immunoglobulin C region; immunoglobulin homology						
C:Keywords: immunoglobulin						
F:20-84/Domain: immunoglobulin homology <IMM>						
Query Match 15.6%; Score 550; DB 2; Length 326;						
Best Local Similarity 27.7%; Pred. No. 9.5e-22;						
Matches 150; Conservative 64; Mismatches 90; Indels 238; Gaps 14;						
QY	121	AKTTPSVVPLAPGSAQTNSMTLGLVKGYFPEPVTYTNWSGSLSSGVHIFPAVLQSD	180			
DB	1	AEITAPSVVPLAPGATALKNSMTLGLVKGYFPEPVTYTNWSGALSSGVHIFPAVLQSG	60			
QY	181	LYTLSSSVTPSPSTWTPSETVTCNVAHPASSTKVDDKIIVPRDSGGPSEKSEINEKDLRKK	240			
DB	61	LYTLTSSVTPSPSTWTPSETVTCNVAHPASSTKVDDKIIVPRNCGGCKPC-	109			
QY	241	SELQGTALGNLKOIYYNKAITSSEKSDAQFLTNTLLFKGPTGHPWYNLLVDLGSTA	300			
DB	110	-----	130			
QY	301	ATSEYEGSSVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLTEKKVPINLWDG--	358			
DB	131	-----	162			
QY	359	---KQTTVPIDKVKTSKEVTVQELDLQARHLYHGKFLGYNDSFGGKVQVGRGLIVFHSS	415			
DB	163	VHTAQTRPPEEQFNSTFR--SVSELPILHQDWLNGR-	196			
QY	416	GSTVSDVLFDAQQGYPDTLRIYRNTTISLSLSLYLTTISIVMTQTPTSLLVSAGD	475			
DB	197	-----	196			
QY	476	RVITITCKASQSVNDVAVYQKPGSKLLISYTSRRYAGVDPDRFSGSGYGTDTLTITISS	535			
DB	197	--TFRCV-	217			
QY	536	VOAEADAVYFCQDYNSPPTFGGGTKLEIKRADAAPTIVIFPPSSQLTSGGASVVCFLN	595			
DB	218	PE-----	249			
QY	596	NFYPKDINVKWKIDGSRQNGVLNSWTDQDSDKSTYSMSSTLTLTKDEYERHNSYTCEAT	655			
DB	250	GRYPDIYVYEWQMGQPOEN-YKNTPTTMDT-DGSYFLYSLKLVNKKERKQCGNFTICSVL	307			
QY	656	HK	657			

Db 308 HE 309
RESULT 57
PS0019
IG gamma-2a chain C region - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C;Accession: PS0019; D25941
R;Bruggemann, M.
Gene 74, 473-482, 1988
A;Title: Evolution of the rat immunoglobulin gamma heavy-chain gene family.
A;Reference number: PS0017; MUID:89232738; PMID:3149946
A;Accession: PS0019
A;Molecule type: DNA
A;Residues: 1-322 <BRU>
A;Cross-references: UNIPROT:P20760; UNIPARC:UPI000012B28D
R;Bruggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, S.; Waldmann, H.
Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986
A;Title: Immunoglobulin heavy chain locus of the rat: striking homology to mouse antibody
A;Reference number: A25941; MUID:86287397; PMID:3016742
A;Accession: D25941
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 216-322 <BR2>
A;Cross-references: UNIPARC:UPI0000176F03
C;Genetics:
A;Introns: 98/1; 109/1; 216/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-84/Domain: immunoglobulin homology <IMM>
Query Match 15.3%; Score 539; DB 2; Length 322;
Best Local Similarity 28.2%; Pred. No. 3.5e-21;
Matches 153; Conservative 55; Mismatches 92; Indels 242; Gaps 15;
Qy 121 AKTTPSVYPLAPGSAQAQNSMTVLGCLVKGYPEPVTVTWNSGSLSSGVTTPAVLQSD 180
Db 1 AETTFSVYPLAFGTALKNSMTVLGCLVKGYPEPVTVTWNSGSLSSGVTTPAVLQSG 60
Qy 181 LYTLSSVTVPSTWSETVTCNVAHPASTKVDKIVPRDSGGPSEKSEINEKDLKK 240
Db 61 LYTLSSVTVPSTWSSQAVTCNVAHPASTKVDKIVPREC-----VFIFPKTKDVL----- 102
Qy 241 SELQGTALGNLKIIYYNSKAITSSSEKSAQDLTNTLLPKGFTHGHWYNDLLVLDGSTA 300
Db 103 -----NPGCGCTGSEVSS-----VFIFPKTKDVL----- 126
Qy 301 ATSEYEGSSVDLYGAYGYOCAGTGNKTKACMYGGVTLHDNNRLTEKKVPINLWIDG-- 358
Db 127 -----TITL-----TP-KVTCVVVDISQND-----PEVRFSGWFIIDVVE 158
Qy 359 ---KQTVPTDKVTSKKEVTVQELDQARHYLHGKFLYNSDSFGKVGQRLIVFHSSE 415
Db 159 VHTAQTHAPEKQNSLTL--SVSELPIVHRDLNGK-----TFKCKVN----- 199
Qy 416 GSTVSVDLFDQAQGYPTLLRIYRDNTTISSTLSISLYLYTTSIVMTQPTTSLLSAGD 475
Db 200 -----SGAFAPV----- 207
Qy 476 RVITTKASQSVGNDVAMVYQKFGQSPKLLIYSTSSRYAGVPRFSGSGYGTDTLTITSS 535
Db 208 -----EKSIS-----KEGTPR----- 219
Qy 536 VQAEADAVYFCQDYNSSPTFFGGGTGLEIKRADAAPTVSIFFPSSSEQLTSGGASVVCFLN 595
Db 220 -----GQVYTMAPPKKEMTQSQVSITCMVK 245
Qy 596 NEYPKDIINVKIKDGSBRQVNLNMTDQDSKDYSSMSSTLTLTKDVEYERHNSYTCAT 655
Db 246 GFYPDPDIYEWKNGQPOEN-YKNTPTMTDT-DGSYFLYSKLVNKKETWQOQNTFTCSVL 303

Qy 656 HK 657
Db 304 HE 305
RESULT 58
S29690
IG heavy chain VDJ region - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 30-Jan-1998 #text_change 20-Jun-2000
C;Accession: S29690
R;Dammers, P.M.; Bos, N.A.; Kroese, F.G.M.
submitted to the EMBL Data Library, October 1992
A;Description: Analysis of the rat B cell repertoire: cloning of rat Vh genes.
A;Reference number: S29690
A;Accession: S29690
A;Molecule type: mRNA
A;Residues: 1-288 <DAM>
A;Cross-references: UNIPARC:UPI0000176F0E; EMBL:X68782; NID:g56442; PID:g1334294
A;Experimental source: strain D2B
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;12-95/Domain: immunoglobulin homology <IMM>
Query Match 15.2%; Score 536; DB 2; Length 288;
Best Local Similarity 45.0%; Pred. No. 4.4e-21;
Matches 113; Conservative 36; Mismatches 78; Indels 24; Gaps 7;
Qy 4 LQSGPDLVKPGASVKISKACSGYFTGYMHVWVKSPGKLEWIGRIINPNNGVTLYNQK 63
Db 1 LQESGTELVRPSSSVKISKASGYTFTDYMHVWVKORPEQGLVWIGRIINPANGNTEYAEK 60
Qy 64 FKDKATLTVDKSTTAYMEILSLTSDSAVYVCARSTMITNMYDMYWGQGTSTVTSASAKT 123
Db 61 FKSRATLTADKSNATYMQLSLTSDTATYFTCTINGTVVFP--DYNGQGVMTVTSSESQ 118
Qy 124 TTPSVVYPLAP-GSAAQTNSMTVLGCLVKGYFPFPVTVTW---NSGSLSSGVTTPAVLQS 179
Db 119 SSPTPLVLVSCSPISDENLVAMGCLARDFLPSSISFSWYQNTVMQGVRTFTLTGT 178
Qy 180 DLYTLSSSVTVPSST---WPSETVTCNVAH-----PA---SSTKVDKKIVPRDS 222
Db 179 DKYATATSVLLSAKNVLEGSDEYLVCKIHGKNKDLHPVPAVEMNPNVSVFIPPRDA 238
Qy 223 -GGPSEKSEBEI 232
Db 239 FSGPAPRKSRSL 249
RESULT 59
A35944
IG gamma-2a chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Nov-1990 #sequence_revision 30-Nov-1990 #text_change 16-Jul-1999
C;Accession: A35944
R;Igarashi, T.; Sato, M.; Katsube, Y.; Takio, K.; Tanaka, T.; Nakanishi, M.; Arata, Y.
Biochemistry 29, 5727-5733, 1990
A;Title: Structure of a mouse immunoglobulin G that lacks the entire C-H1 domain: protein
A;Reference number: A35944; MUID:90344795; PMID:2116900
A;Accession: A35944
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-170 <IGA>
A;Cross-references: UNIPARC:UPI0000176F39
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;56-120/Domain: immunoglobulin homology <IMM>
Query Match 15.0%; Score 530; DB 2; Length 170;
Best Local Similarity 73.1%; Pred. No. 4.6e-21;
Matches 106; Conservative 13; Mismatches 20; Indels 6; Gaps 3;
Qy 85 SLTSDSAVYVCARSTMITNYV-MDYWGQGTSTVTSASAKTTPSPVPLAPGSAQAQNSMV 143

Db 2 TLRAEDTGIYC--TGIYYHPWFAYMGQGLTVLTVSAAKTAPSVYPLAVCGDITGSSV 59

QY 144 TLGCLVKGYPBPVTVTNWSGSLSSGVHTFPFPAVLQSDLYTLSSVTVPSSTWSPSETVTCN 203

Db 60 TLGCLVKGYPBPVTVTNWSGSLSSGVHTFPFPAVLQSDLYTLSSVTVTSSTWSPQSITCN 119

QY 204 VAHPASSTKVDKIVPRDSGGPSEK 228

Db 120 VAHPASSTKVDKIEPR---GPTIK 141

RESULT 60

S41374

single chain Fv antibody - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

C:Accession: S41374

R:Artechenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.

submitted to the EMBL Data Library, January 1994

A:Description: Construction and functional characterization of a single chain Fv antibody

A:Reference number: S41374

A:Accession: S41374

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-249 <ART>

A:Cross-references: UNIPARC:UPI000017C74A; EMBL:Z29480

Query Match 15.0%; Score 529.5; DB 2; Length 249;

Best Local Similarity 25.7%; Pred. No. 7.9e-21;

Matches 147; Conservative 41; Mismatches 54; Indels 331; Gaps 9;

QY 1 EVLOQSGDPLVKPGASVKISCKASGYSTGYMHVWVKSPGKLEWIGRINPNNGVTLY 60

Db 1 QVLOQSGAELVRPGASVLSCTASGTFKDDYIHWVKRPEKLEWIAIAPASGVKY 60

QY 61 NQKFKDKATLVKDSSTAYMELRLSTSDSAVYYCA-RSTMITNVMDYWGQGSTVTVS 119

Db 61 VRFQDKAITADTSNTAYLLSSITSEDTAVYYCARRDTLYTS--LGWGGQGSIVTVS 118

QY 120 SAKTTPPSVYPLAPGSAQTNSMVTLGCLVKGYPFPEVTVTNWSGSLSGVHTFPVLOS 179

Db 119 S-----RGGG----- 123

QY 180 DLYTLSSVTVPSSTWSPSETVCNVAHPASSTKVDKKIVPRDSGGPSEKSEINEKDLRK 239

Db 124 -----SGG----- 126

QY 240 KSELQGTALGNLKQIYYYNKAITSSSEKSADQPLTNTLLFKGFFTGHPPWYNDLLVLDGST 299

Db 127 ----- 126

QY 300 AATSEYEGSDVLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGK 359

Db 127 -----GG----- 131

QY 360 QITVPIDKVKTSKKEVTQELDLQAHYHLGKFGVNSDSFGCKVQVGLIVFHSSEGSIV 419

Db 132 -----GG----- 133

QY 420 SYDLFDAQGYPTLLRIYRDNTTISSTLSISLYLTTYSIVMTQPTSLVLSAGDRVTI 479

Db 134 -----SDIELTQSPSPVWVTPGESVSI 155

QY 480 TKCASQSV-----SNDAVYQQKPGQSKLLISYTSRSVAGVDPDRFSGGSGYGTDFLTLS 534

Db 156 SCRSSKSLLYSDGSLYFLWFLQRPQSGSPQLLIYRMSNLASGVDPDRFSGSGSGTSFTLRIS 215

QY 535 SVQAEAAVYFCOODYNSPPTFGGKLEIKRA 567

Db 216 RVEAEDVGVTYCMQHREYPLTFGAGTKLEIKRA 248

RESULT 61

PN0444

Ig heavy chain V region precursor - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C:Accession: PN0444

R:Kaluza, B.; Betz, G.; Shao, H.; Diamantstein, T.; Weidle, U.H.

Gene 122, 321-328, 1992

A:Title: A general method for chimeraization of monoclonal antibodies by inverse polymerase

A:Reference number: PN0444; MUID:93138402; PMID:1339379

A:Accession: PN0444

A:Molecule type: mRNA

A:Residues: 1-150 <KAL>

A:Cross-references: UNIPARC:UPI0000176A08; GB:I02346

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-150/Product: Ig heavy chain V region #status predicted <MAT>

F:20-117/Domain: variable region <VRG>

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 15.0%; Score 527; DB 2; Length 150;

Best Local Similarity 79.7%; Pred. No. 5.6e-21;

Matches 106; Conservative 4; Mismatches 21; Indels 2; Gaps 1;

QY 1 EVLOQSGDPLVKPGASVKISCKASGYSTGYMHVWVKSPGKLEWIGRINPNNGVTLY 60

Db 20 EVLOQFGAELVKPGTSVKISCKASGYIFTDYNMDVWVKSHGKSLWIGDIDPNFSSSY 79

QY 61 NQKFKDKATLVKDSSTAYMELRLSTSDSAVYYCARSTMITNVMDYWGQGSTVTVSS 120

Db 80 NQKFKGKATLVKDSSTAYMELRLSTSEDTAVYYCARGGF--PYGMDYWGQGSTVTVSS 137

QY 121 AKTTPPSVYPLAP 133

Db 138 AKTTPPSVYPLAP 150

RESULT 62

A46507

Ig alpha chain - chicken

C:Species: Gallus gallus (chicken)

C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999

C:Accession: A46507

R:Mansikka, A.

J:Immunol. 149, 855-861, 1992

A:Title: Chicken IGA H chains. Implications concerning the evolution of H chain genes.

A:Reference number: A46507; MUID:92340889; PMID:1634774

A:Accession: A46507

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-585 <MAN>

A:Cross-references: UNIPARC:UPI0000176F32; GB:S40610; NID:g251907; PID:g251908

A>Note: sequence inconsistent with the nucleotide translation

A:Note: sequence extracted from NCBI backbone (NCBIN:109906, NCBIIP:109907)

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 14.7%; Score 516.5; DB 2; Length 585;

Best Local Similarity 24.4%; Pred. No. 1.1e-19;

Matches 174; Conservative 99; Mismatches 228; Indels 211; Gaps 25;

QY 2 VOLQSGDPLVKPGASVKISCKASGYSTGYMHVWVKSPGKLEWIGRINPNNGVTLYN 61

Db 21 VTLDSEGGGLQTFGGALSLVCKASGFTFSYSGNWRQAPGKLEWVAGIDDDGSGTGYG 80

QY 62 QKFQDKATLVKDSSTAYMELRLSTSDSAVYYCARSTMITNVY---MDYWGQGSTVTV 118

Db 81 PAVQGRATISRDNGQSTVRLQLNNLRAEDTATYYCAKASGCCACAGSIDAWHGTEVIV 140

QY 119 SSAKTTPPSVYPLAPGSAQTNSMVTLGCLVKGYPFPEVTVTNWSGSL--SSGVHTFPVAV 176

Db 141 SSASASRPTLYQLLPLPFDPCPDNVTIGCLVTSFLPPPTVTVTTGGAADATATVSLPVA 200

Db	93	KENFKGRTATVTDKSSSTVYMQLSLTSSEDSAVYYCAREGGRCN-SLDYWGQGTSVNVSS	151
QY	121	AKTTPSPVYPLAPG	134
Db	152	AKTTPSPVYPLAPG	165
RESULT 66			
A27609			
Ig heavy chain precursor V region (I29) - mouse			
C:Species: Mus musculus (house mouse)			
C:Date: 15-Dec-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999			
C:Accession: A27609			
R:Klein, D.; Nieuwkoop, J.; Sirlin, S.; Stavnezer, J.			
J. Immunol. 140, 1676-1684, 1988			
A:Title: I.29 lymphoma cells express a nonmutated V-H gene before and after H chain switch			
A:Reference number: A27609; MUID:88154467; PMID:3126234			
A:Accession: A27609			
A:Molecule type: DNA			
A:Residues: 1-139 <KLE>			
A:Cross-references: UNIPARC:UPI0000114D5D; EMBL:M19401; NID:g195441; PIDN:AAA38303.1; PID:9			
C:Genetics: 16/1			
C:Superfamily: immunoglobulin V region; immunoglobulin homology			
C:Keywords: heterotetramer; immunoglobulin			
F:1-19/Domain: signal sequence #status predicted <SIG>			
F:20-139/Product: Ig heavy chain V region I29 #status predicted <VAR>			
F:34-117/Domain: immunoglobulin homology <IMM>			
Query Match 14.4%; Score 506; DB 2; Length 139;			
Best Local Similarity 80.8%; Pred. No. 6.3e-20;			
Matches 97; Conservative 7; Mismatches 16; Indels 0; Gaps 0;			
QY	1	EVLOQSGPDLVKPGASVKISCKASGYSTGYMHVWKSPGKLEWIGRINPNNGVTLY	60
Db	20	EVLOQSGPELVKPGASVKISCKASGYSTGYMHVWKSPGKLEWIGINPNNDYTSY	79
QY	61	NQKFKDKATLTVDKSSSTAYMELRLSLTSEDSAVYYCARSTMTITNYMDYWGQGTSTVVS	120
Db	80	NQKFKGKATLTVDKSSSTAYMQLSLTSEDSAVYYCARYSYAYMDYWGQGTSTVVS	139
RESULT 67			
I37267			
Ig heavy chain V region (I29) - mouse			
C:Species: Mus musculus (house mouse)			
C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996			
C:Accession: I37267			
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.			
J. Biol. Chem. 266, 6607-6613, 1991			
A:Title: Heavy and light chain variable region sequences and antibody properties of anti			
A:Reference number: A38740; MUID:91177923; PMID:1706720			
A:Accession: I37267			
A:Status: preliminary; not compared with conceptual translation			
A:Molecule type: mRNA			
A:Residues: 1-128 <RUF>			
A:Cross-references: UNIPARC:UPI0000176C52			
C:Superfamily: immunoglobulin V region; immunoglobulin homology			
C:Keywords: heterotetramer; immunoglobulin			
F:19-102/Domain: immunoglobulin homology <IMM>			
Query Match 14.3%; Score 503; DB 2; Length 128;			
Best Local Similarity 79.7%; Pred. No. 8.2e-20;			
Matches 98; Conservative 7; Mismatches 14; Indels 4; Gaps 1;			
QY	2	VOLOQSGPDLVKPGASVKISCKASGYSTGYMHVWKSPGKLEWIGRINPNNGVTLYN	61
Db	6	VOLOQSGPELVKPGASVKISCKTSGTFTFYTHVHWKQSHGKSLWIGINPNNGTSYN	65
QY	62	QKFKDKATLTVDKSSSTAYMELRLSLTSEDSAVYYCARSTMTITNYMDYWGQGTSTV	117
Db	66	QKFKGKATLTVDKSSSTAYMELRLSLTSEDSAVYYCARRGLTTVWAKSYFYDWGQGTTLT	125

QY	118	VSS	120
Db	126	VSS	128
RESULT 68			
PS0057			
Ig heavy chain precursor V region (PAR) - mouse			
C:Species: Mus musculus (house mouse)			
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Jun-2000			
C:Accession: PS0057			
R:Yaota, Y.; Takahashi, M.; Azuma, C.; Kanai, Y.; Honjo, T.			
J. Biochem. 104, 337-343, 1988			
A:Title: Biased expression of variable region gene families of the immunoglobulin heavy			
A:Reference number: PS0057; MUID:89197817; PMID:2467902			
A:Accession: PS0057			
A:Molecule type: DNA			
A:Residues: 1-135 <YAO>			
A:Cross-references: UNIPARC:UPI000011B257; GB:D00307; NID:g220448; PIDN:BAA00213.1; PID:9			
A:Note: the authors translated the codon AAG for residue 32 as Asn and GAC for 92 as Gly			
C:Comment: the gene encoding this protein was isolated from a hybridoma that produces an			
C:Superfamily: immunoglobulin V region; immunoglobulin homology			
C:Keywords: heterotetramer; immunoglobulin			
F:1-19/Domain: signal sequence #status predicted <SIG>			
F:20-135/Product: Ig heavy chain V region PAR #status predicted <MAT>			
F:34-117/Domain: immunoglobulin homology <IMM>			
Query Match 14.3%; Score 502; DB 2; Length 135;			
Best Local Similarity 82.5%; Pred. No. 9.8e-20;			
Matches 99; Conservative 6; Mismatches 11; Indels 4; Gaps 1;			
QY	1	EVLOQSGPDLVKPGASVKISCKASGYSTGYMHVWKSPGKLEWIGRINPNNGVTLY	60
Db	20	EVLOQSGPELVKPGASVKISCKASGYSTGYMHVWKSPGKLEWIGRINPNNGDTFY	79
QY	61	NQKFKDKATLTVDKSSSTAYMELRLSLTSEDSAVYYCARSTMTITNYMDYWGQGTSTVVS	120
Db	80	NQKFKGKATLTVDKSSSTAHMELRLSLTSEDSAVYYCAR----LNVRGAYWGQGTTLTVSA	135
RESULT 69			
A34891			
Ig heavy chain precursor V region - ladyfish			
C:Species: Elops saurus (ladyfish)			
C:Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 21-Jul-2000			
C:Accession: A34891			
R:Ameniya, C.T.; Litman, G.W.			
Proc. Natl. Acad. Sci. U.S.A. 87, 811-815, 1990			
A:Title: Complete nucleotide sequence of an immunoglobulin heavy-chain gene and analysis			
A:Reference number: A34891; MUID:90138916; PMID:2105490			
A:Accession: A34891			
A:Status: preliminary			
A:Molecule type: mRNA			
A:Residues: 1-568 <AME>			
A:Cross-references: UNIPARC:UPI0000114B5D; GB:M26182; NID:g213134; PIDN:AAA49238.1; PID:9			
C:Superfamily: immunoglobulin C region; immunoglobulin homology			
C:Keywords: heterotetramer; immunoglobulin			
F:33-116/Domain: immunoglobulin homology <IMM>			
Query Match 14.1%; Score 495.5; DB 2; Length 568;			
Best Local Similarity 22.8%; Pred. No. 1.3e-18;			
Matches 159; Conservative 109; Mismatches 225; Indels 203; Gaps 24;			
QY	4	IQQSGPDLVKPGASVKISCKASGYSTGYMHVWKSPGKLEWIGRINPNNGVTLYNQK	63
Db	22	LTSEPAVKKPGESHKLTCTASGFTFSNYMGWIRQAPGKLEWLATLKNSAEYYIS	81
QY	64	FKDKATLTVDKSSSTAYMELRLSLTSEDSAVYYCARSTMTITNYMDYWGQGTSTVVS	123
Db	82	VKGRFTIGRDNKNQLYQMNSLRADTAVYYCAR--VYGYWAFDWGRTWVTVTGEQ	139
QY	124	TPPSVYPLAPGSAATNSMVTLCGLVKGYFPFVTVTNWNSGLS-SGVHTFPFVAVLQSDLY	182

Db 140 ASPTVPFLV--SCGATSGYVTMGICGKYLPLDLSLTFWSKSDTLTDYLYQPVLSGGKY 197
QY 183 TLSSSVTPSSSTWPSSTVTCNVAHPASSTKVDKIVPRDSGSPSEKSEENEXDLRKSE 242
Db 198 D-----RVSH-----ARTEGDFKSAE 215
QY 243 LQ-GTALGNLKIYYNSKAITSE--KSADQFLTNLLPKGFTGHPWYNLDLLVLGST 299
Db 216 FKCTTELGGKK-----TPVVIKPEPKPPRPQVLSIMT-----PSQEELTLN--- 258
QY 300 AATSEYEGSSVDLYGAYGYQCAGGTPNKTCACMGVGTLLHNNRLTEKKVPINLMI-DG 358
Db 259 -KTATFACLATDYPKGHSFK-----MURDG 283
QY 359 KQTVTPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKQVQRGLIVFHSSEGST 418
Db 284 KEVTDGIATLTCQKK-----GDKSFATSSFLQASESQW 317
QY 419 VSYD-----LFDAGQVDPDLLRIYRDNWTTISSTLSISLYVTTSIVMTQTPTSLLSVA 473
Db 318 KRLDGTFTCFIQEGETE-----QTVKYSSAECSPQAQIDAKISPTPEELFLQ- 367
QY 474 GDRVTTTCASQSVS--NDVAV--YQKPGQ-----SPKLISYTSRRYAGVDPDRFG 522
Db 368 -QRTLTCTKITGVDGVRNVTVWEGSEVRVQGFDEQRMISKLLIDYE----- 413
QY 523 SGYGTDTLTISSVOAEDAAVYFCQDYNSSPPT-----FGGGTKLEIKRADAAPTV 573
Db 414 -----EWKNTREYTCVKVEHSDLPFLTSYRRCGGKWQ-----SPTV 451
QY 574 SIPTPSSEQITSGASVVCFLNNFYPKDINVKWKIDGSEQRQNGVLSWTDQDSKDSYSM 633
Db 452 FILAP-AEQRLNSTVTLLICVAKDFYEQVLISMLVDDQPVETDV--PTTEVWTEGTYSV 508
QY 634 SSTLTITKDEYERHNSYTCATHKTSPIVKSFN 669
Db 509 FSQLTIPASDWDSGVVYSCAVHHETVMSVVKTVR 544

RESULT 70

C37267

Ig heavy chain V region (Py69) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000

C:Accession: C37267

R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.

J. Biol. Chem. 266, 6607-6613, 1991.

A:Title: Heavy and light chain variable region sequences and antibody properties of anti

A:Reference number: A38740; MUID:91177923; PMID:1706720

A:Accession: C37267

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-128 <RUF>

A:Cross-references: UNIPARC:UPI0000176B3A

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:19-102/Domain: immunoglobulin homology <IMM>

Query Match 14.1%; Score 495; DB 2; Length 128;
Best Local Similarity 77.2%; Pred. No. 2.1e-19;
Matches 95; Conservative 9; Mismatches 15; Indels 4; Gaps 1;

QY 2 VQLQQSGPDLVKPGASVKISCKASGYSTFGYMHVWKQSPGKGLEWIGRINPNNGVTLYN 61

Db 6 VQLQQSGPELVKPGASVKISCKTSGYFTFTYTHWVWKQSHGKSLWIGRINPNNGGSTYN 65

QY 62 QKFKDKATLTVDKSSSTAYMELSLTSDSAVYVCAR----STMITNYMDYWGQGTSTV 117

Db 66 QKFKGKATLTVDKSSSTAYMELSLTSDSAVYVCARRPGYGNVYTSYYPDYWGQGTTLT 125

QY 118 VSS 120

Db 126 VSS 128

RESULT 71

PS0024

Ig heavy chain precursor V region (6A4) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 22-Nov-1996

C:Accession: PS0024

R:Marget, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Domdey, H.

Gene 74, 335-345, 1988

A:Title: Cloning and characterization of cDNAs coding for the heavy and light chains of

A:Reference number: PS0023; MUID:89232725; PMID:3149944

A:Accession: PS0024

A:Molecule type: mRNA

A:Residues: 1-139 <MAR>

A:Cross-references: UNIPARC:UPI0000176D41

A:Experimental source: strain BALB/c

C:Comment: This chain is obtained from an IgG2a monoclonal antibody against Pseudomonas

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin; pyroglytamic acid

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-139/Domain: Ig heavy chain V region #status predicted <IGV>

F:34-117/Domain: immunoglobulin homology <IMM>

F:20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted

Query Match 14.0%; Score 492; DB 2; Length 139;
Best Local Similarity 77.5%; Pred. No. 3.4e-19;
Matches 93; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 EVLQSQGPDLVKPGASVKISCKASGYSTFGYMHVWKQSPGKGLEWIGRINPNNGVTLY 60

Db 20 QVQLQQSGAELAKPGASVKRMSKASGYFTAYWMHWKQRPQGQGLEWIGVINPTGYTEY 79

QY 61 NQKFKDKATLTVDKSSSTAYMELSLTSDSAVYVCARSTMITNYMDYWGQGTSTVSS 120

Db 80 NQKFKDKATLTADKSSSTAYMQLSLTSDSAVYCTRYYNYEGAMDYWGQGTSTVSS 139

RESULT 72

G2MSA

Ig gamma-2a chain C region, secreted form (allele a) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1980 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004

C:Accession: A02152; A32657; A32658

R:Sikorav, J.L.; Aufray, C.; Rougeon, F.

Nucleic Acids Res. 8, 3143-3155, 1980

A:Title: Structure of the constant and 3' untranslated regions of the murine Balb/C gamma

A:Reference number: A02152; MUID:81076554; PMID:6777755

A:Accession: A02152

A:Molecule type: mRNA

A:Residues: 1-330 <SIK>

A:Cross-references: UNIPROT:P01863; UNIPARC:UPI00000272CF; GB:V00798; MID:g51835; PIDN:CI

R:Yamawaki-Kataoka, Y.; Miyata, T.; Honjo, T.

Nucleic Acids Res. 9, 1365-1381, 1981

A:Title: The complete nucleotide sequence of mouse immunoglobulin gamma 2 A gene and evol

A:Reference number: A32657; MUID:81198976; PMID:6262729

A:Accession: A32657

A:Molecule type: DNA

A:Residues: 1-330 <YAM>

A:Cross-references: UNIPARC:UPI00000272CF; GB:J00470

A:Note: the sequence was determined from the germline gene

R:Ollo, R.; Auffray, C.; Mochamps, C.; Rougeon, F.

Proc. Natl. Acad. Sci. U.S.A. 78, 2442-2446, 1981

A:Title: Comparison of mouse immunoglobulin gamma-2A and gamma-2B chain genes suggests t

A:Reference number: A32658; MUID:81223894; PMID:6787604

A:Accession: A32658

A:Molecule type: DNA

A:Residues: 1-330 <OLL>

A:Cross-references: UNIPARC:UPI00000272CF

A:Note: the sequence was determined from the germline gene

R:Lyons, A.; Fougereau, M.; Rocca-Serra, J.

Eur. J. Biochem. 43, 423-435, 1974

A:Title: Determination of the primary structure of a mouse IgG2a immunoglobulin: amino-
A:Reference number: A32659; MUID:74175517; PMID:4831970
A:Contents: annotation; myeloma protein MOPC 173
A:Note: this is one paper in a series reporting the sequence; for additional references,
A:Note: this sequence differs from that shown at a number of positions
R:de Preval, C.; Fougereau, M.
Eur. J. Biochem. 30, 452-462, 1972
A:Title: Determination of the primary structure of a mouse gammaG2a immunoglobulin. Ident
A:Reference number: A32660; MUID:73056887; PMID:4565406
A:Contents: annotation; MOPC 173, disulfide bonds
C:Genetics:
A:Introns: 1/1; 98/1; 114/1; 224/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob
F:20-84/Domain: immunoglobulin homology <IM1>
F:98-113/Region: hinge
F:137-206/Domain: immunoglobulin homology <IM2>
F:243-310/Domain: immunoglobulin homology <IM3>
F:15/Disulfide Bonds: interchain (to light chain) #status experimental
F:27-82,144-204,250-308/Disulfide bonds: #status experimental
F:107,110,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 14.0%; Score 491.5; DB 1; Length 330;
Best Local Similarity 26.4%; Pred. No. 1.1e-18;
Matches 151; Conservative 43; Mismatches 110; Indels 267; Gaps 13;
QY 121 AKTTSPVYPLAPGSAQAOTNSMTLGLVKGYFPEPTVTWNSGSLSSGVHFFPAVLQSD 180
DB 1 AKTTAPSVYPLAPVCGDGTGSSVTLGLVKGYFPEPTVTWNSGSLSSGVHFFPAVLQSD 60
QY 181 LYTLSSTVTPSPSTWSPSETVTCNVAHPASSTKVKKIVPRDSGGPSEKEEINEKDLRKK 240
DB 61 LYTLSSTVTPSTWSPSQSITCNVAHPASSTKVKKIEPR---GPTIKPCP----- 108
QY 241 SELQGTALGNLQIYYNNSKAITSSSEKSDQFLTNTLLFKGPTGHPYNDLLVDLGSTA 300
DB 109 ----- 108
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLTBEKKVPIINLWDGKQ 360
DB 109 -----PCKCPAPN-----LLGGPSVF----- 124
QY 361 TTVPIDKVTSKKEVTVQELDLOARHYLHGKFGLYNSDSFGGKVQGLIVFHSSEGSTVS 420
DB 125 -----IPPPKIKDVLMI---SLSPIVT 143
QY 421 YDLFDAQGOYPTDLLRIYRDNTTISSTLSISLYLTTISIVMTQTPTSLLSVAGDRVITIT 480
DB 144 CVVDVSEDDPD-----VOISWFVNNVEVHTAQTOT----- 174
QY 481 CKASQSVSNDVAWYQKPGSQPKLLISYTSRYAGVDRFSGSGYGTDFTLTISSSVQAE 540
DB 175 -----HREDYNSILRVV----- 186
QY 541 AAVYFCQDYNPPTFGGKTLEIKRAD-----AAPTYSIPPPSEQT 584
DB 187 SALPIQHODWMSGKEF---KCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPEEEMT 242
QY 585 SGGASVVCFLNFPYKDIYKWKIDGSRQN-----GVLSNMTDQDSKDSYMSSTLT 639
DB 243 KQVTLTVMVTFMPEDIIVETVNNKGTLEYNKTEPFLVDS-----DGSFMYSKLRV 295
QY 640 TKDEYERHNSYTCETHK-TSTSPIVKSFRN 669
DB 296 EKKWVERNYSYCSVVHEGLNHHHTTKSFR 326
RESULT 73
G2MSAM
Ig gamma-2a chain C region, membrane-bound form - mouse

C:Species: Mus musculus (house mouse)
C>Date: 19-Feb-1984 #sequence revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: A02154; B32657; I57809
R:Yamawaki-Kataoka, Y.; Nakai, S.; Miyata, T.; Honjo, T.
Proc. Natl. Acad. Sci. U.S.A. 79, 2623-2627, 1982
A:Title: Nucleotide sequences of gene segments encoding membrane domains of immunoglobuli
A:Reference number: A02154; MUID:82222190; PMID:6283537
A:Accession: A02154
A:Molecule type: DNA
A:Residues: 329-399 <YAM>
A:Cross-references: UNIPROT:P01865; UNIPARC:UPI00001737A4; GB:J00471
A:Note: the sequence was determined from the germline gene
R:Yamawaki-Kataoka, Y.; Miyata, T.; Honjo, T.
Nucleic Acids Res. 9, 1365-1381, 1981
A:Title: The complete nucleotide sequence of mouse immunoglobulin gamma 2 A gene and evol
A:Reference number: A32657; MUID:81198976; PMID:6262729
A:Accession: B32657
A:Molecule type: DNA
A:Residues: 1-329, 'K' <YA2>
A:Cross-references: UNIPARC:UPI00000272CF
R:Hall, B.; Milcarek, C.
Mol. Immunol. 26, 819-826, 1989
A:Title: Sequence and polyadenylation site determination of the murine immunoglobulin gan
A:Reference number: I57809; MUID:90097953; PMID:2513486
A:Accession: I57809
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 373-399 <RES>
A:Cross-references: UNIPARC:UPI000011508C; GB:M35032; NID:gl94478; PIDN:AAA37919.1; PID:f
C:Comment: The sequence of residues 1-328 was assumed to be identical with the correspond
C:Comment: Cell lines producing IgG contain two mRNA species for Ig gamma chains. The ma
hat it contains an alternative 3' end, encoded in separate exons, that is homologous wit
C:Genetics:
A:Introns: 1/1; 98/1; 114/1; 224/1; 329/1; 372/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobul
F:137-206/Domain: immunoglobulin homology <IM1>
F:346-363/Domain: transmembrane #status predicted <TM>
F:364-399/Domain: intracellular #status predicted <INT>
F:180/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 14.0%; Score 491.5; DB 1; Length 399;
Best Local Similarity 26.4%; Pred. No. 1.3e-18;
Matches 151; Conservative 43; Mismatches 110; Indels 267; Gaps 13;
QY 121 AKTTSPVYPLAPGSAQAOTNSMTLGLVKGYFPEPTVTWNSGSLSSGVHFFPAVLQSD 180
DB 1 AKTTAPSVYPLAPVCGDGTGSSVTLGLVKGYFPEPTVTWNSGSLSSGVHFFPAVLQSD 60
QY 181 LYTLSSTVTPSPSTWSPSETVTCNVAHPASSTKVKKIVPRDSGGPSEKEEINEKDLRKK 240
DB 61 LYTLSSTVTPSTWSPSQSITCNVAHPASSTKVKKIEPR---GPTIKPCP----- 108
QY 241 SELQGTALGNLQIYYNNSKAITSSSEKSDQFLTNTLLFKGPTGHPYNDLLVDLGSTA 300
DB 109 ----- 108
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLTBEKKVPIINLWDGKQ 360
DB 109 -----PCKCPAPN-----LLGGPSVF----- 124
QY 361 TTVPIDKVTSKKEVTVQELDLOARHYLHGKFGLYNSDSFGGKVQGLIVFHSSEGSTVS 420
DB 125 -----IPPPKIKDVLMI---SLSPIVT 143
QY 421 YDLFDAQGOYPTDLLRIYRDNTTISSTLSISLYLTTISIVMTQTPTSLLSVAGDRVITIT 480
DB 144 CVVDVSEDDPD-----VOISWFVNNVEVHTAQTOT----- 174
QY 481 CKASQSVSNDVAWYQKPGSQPKLLISYTSRYAGVDRFSGSGYGTDFTLTISSSVQAE 540
DB 481 CKASQSVSNDVAWYQKPGSQPKLLISYTSRYAGVDRFSGSGYGTDFTLTISSSVQAE 540

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OM protein - protein search, using sw model

Run on: February 15, 2006, 20:08:30 ; Search time 221.277 Seconds
(without alignments)
2142.628 Million cell updates/sec

Title: US-09-900-766-1

Perfect score: 3522

Sequence: 1 EVOLQSGDPLVKPGASVKI.....EATHKTSTPIVKSFNRNES 672

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Uniprot_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1107	31.4	257	1	ETXE_STAAU
2	1010	28.7	463	2	Q99LC4_MOUSE
3	983.5	27.9	458	2	Q5BJZ2_RAT
4	975	27.7	472	2	Q6PUJ7_MOUSE
5	951	27.0	261	2	Q5PSP6_STAAU
6	948	26.9	257	1	ETXA_STAAU
7	948	26.9	257	1	ETXA_STAAU
8	948	26.9	257	2	Q6GY77_STAAS
9	948	26.9	260	2	Q931M4_STAAU
10	945.5	26.8	465	2	Q6PUB2_MOUSE
11	945	26.8	468	2	Q5G9W9_MOUSE
12	944.5	26.8	458	2	Q5BK05_RAT
13	941	26.7	240	2	Q521L6_MOUSE
14	938	26.6	238	2	Q58EU4_MOUSE
15	935	26.6	257	2	Q6GFA8_STAAU
16	929.5	26.4	477	2	Q58E56_MOUSE
17	924.5	26.2	473	2	Q9D814_MOUSE
18	918	26.1	260	2	Q99SU3_STAAU
19	910	25.8	238	2	Q66U57_MOUSE
20	904	25.7	241	2	Q632X4_MOUSE
21	901.5	25.6	219	2	Q652C0_MOUSE
22	900.5	25.6	464	2	Q6PF95_MOUSE
23	899.5	25.5	470	2	Q7TWK1_MOUSE
24	898	25.5	219	2	Q6XZE9_STAAU
25	897	25.5	468	2	Q505N9_MOUSE
26	891	25.3	467	2	Q4VBH1_RAT
27	888.5	25.2	474	2	Q8R3H6_MOUSE
28	886	25.2	236	2	Q7TS98_MOUSE
29	880.5	25.0	237	2	Q569Y8_MOUSE
30	879.5	25.0	239	2	Q58EU8_MOUSE
31	871	24.7	236	2	Q521L9_MOUSE

32	870.5	24.7	235	2	Q5XEY8_MOUSE	Q5xfy8 mus musculus
33	867.5	24.6	235	2	Q58EV6_MOUSE	Q58ev6 mus musculus
34	867.5	24.6	458	2	Q65ZQ1_HUMAN	Q65zq1 homo sapien
35	858.5	24.4	234	2	Q5XKG4_MOUSE	Q5xkg4 mus musculus
36	858.5	24.4	468	2	Q569B4_RAT	Q569b4 rattus norv
37	852	24.2	461	2	Q5M7V3_RAT	Q5m7v3 rattus norv
38	851	24.2	465	2	Q510J0_RAT	Q510j0 rattus norv
39	836.5	23.8	476	2	Q569X1_MOUSE	Q569x1 mus musculus
40	832.5	23.6	458	2	Q5M842_RAT	Q5m842 rattus norv
41	815.5	23.2	471	2	Q66K04_MOUSE	Q66k04 mus musculus
42	803	22.8	464	2	Q6PIP8_MOUSE	Q6pip8 mus musculus
43	803	22.8	473	2	Q91205_MOUSE	Q91205 mus musculus
44	791	22.5	234	2	Q4KM66_RAT	Q4km66 rattus norv
45	787	22.3	234	2	Q5M838_RAT	Q5m838 rattus norv
46	775	22.0	268	2	Q76LS7_STAAU	Q76ls7 staphylococ
47	768	21.8	268	2	Q85217_STAAU	Q85217 staphylococ
48	765	21.7	154	2	Q6R2G0_STAAU	Q6r2g0 staphylococ
49	755.5	21.5	518	2	Q6N030_HUMAN	Q6n030 homo sapien
50	750	21.3	469	2	Q7Z7P5_HUMAN	Q7z7p5 homo sapien
51	747.5	21.2	469	2	Q5M839_RAT	Q5m839 rattus norv
52	741.5	21.1	470	2	Q4G060_RAT	Q4g060 rattus norv
53	741.5	21.1	480	2	Q6PJF1_HUMAN	Q6pjf1 homo sapien
54	741	21.0	519	2	Q5EBM2_HUMAN	Q5ebm2 homo sapien
55	734	20.8	236	2	Q6GMW1_HUMAN	Q6gmw1 homo sapien
56	733	20.8	475	2	Q6N095_HUMAN	Q6n095 homo sapien
57	721.5	20.5	472	2	Q6N089_HUMAN	Q6n089 homo sapien
58	719	20.4	469	2	Q569F4_HUMAN	Q569f4 homo sapien
59	717.5	20.4	478	2	Q6PI81_HUMAN	Q6pi81 homo sapien
60	715	20.3	465	2	Q6GMX6_HUMAN	Q6gmx6 homo sapien
61	714	20.3	475	2	Q5RE17_PONPY	Q5re17 pongo pygma
62	712	20.2	234	2	Q5EFE6_HUMAN	Q5efe6 homo sapien
63	710	20.2	236	2	Q6PIH7_HUMAN	Q6pih7 homo sapien
64	707.5	20.1	235	2	Q6GMW0_HUMAN	Q6gmw0 homo sapien
65	706	20.0	236	2	Q6GMX0_HUMAN	Q6gmx0 homo sapien
66	705	20.0	236	2	Q6GMX8_HUMAN	Q6gmx8 homo sapien
67	703.5	20.0	470	2	Q68CN4_HUMAN	Q68cn4 homo sapien
68	699	19.8	236	2	Q6GMX9_HUMAN	Q6gmx9 homo sapien
69	698.5	19.8	470	2	Q6PUA4_HUMAN	Q6puj4 homo sapien
70	697.5	19.8	466	2	Q6IN78_HUMAN	Q6in78 homo sapien
71	696	19.8	236	2	Q502W4_HUMAN	Q502w4 homo sapien
72	694.5	19.7	235	2	Q6GMV9_HUMAN	Q6gmv9 homo sapien
73	694	19.7	475	2	Q6MZQ6_HUMAN	Q6mzq6 homo sapien
74	691	19.6	234	2	Q7Z473_HUMAN	Q7z473 homo sapien
75	689	19.6	236	2	Q6P5S8_HUMAN	Q6p5s8 homo sapien
76	689	19.6	236	2	Q7Z3Y4_HUMAN	Q7z3y4 homo sapien
77	689	19.6	465	2	Q6P6C4_HUMAN	Q6p6c4 homo sapien
78	689	19.6	475	2	Q6GMW7_MOUSE	Q6gmw7 homo sapien
79	687.5	19.5	617	2	Q4KML5_MOUSE	Q4kml5 mus musculus
80	687	19.5	473	2	Q6MZV7_HUMAN	Q6mzv7 homo sapien
81	687	19.5	475	2	Q5EFE5_HUMAN	Q5efe5 homo sapien
82	686.5	19.5	482	2	Q7Z351_HUMAN	Q7z351 homo sapien
83	686	19.5	544	2	Q6PJ95_HUMAN	Q6pj95 homo sapien
84	684.5	19.4	235	2	Q6PJF2_HUMAN	Q6pjf2 homo sapien
85	684	19.4	236	2	Q6PIT5_HUMAN	Q6pit5 homo sapien
86	683.5	19.4	480	2	Q6N094_HUMAN	Q6n094 homo sapien
87	682	19.4	473	2	Q6P055_HUMAN	Q6p055 homo sapien
88	681.5	19.3	464	2	Q6MZU6_HUMAN	Q6mzu6 homo sapien
89	681.5	19.3	466	2	Q6N096_HUMAN	Q6n096 homo sapien
90	679	19.3	236	2	Q6PIL8_HUMAN	Q6pil8 homo sapien
91	678.5	19.3	476	2	Q6GMX1_HUMAN	Q6gmx1 homo sapien
92	669.5	19.0	239	2	Q8NEK0_HUMAN	Q8nek0 homo sapien
93	667	18.9	236	2	Q6PIH4_HUMAN	Q6pih4 homo sapien
94	666.5	18.9	470	2	Q7Z5W1_HUMAN	Q7z5w1 homo sapien
95	666	18.9	240	2	Q6PIH6_HUMAN	Q6pih6 homo sapien
96	665	18.9	481	2	Q6N097_HUMAN	Q6n097 homo sapien
97	662.5	18.8	473	2	Q8TC63_HUMAN	Q8tc63 homo sapien
98	654.5	18.6	239	2	Q8TCDD_HUMAN	Q8tcdd homo sapien
99	652	18.5	234	2	Q56919_HUMAN	Q56919 homo sapien
100	651.5	18.5	590	2	Q4V9V8_MOUSE	Q4v9v8 mus musculus
101	648	18.4	487	2	Q65ZL2_9MUR1	Q65zl2 mus sp. fv/
102	648	18.4	614	2	Q7TWT6_MOUSE	Q7twt6 mus musculus
103	646.5	18.4	239	2	Q6P491_HUMAN	Q6p491 homo sapien
104	643.5	18.3	560	2	Q4V801_XENLA	Q4v801 xenopus lae

105	641	18.2	521	2	Q8N4Y9_HUMAN	Q8N4Y9 homo sapien
106	640	18.2	476	2	Q6MXZ7_HUMAN	Q6mxz7 homo sapien
107	639	18.1	616	2	Q504M7_MOUSE	Q504m7 mus musculus
108	631	17.9	483	2	Q4VAB6_MOUSE	Q4vab6 mus musculus
109	619.5	17.6	488	2	Q8KOF2_MOUSE	Q8kof2 mus musculus
110	619	17.6	598	2	Q56BY0_RAT	Q56by0 rattus norv
111	618.5	17.6	482	2	Q8K172_MOUSE	Q8k172 mus musculus
112	618.5	17.6	613	2	Q8VCX7_MOUSE	Q8vcx7 mus musculus
113	612.5	17.4	591	2	Q4QQM0_RAT	Q4qqm0 rattus norv
114	611	17.3	258	1	ETXD_STAAU	ETXD23 staphylococ
115	609	17.3	584	2	Q61NK3_XENLA	Q61nk3 xenopus lae
116	606	17.2	243	2	Q7TQM2_MOUSE	Q7tqm2 mus musculus
117	602.5	17.1	488	2	Q91WR1_MOUSE	Q91wr1 mus musculus
118	598.5	17.0	417	2	Q6N093_HUMAN	Q6n093 homo sapien
119	589.5	16.7	585	2	Q6GPX4_XENLA	Q6gpx4 xenopus lae
120	587	16.7	244	2	Q65ZC8_HUMAN	Q65zc8 homo sapien
121	585	16.6	485	2	Q5BEM1_MOUSE	Q5bem1 mus musculus
122	594	16.6	593	2	Q61NM5_XENLA	Q61nm5 xenopus lae
123	593	16.6	481	2	Q91WT1_MOUSE	Q91wt1 mus musculus
124	576.5	16.4	243	2	Q6NTU5_XENLA	Q6ntu5 xenopus lae
125	575	16.3	589	2	Q5XHD5_XENLA	Q5xhd5 xenopus lae
126	573	16.3	481	2	Q8VCV5_MOUSE	Q8vcv5 mus musculus
127	572.5	16.3	555	2	Q5FW04_XENTR	Q5fw04 xenopus tro
128	570	16.2	498	2	Q6N041_HUMAN	Q6n041 homo sapien
129	566.5	16.1	480	2	Q8K0Z4_MOUSE	Q8k0z4 mus musculus
130	565.5	16.1	239	2	Q5HZC6_XENTR	Q5hzc6 xenopus tro
131	565	16.0	489	2	Q8VCX4_MOUSE	Q8vcx4 mus musculus
132	563.5	16.0	486	2	Q5HZY6_MOUSE	Q5hzy6 mus musculus
133	561	15.9	597	2	Q96BB9_HUMAN	Q96bb9 homo sapien
134	560	15.9	475	2	Q5FVP3_RAT	Q5fvp3 rattus norv
135	559	15.9	483	2	Q52L51_MOUSE	Q52l51 mus musculus
136	557	15.8	324	1	IGHG1_MOUSE	IGHG1 mus musculus
137	557	15.8	393	1	IGHI1_MOUSE	IGHI1 mus musculus
138	556	15.8	106	1	KAC_MOUSE	KAC_MOUSE
139	554	15.7	255	2	Q6KE05_MOUSE	Q6keb05 mus musculus
140	553	15.7	367	2	Q5M8X4_XENTR	Q5m8x4 xenopus tro
141	550.5	15.6	606	2	Q6GNW2_HUMAN	Q6gmn2 homo sapien
142	550	15.6	326	1	GCL_RAT	GCL_RAT
143	548	15.6	237	2	Q7S236_XENLA	Q7s236 xenopus lae
144	546.5	15.5	614	2	Q6DDQ7_XENLA	Q6ddq7 xenopus lae
145	545.5	15.5	480	2	Q9P089_HUMAN	Q9p089 homo sapien
146	545	15.5	597	2	Q9BQB8_HUMAN	Q9bqb8 homo sapien
147	542.5	15.4	500	2	Q6N091_HUMAN	Q6n091 homo sapien
148	540	15.3	208	2	Q6ZPB7_HUMAN	Q6zpb7 homo sapien
149	540	15.3	595	2	Q8WUX4_HUMAN	Q8wux4 homo sapien
150	540	15.3	597	2	Q9BU10_HUMAN	Q9bu10 homo sapien
151	540	15.3	597	2	Q6GNX5_HUMAN	Q6gnx5 homo sapien
152	540	15.3	625	2	Q96AA6_HUMAN	Q96aa6 homo sapien
153	539	15.3	322	1	GCA_RAT	GCA_RAT
154	537.5	15.3	613	2	Q8WUK1_HUMAN	Q8wuk1 homo sapien
155	535	15.2	145	2	Q924Q9_MOUSE	Q924q9 mus musculus
156	535	15.2	481	2	Q91WT3_MOUSE	Q91wt3 mus musculus
157	534	15.2	145	2	Q924Q6_MOUSE	Q924q6 mus musculus
158	533	15.1	136	2	Q7TPE3_MOUSE	Q7tpe3 mus musculus
159	527.5	15.0	484	2	Q91LA6_MOUSE	Q91la6 mus musculus
160	527	15.0	145	2	Q924R4_MOUSE	Q924r4 mus musculus
161	525.5	14.9	620	2	Q96EY0_HUMAN	Q96ey0 homo sapien
162	523.5	14.9	500	2	Q9BRV0_HUMAN	Q9brv0 homo sapien
163	519	14.7	145	2	Q924R1_MOUSE	Q924r1 mus musculus
164	518.5	14.7	146	2	Q924Q3_MOUSE	Q924q3 mus musculus
165	515	14.6	145	2	Q924P7_MOUSE	Q924p7 mus musculus
166	514	14.6	143	2	Q924R0_MOUSE	Q924r0 mus musculus
167	514	14.6	573	2	Q8WUJ8_HUMAN	Q8wu38 homo sapien
168	512.5	14.6	477	2	Q659B1_RAT	Q659b1 rattus norv
169	511.5	14.5	134	2	Q65ZR6_MOUSE	Q65zr6 mus musculus
170	509	14.5	189	2	Q56917_HUMAN	Q56917 homo sapien
171	508.5	14.4	117	2	Q9QXE9_MOUSE	Q9qxe9 mus musculus
172	507.5	14.4	142	2	Q924Q1_MOUSE	Q924q1 mus musculus
173	507	14.4	143	2	Q924P6_MOUSE	Q924p6 mus musculus
174	507	14.4	594	2	Q5FW13_XENTR	Q5fw13 xenopus tro
175	506.5	14.4	140	2	Q924R2_MOUSE	Q924r2 mus musculus
176	506	14.4	497	2	Q8WY24_HUMAN	Q8wy24 homo sapien
177	505.5	14.4	146	2	Q924R8_MOUSE	Q924r8 mus musculus

178	505	14.3	240	2	Q65ZC9_HUMAN	Q65zc9 homo sapien
179	504.5	14.3	496	2	Q96DK0_HUMAN	Q96dk0 homo sapien
180	504	14.3	615	2	Q569B6_RAT	Q569b6 rattus norv
181	502.5	14.3	168	2	Q8VDC9_MOUSE	Q8vdc9 mus musculus
182	502.5	14.3	591	2	Q51OL9_RAT	Q51ol9 rattus norv
183	501	14.2	493	2	Q6GMX2_HUMAN	Q6gmx2 homo sapien
184	500	14.2	145	2	Q924Q7_MOUSE	Q924q7 mus musculus
185	500	14.2	145	2	Q924R3_MOUSE	Q924r3 mus musculus
186	498.5	14.2	117	2	Q9QXF0_MOUSE	Q9qxf0 mus musculus
187	498.5	14.2	146	2	Q924Q8_MOUSE	Q924q8 mus musculus
188	497	14.1	576	2	Q6P4I8_HUMAN	Q6p4i8 homo sapien
189	496	14.1	137	2	Q924R6_MOUSE	Q924r6 mus musculus
190	493	14.0	241	2	Q921A6_MOUSE	Q921a6 mus musculus
191	492	14.0	141	2	Q924Q4_MOUSE	Q924q4 mus musculus
192	492	14.0	475	2	Q5FQS1_RAT	Q5fqsl rattus norv
193	492	14.0	587	2	Q7T0R1_XENLA	Q7t0r1 xenopus lae
194	491.5	14.0	140	2	Q924P8_MOUSE	Q924p8 mus musculus
195	491.5	14.0	330	1	GCAA_MOUSE	Q91863 mus musculus
196	491	13.9	590	2	Q569B8_RAT	Q569b8 rattus norv
197	490.5	13.9	588	2	Q61R66_XENLA	Q61r66 xenopus lae
198	488	13.9	143	2	Q924R7_MOUSE	Q924r7 mus musculus
199	487.5	13.8	398	1	GCAI_MOUSE	Q91865 mus musculus
200	487.5	13.8	605	2	Q6GN83_XENLA	Q6gn83 xenopus lae
201	484	13.7	493	2	Q8NCL6_HUMAN	Q8ncl6 homo sapien
202	483	13.7	143	2	Q91VA2_MOUSE	Q91va2 mus musculus
203	483	13.7	143	2	Q924Q5_MOUSE	Q924q5 mus musculus
204	481.5	13.7	117	1	HV12_MOUSE	Q91756 mus musculus
205	481.5	13.7	144	2	Q924P5_MOUSE	Q924p5 mus musculus
206	481	13.7	139	1	HV07_MOUSE	Q91751 mus musculus
207	480.5	13.6	117	1	HV13_MOUSE	Q91757 mus musculus
208	480	13.6	118	1	HV51_MOUSE	Q66330 mus musculus
209	480	13.6	477	2	Q6GMX7_HUMAN	Q6gmx7 homo sapien
210	479.5	13.6	570	2	Q5BJ31_BRARE	Q5bj31 brachydanio
211	479	13.6	336	1	GCB_MOUSE	Q91866 mus musculus
212	477	13.5	487	2	Q6ZVX0_HUMAN	Q6zvx0 homo sapien
213	475	13.5	404	1	GCBM_MOUSE	Q91867 mus musculus
214	474.5	13.5	506	2	Q6N090_HUMAN	Q6n090 homo sapien
215	474	13.5	139	2	Q924R5_MOUSE	Q924r5 mus musculus
216	474	13.5	479	2	Q5PQK9_RAT	Q5pqk9 rattus norv
217	472.5	13.4	225	2	Q6FAF5_XENLA	Q6faf5 xenopus lae
218	472	13.4	106	1	KACA_RAT	Q91836 rattus norv
219	471	13.4	506	2	Q6MZW0_HUMAN	Q6mzw0 homo sapien
220	469	13.3	485	2	Q6PDB8_MOUSE	Q6pdb8 mus musculus
221	468.5	13.3	483	2	Q5U413_MOUSE	Q5u413 mus musculus
222	468	13.3	499	2	Q8N5K4_HUMAN	Q8nsk4 homo sapien
223	467.5	13.3	494	2	Q96K68_HUMAN	Q96k68 homo sapien
224	467	13.3	335	1	GCAI_MOUSE	Q91864 mus musculus
225	465.5	13.2	123	2	Q8VIJ1_MOUSE	Q8vij1 mus musculus
226	465	13.2	143	2	Q924P9_MOUSE	Q924p9 mus musculus
227	464	13.2	348	2	Q6PVX1_HUMAN	Q6pvx1 homo sapien
228	462	13.1	143	2	Q91V67_MOUSE	Q91v67 mus musculus
229	462	13.1	152	2	Q6R2F9_STAAU	Q6r2f9 staphylococ
230	461	13.1	143	2	Q924Q0_MOUSE	Q924q0 mus musculus
231	461	13.1	476	2	Q4V9Z4_MOUSE	Q4v9z4 mus musculus
232	461	13.1	479	2	Q6MZV6_HUMAN	Q6mzv6 homo sapien
233	460.5	13.1	142	2	Q924Q2_MOUSE	Q924q2 mus musculus
234	458.5	13.0	120	1	HV03_MOUSE	Q91747 mus musculus
235	458.5	13.0	482	2	Q91X92_MOUSE	Q91x92 mus musculus
236	458.5	13.0	572	2	Q661Q7_XENLA	Q661q7 xenopus lae
237	458	13.0	99	2	Q9JL74_MOUSE	Q9jl74 mus musculus
238	457	13.0	106	1	KACB_RAT	Q91835 rattus norv
239	456.5	13.0	248	2	Q65ZQ7_9MURI	Q65zq7 mus sp. b3 (
240	454	12.9	137	1	HV11_MOUSE	Q91755 mus musculus
241	454	12.9	477	2	Q510J1_RAT	Q510j1 rattus norv
242	454	12.9	479	2	Q91WP5_MOUSE	Q91wp5 mus musculus
243	453.5	12.9	478	2	Q5FVQ3_RAT	Q5fvq3 rattus norv
244	451.5	12.8	478	2	Q6NVH3_HUMAN	Q6nvh3 homo sapien
245	451.5	12.8	494	2	Q6ZM64_HUMAN	Q6zm64 homo sapien
246	450.5	12.8	140	1	HV02_MOUSE	Q91746 mus musculus
247	450.5	12.8	496	2	Q96KX8_HUMAN	Q96kx8 homo sapien
248	449.5	12.8	119	2	Q9GYZ2_MOUSE	Q9gyz2 mus musculus
249	449.5	12.8	120	2	Q920E8_MOUSE	Q920e8 mus musculus
250	448	12.7	483	2	Q6MZX9_HUMAN	Q6mzx9 homo sapien

251	448	12.7	487	2	Q99KA4_MOUSE	Q99ka4 mus musculus	RT
252	447	12.7	479	2	Q5BK12_RAT	Q5bk12 rattus norv	RL
253	446	12.7	114	2	Q9JL81_MOUSE	Q9jl81 mus musculus	RN
254	446	12.7	333	1	QCB_RAT	R20761 rattus norv	RP
255	446	12.7	487	2	Q80Z17_MOUSE	Q80z17 mus musculus	RX
256	445	12.6	234	2	Q8N355_HUMAN	Q8n355 homo sapien	RA
257	444.5	12.6	484	2	Q8VBA0_MOUSE	Q8vea0 mus musculus	RB
258	444	12.6	479	2	Q7TWK4_MOUSE	Q7tmk4 mus musculus	RT
259	443	12.6	236	2	Q6GMX4_HUMAN	Q6gmx4 homo sapien	RL
260	443	12.6	478	2	Q7Z379_HUMAN	Q7z379 homo sapien	CC
261	442	12.5	487	2	Q5BK15_RAT	Q5bk15 rattus norv	CC
262	441	12.5	110	2	Q9JU77_MOUSE	Q9ju77 mus musculus	CC
263	440.5	12.5	234	2	Q5HFG0_STAAC	Q5hfg0 staphylococ	CC
264	440.5	12.5	492	2	Q7Z374_HUMAN	Q7z374 homo sapien	CC
265	439.5	12.5	233	2	Q8TBC9_HUMAN	Q8tbc9 homo sapien	CC
266	439	12.5	234	2	Q6GMW3_HUMAN	Q6gmw3 homo sapien	CC
267	439	12.5	234	2	Q6NS95_HUMAN	Q6ns95 homo sapien	CC
268	438.5	12.5	229	2	Q6GBW7_STAAS	Q6gbw7 staphylococ	CC
269	438.5	12.5	229	2	Q8NW97_STAAM	Q8nw97 staphylococ	CC
270	438	12.4	236	2	Q6GMX3_HUMAN	Q6gmx3 homo sapien	CC
271	437.5	12.4	138	1	HV48_MOUSE	P03980 mus musculus	CC
272	437.5	12.4	329	1	GCC_RAT	P20762 rattus norv	CC
273	437.5	12.4	479	2	Q9RM22_MOUSE	Q9rm22 mus musculus	CC
274	437	12.4	236	2	Q6GMV7_HUMAN	Q6gmv7 homo sapien	CC
275	434.5	12.3	235	2	Q567P1_HUMAN	Q567p1 homo sapien	CC
276	434.5	12.3	617	2	Q569B3_RAT	Q569b3 rattus norv	DR
277	434	12.3	236	2	Q8NEJ1_HUMAN	Q8nej1 homo sapien	DR
278	433.5	12.3	486	2	Q91207_MOUSE	Q91207 mus musculus	DR
279	433	12.3	96	2	Q5R3X6_MOUSE	Q5r3x6 mus musculus	DR
280	433	12.3	120	1	HV50_MOUSE	P06329 mus musculus	DR
281	432	12.3	109	2	Q9JU75_MOUSE	Q9ju75 mus musculus	DR
282	432	12.3	118	2	Q5R3X0_MOUSE	Q5r3x0 mus musculus	DR
283	432	12.3	483	2	Q566J7_MOUSE	Q566j7 mus musculus	DR
284	431	12.2	97	2	Q5R3Y0_MOUSE	Q5r3y0 mus musculus	DR
285	430.5	12.2	235	2	Q6GMW6_HUMAN	Q6gmw6 homo sapien	DR
286	428.5	12.2	235	2	Q6IN99_HUMAN	Q6in99 homo sapien	DR
287	428	12.2	118	2	Q9ZIC4_MOUSE	Q9zic4 mus musculus	DR
288	427	12.1	519	2	Q6N092_HUMAN	Q6n092 homo sapien	DR
289	426.5	12.1	233	2	Q6NS96_HUMAN	Q6ns96 homo sapien	KW
290	426	12.1	236	2	Q6IPQ0_HUMAN	Q6ipq0 homo sapien	FT
291	426	12.1	262	2	Q65Z11_MOUSE	Q65z11 mus musculus	FT
292	425	12.1	117	1	HV05_MOUSE	P01753 mus musculus	FT
293	425	12.1	232	2	Q5FWF9_HUMAN	Q5fwf9 homo sapien	FT
294	424.5	12.1	147	2	Q925S3_MOUSE	Q925s3 mus musculus	FT
295	424.5	12.1	231	2	Q6GNB8_XENLA	Q6gnb8 xenopus lae	FT
296	424.5	12.1	237	2	Q6DHW4_HUMAN	Q6dhw4 homo sapien	FT
297	424	12.0	234	2	Q6GMV8_HUMAN	Q6gmv8 homo sapien	FT
298	423	12.0	149	1	KV5A_MOUSE	P01633 mus musculus	FT
299	422	12.0	117	1	HV14_MOUSE	P01758 mus musculus	FT
300	422	12.0	233	2	Q6GMW4_HUMAN	Q6gmw4 homo sapien	FT

enterotoxin gene.";
J. Bacteriol. 170:2954-2960(1988).
[2]
3D-STRUCTURE MODELING.
MEDLINE=96022987; PubMed=7552730;
Swaminathan S., Pury W.F. Jr., Fletcher J., Sax M.;
"Residues defining V beta specificity in staphylococcal
enterotoxins.";
Nat. Struct. Biol. 2:680-686(1995).
-I- FUNCTION: Staphylococcal enterotoxins cause the intoxication
staphylococcal food poisoning syndrome. The illness characterized
by high fever, hypotension, diarrhea, shock, and in some cases
death.
-I- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
for the toxin interaction with MHC class II (By similarity).
-I- SUBCELLULAR LOCATION: Secreted.
-I- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
family.

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removed.

EMBL; M21319; AAA26617.1; -; Genomic_DNA.
PIR; A28179; A28179.
PDB; 1SBE; Model; @=28-257.
InterPro; IPR006177; Bctrl tox.
InterPro; IPR006123; Stap/Strep toxin.
InterPro; IPR006126; Staph/Strept_cox.
Pfam; PF02876; Stap_Strep_tox_C; 1.
Pfam; PF01123; Stap_Strep_toxin; 1.
PRINTS; PR00279; BACTELTOXIN
PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
3D-structure; Antigen; Direct protein sequencing; Enterotoxin;
Metal-binding; Signal; Superantigen; Toxin; Zinc.

CHAIN 1 27 Enterotoxin type E.
METAL 211 211 Zinc (By similarity).
METAL 249 249 Zinc (By similarity).
METAL 251 251 Zinc (By similarity).
HELIX 33 35
HELIX 39 41
STRAND 42 42
TURN 46 47
HELIX 48 51
HELIX 52 54
STRAND 59 64
TURN 66 67
STRAND 69 69
TURN 73 74
STRAND 75 79
TURN 83 84
STRAND 90 94
HELIX 98 104
TURN 105 106
STRAND 109 113
TURN 115 116
STRAND 118 119
STRAND 128 132
STRAND 135 137
TURN 139 140
STRAND 142 142
STRAND 152 152
STRAND 154 155
TURN 156 157
STRAND 163 163
STRAND 171 171
STRAND 173 175
HELIX 176 190

ALIGNMENTS

RESULT 1	ETXE_STAAM	STANDARD;	PRT;	257 AA.
AC	P12933;			
DT	01-JAN-1990 (Rel. 13, Created)			
DT	01-JAN-1990 (Rel. 13, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Enterotoxin type E precursor (SEE).			
GN	Name=entE;			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=1280;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 28-74.			
RC	STRAIN=MJB265;			
RX	MEDLINE=88257005; PubMed=3384800;			
RA	Couch J.D., Soltis M.T., Betley M.J.;			
RT	"Cloning and nucleotide sequence of the type E staphylococcal			

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FT TURN 191
FT STRAND 203
FT STRAND 211
FT STRAND 219
FT STRAND 221
FT STRAND 227
FT STRAND 234
FT STRAND 239
FT STRAND 242
FT STRAND 244
FT TURN 245
FT TURN 247
FT STRAND 249
SQ SEQUENCE 257 AA; 29358 MW; 27EDA94B97770CE3 CRC64;

Query Match
Best Local Similarity 31.4%; Score 1107; DB 1; Length 257;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKXSELGSTALGNLKIYYNSKAITSEKSDQFLNTLLFKGFFTG 285
DQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 25 SEKSEINEKDLRKXSELGSTALGNLKIYYNSKAITSEKSDQFLNTLLFKGFFTG 84
QY 286 HPWYNDLLVLDGSTAATSEYSSVDLYGAYGYQCAGGTPNKTCMGYGVTLHNNRLT 345
DQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 85 HPWYNDLLVLDGSKDATNKYKGKVDLYGAYGYQCAGGTPNKTCMGYGVTLHNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDIKVTSKKEVTVQELDLQARHYLHGKFLYNSDSFGKQV 405
DQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 145 EEKVPINLWIDGKQTTVPIDIKVTSKKEVTVQELDLQARHYLHGKFLYNSDSFGKQV 204
QY 406 RGLIVHSEGSTSVSDLDFAQQYPTDLLRIYRDNNTSSLSLSLYTT 458
DQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 205 RGLIVHSEGSTSVSDLDFAQQYPTDLLRIYRDNNTSSLSLSLYTT 257

RESULT 2
Q99LC4 MOUSE PRELIMINARY; PRT; 463 AA.
AC Q99LC4;
DT 01-JUN-2001 (trEMBLrel. 17, Created)
DT 01-JUN-2001 (trEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (trEMBLrel. 26, Last annotation update)
DE Igh-4 protein.
GN Name=Igh-4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N;
RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
RC virgin mouse. Taken by biopsy.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hake S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.

```

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RC STRAIN=FVB/N;
RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old
RC virgin mouse. Taken by biopsy.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; -; mRNA.
DR PIR; B45837; B45837.
DR HSSP; P01869; 1CLJ7.
DR SMR; Q99LC4; 21-459.
DR MGI; MGI:96446; Igh-4.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR GO; GO:0003823; P:antigen binding; IDA.
DR GO; GO:0019733; P:antibacterial humoral response (sensu Verte. .; IDA.
DR GO; GO:0001788; P:antibody-dependent cellular cytotoxicity; IDA.
DR GO; GO:0006958; P:complement activation, classical pathway; IDA.
DR GO; GO:0042830; P:defense response to pathogenic bacteria; IDA.
DR GO; GO:0006911; P:phagocytosis, engulfment; IDA.
DR GO; GO:0006910; P:phagocytosis, recognition; IDA.
DR GO; GO:0050778; P:positive regulation of immune response; IDA.
DR GO; GO:0050766; P:positive regulation of phagocytosis; IDA.
DR GO; GO:0003812; P:positive regulation of type I hypersensitivity; IDA.
DR GO; GO:0001798; P:positive regulation of type I hypersensit. .; IDA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
KW Immunoglobulin domain.
SQ SEQUENCE 463 AA; 51008 MW; EAA674C6BBC30783 CRC64;

Query Match
Best Local Similarity 28.7%; Score 1010; DB 2; Length 463;
Matches 240; Conservative 64; Mismatches 114; Indels 248; Gaps 13;

QY 1 EVQLQQSGDPLVKPGASVKISKASGYSTGYTHMWVKSPGKLEWIGRIINPNNGVLY 60
DQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 20 QVQLQQSGAELARPAGASVRLSCKASGYTFTGYGVSMVKQTGQLEWGEIYVPGNTY 79
QY 61 NQKFKDKATLTVDKSSTTHMYELSLTSDSAVYYCARSTMTNYNDYWGQSTVTVSS 120
DQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 80 SEKFKGKATLTDDKSSSTAYMHLSSLTSDSAVYFCARSSYYSDLFAYWGQSTLVVSA 139
QY 121 AKTTTPSVYPLAPGAAQNSMTVLGCLVKGFPEPTVTWNSGSLSSGVHFFPAVLQSD 180
DQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 140 AKTTTPSVYPLAPGAAQNSMTVLGCLVKGFPEPTVTWNSGSLSSGVHFFPAVLQSD 199
QY 181 LYTLSSSVTPSPSTWPFSETVTCNVAHPASSTKVDKIVPRDSDGSPSEKSEINEKDLRK 240
DQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 200 LYTLSSSVTPSPSTWPFSETVTCNVAHPASSTKVDKIVPRDSDGSPSEKSEINEKDLRK 242
QY 241 SELOGTALGNLKIYYNSKAITSEKSDQFLNTLLFKGFFTHPWYNDLLVDLGSTA 300
DQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 243 CKPCICTPEVSSVFIFPKP-----PKDVLITL----- 271
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTCMGYGVTLHNNRLTBEKKVPINLWIDGKQ 360
DQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 272 -----TP-KTCVVVDIS-----KDDPEVQSFVFD--- 296
QY 361 TTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVGQRLIVF 411
DQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 297 -DVEVHTAQTPREEQFNSTFRSVSELPIMHQDLNGKEFKCRVNSAAPPAPTEK----- 350
QY 412 HSEGSTSVSDLDFAQQYPTDLLRIYRDNNTSSLSLSLYTTSIVMTQPTSLLV 471
DQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 351 -----TISK----- 355
QY 472 SAGDRVITTCASQSVSNDVAVYQKPGQSPKLLISYTSRVAGVDPDFSGSGYGTFTL 531
DQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DQ 356 ----- 355
QY 532 TISSVQAEDAAYVFCQDYNSPPTFGGKLEIKRADAAPTYSIFPPSSEQLTSGGASVV 591
DQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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DB 208 RGLVHTSTEPSVNYDLFGAQOQYGNILLRIYDRNKTISSENMHIIDLYLTS 260
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|||||:| :|:|||| |||| :||||||| |||| :| :|||:
208 RGLVHTSTEPSVNYDLFGAQOQYGNILLRIYDRNKTISSENMHIIDLYLTS 260

RESULT 6
ETXA_STRAU
ID ETXA_STRAU STANDARD; PRT; 257 AA.
AC POA0L2; P13163;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Enterotoxin type A precursor (SEA).
GN Name=entA;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
ON NCBI_TaxID=1280;
RX [1]_TaxID=1280;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PRI337;
RX MEDLINE=8722293; PubMed=3335483;
RA Betley M.J., Mekalanos J.J.;
RT "Nucleotide sequence of the type A staphylococcal enterotoxin gene.";
RL J. Bacteriol. 170:34-41 (1988).
RN [2]
RP PROTEIN SEQUENCE OF 25-257.
RX MEDLINE=8722293; PubMed=3584106;
RA Huang I.-Y., Hughes J.L., Bergdoll M.S., Schantz E.J.;
RT "Complete amino acid sequence of staphylococcal enterotoxin A.";
RL J. Biol. Chem. 262:7006-7013 (1987).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95354648; PubMed=7628431;
RA Schad E.M., Zaitseva I., Zaitsev V.N., Dohlsten M., Kalland T.,
RA Schlievert P.M., Ohlendorf D.H., Svensson L.A.;
RT "Crystal structure of the superantigen staphylococcal enterotoxin type
RT A.";
RL EMBO J. 14:3292-3301 (1995).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=97113025; PubMed=8943278; DOI=10.1074/jbc.271.50.32212;
RA Sundstroem M., Hallen D., Svensson A., Schad E., Dohlsten M.,
RA Abrahamson L.;
RT "The Co-crystal structure of staphylococcal enterotoxin type A with
RT Zn2+ at 2.7-A resolution. Implications for major histocompatibility
RT complex class II binding.";
RL J. Biol. Chem. 271:32212-32216 (1996).
RN [5]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=96022987; PubMed=7552730;
RA Swaminathan S., Furey W.F. Jr., Fletcher J., Sax M.;
RT "Residues defining V beta specificity in staphylococcal
RT enterotoxins.";
RL Nat. Struct. Biol. 2:680-686 (1995).
RN [6]
RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
RX MEDLINE=97334373; PubMed=9191070; DOI=10.1006/jmbi.1997.1023;
RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
RT "A structural and functional comparison of staphylococcal enterotoxins
RT A and C2 reveals remarkable similarity and dissimilarity.";
RL J. Mol. Biol. 269:270-280 (1997).
CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication
CC staphylococcal food poisoning syndrome. The illness characterized
CC by high fever, hypotension, diarrhea, shock, and in some cases
CC death.
CC -!- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
CC for the toxin interaction with MHC class II.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MISCELLANEOUS: This toxin seems to be coded by a bacteriophage.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
```

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CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; M18970; AAA26681.1; -; Genomic_DNA.
DR PIR; A28664; A28664.
DR PDB; 1DQ; X-ray; A=25-257.
DR PDB; 1ESF; X-ray; A/B=25-257.
DR PDB; 1I4G; X-ray; A/B=25-257.
DR PDB; 1I4H; X-ray; A/B=25-257.
DR PDB; 1LO5; X-ray; D=25-257.
DR PDB; 1SEA; Model; @=25-257.
DR PDB; 1SXT; X-ray; A/B=25-257.
DR SMR; POA0L2; 25-257.
DR InterPro; IPR006177; Bcrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW 3D-structure; Antigen; Direct protein sequencing; Enterotoxin;
KW Metal-binding; Signal; Superantigen; Toxin; Zinc.
FT SIGNAL 1 24
FT CHAIN 25 257 Enterotoxin type A.
FT METAL 211 211 Zinc.
FT METAL 249 249 Zinc.
FT METAL 251 251 Zinc.
FT DISULFID 120 130
FT CONFLICT 242 242
FT HELIX 33 35
FT HELIX 39 41
FT TURN 44 45
FT HELIX 46 55
FT STRAND 75 78
FT TURN 79 80
FT STRAND 90 94
FT HELIX 98 104
FT TURN 105 106
FT STRAND 109 114
FT STRAND 116 116
FT HELIX 117 119
FT TURN 122 123
FT TURN 126 127
FT STRAND 128 132
FT STRAND 135 137
FT TURN 139 140
FT STRAND 142 148
FT STRAND 151 155
FT TURN 156 157
FT STRAND 158 160
FT TURN 164 165
FT STRAND 168 171
FT STRAND 173 175
FT HELIX 176 191
FT TURN 193 194
FT HELIX 197 199
FT TURN 200 200
FT STRAND 205 211
FT STRAND 218 221
FT TURN 222 223
FT TURN 227 228
FT TURN 230 232
FT HELIX 233 237
FT TURN 238 239
FT STRAND 242 244
FT TURN 245 247
FT STRAND 249 255
FT SEQUENCE 257 AA; 29669 MW; ADEBF5BCAIF14677 CRC64;
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Query Match          26.9%; Score 948; DB 1; Length 257;
Best Local Similarity 76.4%; Pred. No. 7e-51;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDKRKSELGALGNLKOIYYNYSKAITSEKSADQFLNTLLFKGFFTG 285
DB 25 SEKSEINEKDKRKSELGALGNLKOIYYNEKAKTENKESHDOFLOHTILFKGFFTD 84

QY 286 HPWYNLLVDLSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 345
DB 85 HSWYNLLVDFPDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144

QY 346 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
DB 145 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204

QY 406 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNTTISSTLSISLYLYTT 458
DB 205 RGLIVFHTSTEPSVNYDLFGAQGYNTLLRIYRDNTTISENMHIDIYLYTS 257

RESULT 7
ETXA STAAW
ID ETXA STAAW STANDARD; PRT; 257 AA.
AC POA011; P13163;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Enterotoxin type A precursor (SEA).
GN Name=entA; OrderedLocusNames=MW1889;
OS Staphylococcus aureus (strain MW2)
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Aeono K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication
CC Staphylococcal food poisoning syndrome. The illness characterized
CC by high fever, hypotension, diarrhea, shock, and in some cases
CC death (By similarity).
CC -!- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
CC for the toxin interaction with MHC class II (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; BA000033; BAB95754.1; -; Genomic_DNA.
CC SMR; POA011; 25-257.
CC InterPro; IPR006177; Bcrl toxin.
CC InterPro; IPR006123; Staph/Strep toxin.
CC InterPro; IPR006126; Staph/Strep tox.
CC InterPro; IPR006173; Staph tox OB.
CC Pfam; PF02876; Staph_Strep_tox_C; 1.
CC Pfam; PF01123; Staph_Strep_tox; 1.
CC PRINTS; PR00279; BACTRLTOXIN.
CC PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
CC PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
CC Antigen; Complete proteome; Enterotoxin; Metal-binding; Signal;
CC Superantigen; Toxin; Zinc.

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FT SIGNAL          1 24 BY similarity.
FT CHAIN           25 257 Enterotoxin type A.
FT METAL           211 211 Zinc (By similarity).
FT METAL           249 249 Zinc (By similarity).
FT METAL           251 251 Zinc (By similarity).
FT DISULFID        120 130 By similarity.
SQ SEQUENCE 257 AA; 29669 MW; ADEBFSBCAIF14677 CRC64;

Query Match          26.9%; Score 948; DB 1; Length 257;
Best Local Similarity 76.4%; Pred. No. 7e-51;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDKRKSELGALGNLKOIYYNYSKAITSEKSADQFLNTLLFKGFFTG 285
DB 25 SEKSEINEKDKRKSELGALGNLKOIYYNEKAKTENKESHDOFLOHTILFKGFFTD 84

QY 286 HPWYNLLVDLSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 345
DB 85 HSWYNLLVDFPDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144

QY 346 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
DB 145 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204

QY 406 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNTTISSTLSISLYLYTT 458
DB 205 RGLIVFHTSTEPSVNYDLFGAQGYNTLLRIYRDNTTISENMHIDIYLYTS 257

RESULT 8
G6GY7 STAAS
ID G6GY7 STAAS PRELIMINARY; PRT; 257 AA.
AC G6GY7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Enterotoxin type A.
GN OrderedLocusNames=SAS1872;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571857; CA43678.1; -; Genomic_DNA.
DR SMR; Q6GY7; 25-257.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bcrl toxin.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph_Strep_tox; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Complete proteome.
SQ SEQUENCE 257 AA; 29669 MW; ADEBFSBCAIF14677 CRC64;

Query Match          26.9%; Score 948; DB 2; Length 257;

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Best Local Similarity 76.4%; Pred. No. 7e-51;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKKSLOQTALGNLKOIYYNSKAITSEKSDADQPLTNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKKSLOQTALGNLKOIYYNEKAKTENKSHDQPLQHTILFKGFFTD 84
QY 286 HPWYNLLVDLGGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
Db 85 HSWYNLLVDFDSKDIIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWDGKQTPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDFGSKVQ 405
Db 145 EEKVPINLWDGKQNTVPLETVTKNKVNTVQELDLQARRYLQEKYLNYSDFGSKVQ 204
QY 406 RGLIVFHSSGGSTVSYDLFDAQOQYPTLLRIYRDNTTSSLSLSLYTT 458
Db 205 RGLIVFHTSTEPSVNYDLFGAQOQYNTLLRIYRDNTKNTINSENHDIYLYTS 257

RESULT 9
Q931M4 STAA
ID Q931M4 STAA PRELIMINARY; PRT; 260 AA.
AC Q931M4;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Enterotoxin P.
GN Names=sep; OrderedLocuNames=SAV1948;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=2131192; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Iuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekinizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshino K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus";
RL Lancet 357:1225-1240 (2001).
DR EMBL; BA000017; BAB58110.1; -; Genomic_DNA.
DR HSSP; P13163; 1LO5.
DR SMR; Q931M4; 28-260.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR Pfam; PF01123; Staph Strep toxin; 1.
DR Pfam; PF02876; Staph Strep toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH STREP TOXIN 1; 1.
DR PROSITE; PS00278; STAPH STREP TOXIN 2; 1.
DR Complete proteome.
KW SEQUENCE 260 AA; 30016 MW; 15C2D36270FA8241 CRC64;

Query Match 26.9%; Score 948; DB 2; Length 260;
Best Local Similarity 76.4%; Pred. No. 7.1e-51;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKKSLOQTALGNLKOIYYNSKAITSEKSDADQPLTNTLLFKGFFTG 285
Db 28 SEKSEINEKDLRKKSLOQTALGNLKOIYYNEKAKTENKSHDQPLQHTILFKGFFTD 87
QY 286 HPWYNLLVDLGGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
Db 88 HSWYNLLVDFDSKDIIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 147
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KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51329 MW; 394F43C4E8DB3E21 CRC64;

Query Match 26.8%; Score 945.5; DB 2; Length 465;
Best Local Similarity 34.1%; Pred. No. 2.5e-50;
Matches 236; Conservative 56; Mismatches 136; Indels 255; Gaps 12;

QY 1 EVQLQSGDPLVKPGASVKISKASGYSTGYMHVVKSPGKLEWIGRINPNNGVTLY 60
DB 20 QVQLKQSGAELVKPGASVKLSKASGYTFSNYIMHWKQRPQGGLWIGYFSPYNDTKC 79

QY 61 NQKFKDKATLTVDKSSSTTAYMELRLSTSDSAVYYCARSTMTITNYMYDWGQOSTVTSS 120
DB 80 NEKFKGKATLTADKSSSTAYMELSLSTSDSAVYYCARG----YYVFDWGGQTTITVSS 135

QY 121 AKTTPSVYPLAPGSAQAQNSMTVLCGLVKGYFPEPVTVWNSGSLSSGVHFFPAVLQSD 180
DB 136 AKTTPSVYPLAPVCGDITGSSVTGLCGLVKGYFPEPVTVWNSGSLSSGVHFFPAVLQSD 195

QY 181 LYTLSSTVTPSSTWPSSETVTCNVAPASSTKVDDKI VPRDGGPSEKSEINEKDLRKK 240
DB 196 LYTLSSTVTPSSTWPSQSITCNVAPASSTKVDDKIEPR---GPTIKPCP----- 243

QY 241 SELQGTALGNLQKIYYNKAITSSEKSADQFLTNTLLFKGFTTGHFWYNDLLVDLGSTA 300
DB 244 ----- 243

QY 301 ATSEYEGSSVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLTEBEKVPINLWIDGKQ 360
DB 244 -----PCKCPAPN-----LLGGPSVF----- 259

QY 361 TTVPIDKVKTSKEVTVQELDLQARHYLHGKGLYNSDSFGGKQVQRLIVFHSSEGSTVS 420
DB 260 -----IPPKIKDVLMI-----SLSPMT 278

QY 421 YDLFDAQGYQPTLLRIYRDNNTTISSTLSISLYITTSITVMTQTPTSLVLSAGDRVTIT 480
DB 279 CVVDVDSDDPD-----VQISWFVNVEVLTAQTQT----- 309

QY 481 CKASQSVNDVAWYQKPGQSKLLISYTSRYAGVDRPFSGGYGTDTLTLISSVQA-- 538
DB 310 -----HREDYNSTLRVVVALP 325

QY 539 -----EDAAVFCQDYNPPTFGGKTLEIKRADAAPTVISIFPPSSQLTSGGASVVC 592
DB 326 IQHQMMSKEFKCKRNKALPAPIERTISKPGSVRAPQVYVLPPEEMTKKQVTLTC 385

QY 593 FLNNFYPKDINVKWKIDGSRQKQ-----GVLSNWTDDQSKDSTYSMSSTLTITKDEYERH 647
DB 386 MVTDFMPEDIYVEWTNNGKTELNYKNTPEVLDS-----DGSYFMYSKLRVEKKQWVER 438

QY 648 NSYTCETHK-TSTSPIVKSFNR 669
DB 439 NSYSCSVVHEGLHHHTTKSFSR 461

RESULT 11
ID Q569W3_MOUSE PRELIMINARY; PRT; 468 AA.
AC Q569W3;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN Name=Igh-la;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;

RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Krausberger R.L., Feingold E.A., Grouse L.H., Derge J.G.
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McKellan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RC NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastatized to lung. Tumor arose spontaneously;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC092271; AAH92271.1; -; mRNA.
DR SMR; Q569W3; 20-464.
DR MGI; MGI:96443; Igh-1a.
DR GO; GO:0003823; P:antigen binding; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 468 AA; 51666 MW; 5BF6E527329F8461 CRC64;

Query Match 26.8%; Score 945; DB 2; Length 468;
Best Local Similarity 34.1%; Pred. No. 2.5e-50;
Matches 233; Conservative 62; Mismatches 136; Indels 252; Gaps 12;

QY 1 EVQLQSGDPLVKPGASVKISKASGYSTGYMHVVKSPGKLEWIGRINPNNGVTLY 60
DB 20 EVQLQSGAELVKPGSSVKLSCKTGYTFTSYINWVKQRPQGGLWIGHIYPCNGYTEY 79

QY 61 NQKFKDKATLTVDKSSSTTAYMELRLSTSDSAVYYCARSTMTITNYMYDWGQOSTVTSS 120
DB 80 NEKFKGKATLTSDTSSSTAYMQLRLSLTSENSAIYFCARTGGYDGY-FDYWGQGTITVSS 138

QY 121 AKTTPSVYPLAPGSAQAQNSMTVLCGLVKGYFPEPVTVWNSGSLSSGVHFFPAVLQSD 180
DB 139 AKTTPSVYPLAPVCGDITGSSVTGLCGLVKGYFPEPVTVWNSGSLSSGVHFFPAVLQSD 198

QY 181 LYTLSSTVTPSSTWPSSETVTCNVAPASSTKVDDKI VPRDGGPSEKSEINEKDLRKK 240
DB 199 LYTLSSTVTPSSTWPSQSITCNVAPASSTKVDDKIEPR---GPTIKPCP----- 246

QY 241 SELQGTALGNLQKIYYNKAITSSEKSADQFLTNTLLFKGFTTGHFWYNDLLVDLGSTA 300
DB 247 ----- 246

QY 301 ATSEYEGSSVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLTEBEKVPINLWIDGKQ 360
DB 247 -----PCKCPAPN-----LLGGPSVF----- 262

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QY 361 TTVPIDKVTSKKEVTVQELDLQARHYLHGKGLYNSDSFGKVGQRLIVFHSSEGSTVS 420
Db 263 -----IFPPKIKDVLMI---SLSPWVT 281
QY 421 YDLFDAQGYDPDILLRIYRDNNTISSTLSLSISLYLTTISVMTQPTSLLSVAGDRVTIT 480
Db 282 CVVVDVSEDDPD-----VQISFVANNVEVLTAQTQT----- 312
QY 481 CKASQSVNDVAVYQKQGSQPKLLISYTSRYAGVDPDFSGSGYGTDFTLTISVQA-- 538
Db 313 -----HREDYNSLTRVVSALP 328
QY 539 -----EDAAVYFCQDYNPPTFGGTGKLEIKRADAAPTIVSIFPSSQELTSGGASVVC 592
Db 329 IQHODWMSGKFEKCKVNNKALPAPIERTISKPKGSVRAPQVYVLPPEEEMTKKQVTLTC 388
QY 593 FLNNFPYKDNVKKWDIGSERQ-----GVLSNWTDDSDKSTYSMSSTLTTLTKDYERH 647
Db 389 MVTDFMPEDIYVETWNTNGKTELNYKNTPEVLD-----DGSYFYMSKLRVEKKNVVER 441
QY 648 NSYTCEATHK-TGTSPIVKSFRN 669
Db 442 NSYSCSVVHEGLNHNHTTKSFSR 464

RESULT 12
Q5BK05_RAT PRELIMINARY; PRT; 458 AA.
AC Q5BK05;
DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DE LOC367586 protein.
GN Name=LOC367586;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC -!- histocompatibility complex class I molecules (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
DR EMBL; BC091257; AAH91257.1; -; mRNA.
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DR SMR; Q5BK05; 21-454.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_cl.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGcl; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 4.
KW Immunoglobulin domain; Repeat.
SQ SEQUENCE 458 AA; 49943 MW; 74D964EC1DFCD12F CRC64;

Query Match 26.8%; Score 944.5; DB 2; Length 458;
Best Local Similarity 35.0%; Pred. No. 2.6e-50;
Matches 232; Conservative 71; Mismatches 114; Indels 245; Gaps 16;

QY 1 EYVLOQSGDPLVKGPSKISKASKASYSTGYMHVVKSPGKLEWIGRINPNNGVTLY 60
Db 20 QVLOQSGAELAKPGSVKISKASKGYTTSYDVSVIKQTTGGLEYIYINTSGGIY 79
QY 61 NOKFKDKATLTVDKSTTAYMELRSLTSDSAVYVCARSTMITNYVMDVYMGQTSVTSS 120
Db 80 TEKFKGKATLTVDKSSSTAPMQLSSLTPEDTAVYYCTRD---GTRINDAWGQTSVTSS 136
QY 121 AKTTPEPVYPLAPGSAATNSMVTGLCLVKGFPPEPVTVTWNSGSLSSSGVHTFPVLQSD 180
Db 137 AETTAPSVYPLAPGTALKSNMVTGLCLVKGFPPEPVTVTWNSGALSSSGVHTFPVLQSG 196
QY 181 LYTSSSVTPSPSTWSPSETVTCNVAHPASSTKVDKIVPRDGGPSEKSEINEKDLRKK 240
Db 197 LYTSSSVTPSPSTWSSQAVTCNVAHPASSTKVDKIVPREC----- 238
QY 241 SELQGTALGNLQIYYVYNSKATISSEKSDQFLTNTLLFKGPTGHPYNDLLAVDLGSTA 300
Db 239 -----NPCGCTGSEVSS-----VPFPKTKDVL----- 262
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTEKKVPINLWIDG-- 358
Db 263 -----TITL-----TP-KVTCVVVDISQND-----PEVRFSEFIDDVE 294
QY 359 ---KQTTVIDKVTSKKEVTVQELDLQARHYLHGKGLYNSDSFGKVGQRLIVFHSSE 415
Db 295 VHTAQTHAPEKQSNSTLR--SVSELPVHRDMLNGK-----TPKCKVN----- 335
QY 416 GSTVSVDLPDAQOYDPTLLRIYRDNNTISSTLSLSLYLTTISVMTQPTSLLSVAGD 475
Db 336 -----SGAFPAP----- 343
QY 476 RVITTCASQSVNDVAVYQKQGSQPKLLISYTSRYAGVDPDFSGSGYGTDFTLTIS 535
Db 344 -----EKSIS-----KPEGTFR----- 355
QY 536 VQAEADNAVFCQDYNPPTFGGTGKLEIKRADAAPTIVSIFPSSQELTSGGASVVCFLN 595
Db 356 -----GFQVYTMAPPKEEMTQSQVSIICMVK 381
QY 596 NFVPKDNVKKWDIGSERQNGVLSNWTDDSDKSTYSMSSTLTTLTKDEYERHNSYTCAT 655
Db 382 GFPPDIYTEWRKMGQPOEN-YKNTPTPTWDT-DGSYFLYSKLVNKKETWQQTFTCSVL 439
QY 656 HK 657
Db 440 HE 441

RESULT 13
Q52L64_MOUSE PRELIMINARY; PRT; 240 AA.
AC Q52L64;
ID Q52L64_MOUSE PRELIMINARY; PRT; 240 AA.
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
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146 SEQITGGASVWFLNNFPKIDNVKWKIDGSRQVNLNSWTDQDSKOSTYSMSSTLTL 205
640 TKDEYERHNSYTCETHAKTSTSPIVKSFNRNE 671
206 TKDEYERHNSYTCETHAKTSTSPIVKSFNRNE 237

RESULT 15
Q6GFA8 STAAAR
ID Q6GFA8 STAAAR PRELIMINARY; PRT; 257 AA.
AC Q6GFA8 STAAAR PRELIMINARY; PRT; 257 AA.
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DE Enterotoxin type A.
GN OrderedLocuNames=SAR2043;
OS Staphylococcus aureus (strain MSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Eason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitz E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791 (2004).
DR EMBL: BX571856; CAG41028.1; -; Genomic_DNA.
DR SRR; Q6GFA8; 25-257.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 257 AA; 29674 MW; 56B0A6D952EDFED4 CRC64;

Query Match 26.5%; Score 935; DB 2; Length 257;
Best Local Similarity 75.5%; Pred. No. 4, 5e-50;
Matches 176; Conservative 21; Mismatches 36; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKKSELOQTALGNLKQIYYNSKAITSEKSDQFLNTLLFKGFFTG 285
DB 25 SEKSEINEKDLRKKSELOQTALGNLKQIYYNEKAKTENKESHDPLOHTILFKGFFTN 84

QY 286 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGVCAGGTPNKTACWYGGVTLHDNNRLT 345
DB 85 HSWYNDLLVDLFDSDKQIDVKYKGGKVDLYGAYGYQCAGGTPNKTACWYGGVTLHDNNRLT 144

QY 346 EEKKVPINLWDGQKTTVPIDKVKTSKKEVTQELDLQARHYLHGKFLYNSDSFGKVKQ 405
DB 145 EEKKVPINLWDGQKTTVPLETVTNKNKNTVVELDLQARYLQEKYLNYSNDFGKVKQ 204

QY 406 RGLIVFHSSSGSVSYDLFDAQGQYPTLLRIYRDNTTISSTLSLSLYLTT 458
DB 205 RGLIVFHTSTSPSYVDLFGAQGQNSNTLLRIYRDNKNINSNNHIDIYLYTS 257

RESULT 16
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Q58E56_MOUSE
ID Q58E56_MOUSE PRELIMINARY; PRT; 477 AA.
AC Q58E56;
DT 10-MAY-2005 (T-EMBLrel. 30, Created)
DT 10-MAY-2005 (T-EMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (T-EMBLrel. 30, Last annotation update)
DE Igh-1a protein.
GN Name=Igh-1a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Spletten M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedtin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC092061; AAH92061.1; -; mRNA.
DR MGI; MGI:96443; Igh-1a.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IEA.
DR GO; GO:0005771; C:multivesicular body; IEA.
DR GO; GO:0003823; F:antigen binding; IEA.
DR GO; GO:0001788; P:antibody-dependent cellular cytotoxicity; IEA.
DR GO; GO:0030333; P:antigen processing; IEA.
DR GO; GO:0008958; P:complement activation, classical pathway; IEA.
DR GO; GO:0045022; P:early endosome to late endosome transport; IEA.
DR GO; GO:0008333; P:endosome to lysosome transport; IEA.
DR GO; GO:0006911; P:phagocytosis, engulfment; IEA.
DR GO; GO:0006910; P:phagocytosis, recognition; IEA.
DR GO; GO:0050871; P:positive regulation of B cell activation; IEA.
DR GO; GO:0050778; P:positive regulation of immune response; IEA.
DR GO; GO:0050766; P:positive regulation of phagocytosis; IEA.
DR GO; GO:0001812; P:positive regulation of type I hypersensitivity; IEA.
DR GO; GO:0001798; P:positive regulation of type I hypersensitivity; IEA.
DR GO; GO:0030162; P:regulation of proteolysis and peptidolysis; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGL1; 3.
DR SMART; SM00406; IGV; 1.
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RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK007918; BAB25349.1; -, mRNA.
DR PIR; PH1165; PH1165.
DR PIR; S19966; S19966.
DR PIR; S26746; S26746.
DR HSSP; P01864; IBOG.
DR SMR; Q9DBL4; 20-469.
DR Ensemble; ENSMUSG0000054328; Mus musculus.
DR MGI; MGI:96443; Igh-1a.
DR GO; GO:004543; C:immunoglobulin complex, circulating; IDA.
DR GO; GO:0005771; C:multivesicular body; IDA.
DR GO; GO:0003823; F:antigen binding; IDA.
DR GO; GO:0001788; P:antibody-dependent cellular cytotoxicity; IDA.
DR GO; GO:0030333; P:antigen processing; IDA.
DR GO; GO:0006958; P:complement activation; IDA.
DR GO; GO:0045022; P:early endosome to late endosome transport; IDA.
DR GO; GO:0008333; P:endosome to lysosome transport; IDA.
DR GO; GO:0006911; P:phagocytosis, engulfment; IDA.
DR GO; GO:0006910; P:phagocytosis, recognition; IDA.
DR GO; GO:0050871; P:positive regulation of B cell activation; IDA.
DR GO; GO:0050778; P:positive regulation of immune response; IDA.
DR GO; GO:0050766; P:positive regulation of phagocytosis; IDA.
DR GO; GO:0001812; P:positive regulation of type I hypersensitivity; IDA.
DR GO; GO:0001798; P:positive regulation of type I hypersensitivity; IDA.
DR GO; GO:0030162; P:regulation of proteolysis and peptidolysis; IDA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin domain.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 26.2%; Score 924.5; DB 2; Length 473;
Best Local Similarity 33.8%; Pred. No. 4.7e-49;
Matches 239; Conservative 53; Mismatches 123; Indels 293; Gaps 15;

QY 1 EVQLQSGDPLVRFGASVKISCKASGYFTGYMHVWYKQSPKGLWIGRIINPNNGVTLY 60
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 QVQLKQSGAELVRFGASVKISCKASGYFTDYVINWVKQRPQGLWIGKIGPGSGSTY 79
QY 61 NQFQPKATLTVDKSSSTAYWELRLTSDSAVYFCARSTWITNYVMD---YWGQTSVT 117
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
80 NEKFGKATLTADKSSSTAYWQLSSLTSDSAVYFCARS---GYDYDFWYWGQGTTLT 135
QY 118 VSSAKTTPPSVPLAPGSAAGTSMVTLGCLVKGYPPEVTVTWNSGLSSGVHTTPPAVL 177
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
136 VSAAKTTPSVPLAPVCGGTTGSSVTLGCLVKGYPPEVTVTWNSGLSSGVHTFPALL 195
QY 178 QSDLYTLSSSVTPSPSTWPTVCNVAHPASSTKVDKIIVPRDSGGFSEKSEINEKOL 237
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
196 QSGLYTLSSSVTVTSNTWPSQTICNVAHPASSTKVDKIEPR----- 238
QY 238 RKKSLELQGTALGNLKOIYYNSKAITSSEKSAQDLTNTLLFKGFTGHPWYNDLLVDLG 297
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
239 ----- 238
QY 298 STAATSEYSGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNRLTEKKVPINLWID 357
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
239 -----VPI----- 241
QY 358 GKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGQGLVPHSSEGS 417
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
242 ---TQNPCLKECPCAA-----PDLLGGP----- 264
QY 418 TVSYDLFDAQGVDPDILLRIYRONTTISSTLSISLYLYTTSIVMTQPTSLILVAGDRV 477
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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DB 265 ----SVFIPEPKIKOVLV-----ISLSPWTCVV----- 290
QY 478 TITCKASQSVSNDVAVYQQKQSPKLLISYTSRYAGVDPDRFSGGYGDTFLTITSSVQ 537
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
291 -----DVSED-----DPDVQISW-----FVNVE 309
QY 538 AEDAAYVFCQODVNSPPTFGGTYKLEIKRAD----- 569
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
310 VHTAQQTQTHREDYNS--TLRVVSALPIQHDWMMSGKEFKCKVNNRALPSPIETISKPRG 367
QY 569 --AAPTYSIPPSSEQLTSGASVVCFLNNFYPKDINVKWIKIDGSEKQNGVLSWTDQDS 626
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
368 PVRAPQVYVLPPEAEETKPESLTCTMTGFLPAETAVDWTSGRTQN--YKNTATVLDS 426
QY 627 KDSTYSMSSTLTITKDEYERHNSYTCETHK-----TSTSPIVKSFN 669
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
427 -DGSYFMYSKLRVQKSTWERSLFCACSVVHEGLHNHLTTKTISSRLGK 473

RESULT 18
Q99SU3 STAA
ID Q99SU3 STAA PRELIMINARY; PRT; 260 AA.
AC Q99SU3; 2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin P.
GN Names: OrderedLocNames=SA1761;
OS Staphylococcus aureus (strain N315);
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP MEDLINE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshino A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Sekihisa M., Yamashita N., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240 (2001).
DR EMBL; BA000018; BAB43036.1; -, Genomic DNA.
DR PIR; C89984; C89984.
DR HSSP; P13163; 1SXT.
DR SMR; Q99SU3; 28-260.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bcrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH STREP TOXIN 1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 260 AA; 29708 MW; 087C5B4EC028CFDB CRC64;

Query Match 26.1%; Score 918; DB 2; Length 260;
Best Local Similarity 73.0%; Pred. No. 5.2e-49;
Matches 170; Conservative 21; Mismatches 42; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLKKSELOQTALGNLKOIYYNSKAITSSEKSAQDLTNTLLFKGFTG 285
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
28 SEKSEINEKDLKKSELOQTALGNLKOIYYNSKAITSSEKSAQDLTNTLLFKGFTG 87
QY 286 HPWNVDLLVDLGSSTAESEYSGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNRLT 345
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
88 HPWNVDLLVDLGSSTAESEYSGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNRLT 147

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QY 346 BEKKVPINLWIDGKQTTVPIDKVKTSKVEYVOELDLQARHYLHGKFLYNSDSFGKVKQ 405
DB 148 BEKKVPINLWIDGKQNTVGLTKVKTKVEYVOELDLQSRHYLHETYNLYNTDAFNGKIQ 207
QY 406 RGLIVPHSSEGSVSVYDLFDAQOQYPTDLLRIYRDNTTISSTLSLSLYLYTT 458
DB 208 RGLIEFHPSSGSDSVGYDLFQAQOQYPTQLRIYRDNKTIKSKWHDIDYLYTT 260

RESULT 19
Q66JS7_MOUSE
ID Q66JS7_MOUSE PRELIMINARY; PRT; 238 AA.
AC Q66JS7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE LOC243469 protein.
DE Names=LOC243469;
GN Mus musculus (Mouse)
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Richards S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RG NIH MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC080787; AAH80787.1; -; mRNA.
DR SMR; Q66JS7; 21-237.
DR Ensembl; ENSMUSG0000061260; Mus musculus.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07454; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 238 AA; 26317 MW; C1AF406948D76423 CRC64;

Query Match 25.8%; Score 910; DB 2; Length 238;
Best Local Similarity 80.4%; Pred. No. 1.4e-48;
Matches 176; Conservative 10; Mismatches 29; Indels 4; Gaps 1;

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QY 457 TTSIVMTPTPTSLVYSGDRVTITCKASOSVND----VAMVQOKPGQSPKLLISYTSSR 512
DB 19 TGDIVLTOSPASLAVSLGORATISCRASOSVSTSYMHMTYQOKPGQPKLLIKIASNL 78
QY 513 YAGVDPDRFSGSGYGTDFTLTISVQAEADAATVFCQDYNSPPTFFGGTGTLEIKRADAAPT 572
DB 79 ESGVPARFSGSGSGTDFTLNIHPVEEDATYYCQHSWEIPWTFGGGTNLEIKRADAAPT 138
QY 573 VSIFPPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNWTDDQSKDSTYS 632
DB 139 VSIFPPSSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNWTDDQSKDSTYS 198
QY 633 MSSTLTLTLDKDEYRNHSYTCETHTKTSTSTPIVKSFNRN 671
DB 199 MSSTLTLTLDKDEYRNHSYTCETHTKTSTSTPIVKSFNRN 237

RESULT 20
Q632X4_MOUSE
ID Q632X4_MOUSE PRELIMINARY; PRT; 241 AA.
AC Q632X4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RX TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RX TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
RA Director MGC Project;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC082779; AAH82779.1; -; mRNA.
DR SMR; Q632X4; 22-241.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07454; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IG; 1.

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DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein_1
FT NON_TER 1
SQ SEQUENCE 241 AA; 26865 MW; 3D5C4416D8E8C9B9 CRC64;

Query Match
Best Local Similarity 76.5%; Score 904; DB 2; Length 241;
Matches 182; Conservative 18; Mismatches 28; Indels 10; Gaps 3;

QY 444 ISSTLSISLYLT-----SIWTOPTSLVSAGDRVTITCKASQSV---SND---VAW 493
DB 3 VSETHVLIFLLWVSGACGEIVLTQISPLTISAGERTVTSCKNSQSLWSGNQRYCLW 62

QY 494 YQKPKQSPKLLISYTSRRYAGVDPDRFSGSGYGTDTLTITSSVQAEDAAVYFCQDYNP 553
DB 63 HQWPKQPTPLTWTSDRYSGVDPDRFVSGSVTDTLTITSSVQDEEDVAVYFCQHLHP 122

QY 554 PTFGGTGTGLEIKRADAAPTIVSIPPPSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSR 613
DB 123 PTFGTGTGLEIKRADAAPTIVSIPPPSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSR 182

QY 614 QNGVLNSWTDQDSKSTYSNSSTLTLTCKDEYERHNSYTCEATHTKSTSPIVKSFNRNE 671
DB 183 QNGVLNSWTDQDSKSTYSNSSTLTLTCKDEYERHNSYTCEATHTKSTSPIVKSFNRNE 240

RESULT 21
Q65ZC0_MOUSE PRELIMINARY; PRT; 219 AA.
AC Q65ZC0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Kappa light chain C region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RX MEDLINE=963119505; PubMed=8768802;
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Kappa light chain C region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c; TISSUE=Spleen;
RX MEDLINE=963119505; PubMed=8768802;
RA Kipp B., Schlaak M., Becker W.M.;
RT "Cloning and expression of a recombinant mouse Fab-fragment
RT recognizing a defined linear epitope of Chironomus thummi major
RT allergen Chi t 1.";
RL Int. Arch. Allergy Immunol. 110:348-353(1996).
DR EMBL; Z37499; CAA85724.1; -; mRNA.
DR SMR; Q65ZC0; 1-219.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; 1.
FT NON_TER 1
FT NON_TER 219
SQ SEQUENCE 219 AA; 23944 MW; 7E1B82A14EAF8445 CRC64;

Query Match
Best Local Similarity 80.2%; Score 901.5; DB 2; Length 219;
Matches 174; Conservative 15; Mismatches 23; Indels 5; Gaps 1;

QY 460 IYVTOPTSLVSAGDRVTITCKASQSV-----SNDVAVYQKPGSPKLLISYTSRVA 514
DB 2 LVMTQSPFLSVSLGDAQSISCRSSQSLVHTNGNTYLHWYLPGLSPKLLIYIVSNRFS 61
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QY 515 GVPDRFSGSGYGTDTLTITSSVQAEDAAVYFCQDYNPPTFGGKTKLEIKRADAAPTVS 574
DB 62 GVPDRFSGSGYGTDTLTITSSVQAEDAAVYFCQDYNPPTFGGKTKLEIKRADAAPTVS 121

QY 575 IFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKSTYSMS 634
DB 122 IFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKSTYSMS 181

QY 635 STLTLTCKDEYERHNSYTCEATHTKSTSPIVKSFNRNE 671
DB 182 STLTLTCKDEYERHNSYTCEATHTKSTSPIVKSFNRNE 218

RESULT 22
Q6PF95_MOUSE PRELIMINARY; PRT; 464 AA.
AC Q6PF95;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN Name-Igh-la;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RX Expression driven by an MMTV-LTR enhancer.;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
RA Altshuler R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Viallon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RX Expression driven by an MMTV-LTR enhancer.;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC057672; AAH57672.1; -; mRNA.
DR HSSP; P01865; 1KB5.
DR MGI; MGI:96443; Igh-la.
DR GO; GO:0003823; F-antigen binding; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
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Db 338 ----- 337
QY 474 GDRVTITCKASQSVSNDVAVYQKPGSKLLISYTSRVAGVDPDRFSGGYGDTFLTII 533
Db 338 -----TFCKV-----TSAPFSPFKTI 356
QY 534 SSVQAEADAVYFCQDYNPSPTFGGKTKLEIKRADAAPTVSIFFPSEQLTSGGASVVCVF 593
Db 357 SKPE-----GRQV-----PHYVTMSPTKEEMTQNEVSITCM 388
QY 594 LNNFYPKDINVKWKIDGSRQNGVLNSWTQDQSKDSTYSMSSTLTITLKDEYERHNSVTCE 653
Db 389 VKGYFPDIIYVQMNGQPOEN-YKNTPTPTMDT-DGSYFLYSLNVLNKKVKKQNGTFTCS 446
QY 654 ATHK 657
Db 447 VLHE 450

RESULT 27
Q8R3H6 MOUSE
ID Q8R3H6_MOUSE PRELIMINARY; PRT; 474 AA.
AC Q8R3H6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IgH protein.
GN Name=Ighb; Synonyms=AU044919;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH 11;
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max J., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZECH 11;
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
RA Director MGC Project;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025447; AAH25447.1; -, mRNA.
DR HSSP; P01869; 1CL7.
DR SMR; Q8R3H6; 20-470.
DR MGI; MGI:2144967; AU044919.
DR MGI; MGI:2144967; Ighb.
DR GO; GO:0003823; F-antigen binding; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin domain.
SQ SEQUENCE 474 AA; 51749 MW; 8608B57C6CD2874A CRC64;
Query Match 25.2%; Score 888.5; DB 2; Length 474;
Local Similarity 35.0%; Pred. No. 81e-47;
Matches 234; Conservative 69; Mismatches 124; Indels 241; Gaps 18;
QY 1 EVQLQSGDPLVKPGASVKISKASGYSTFTGYMHVYKQSPGKLEWIGRINPNNGVTLY 60
Db 20 QVQLQSGDPLVKPGASVKISKASGYSTFTGYMHVYKQSPGKLEWIGRINPNNGVTLY 79
QY 61 NQKFKDKATLTVDKSSITAYMELSLTSDSAVYCARSTMTITNYVMYDYGQGTSTVSS 120
Db 80 SGKFGKAKLTADKSSVTAFLQLTSLTSDSAVYFCARDSDYGDY-FDDWGQAGATVTSS 138
QY 121 AKTTPSPVYPLAPGSAQAQNSMVTGLCLVKGYFPEPVTVTWNSGSLSSSGVHTFPAVLQSD 180
Db 139 AKTTPSPVYPLAPGCGDTTGSSTVTLGCLVKGYFPEPVTVTWNSGSLSSSGVHTFPAVLQSG 198
QY 181 LYTLSSTVTPSTWSPSETVTCNVAHPASSTKYDKKIVPRDSCGPGSEKSEINE----KD 236
Db 199 LYTMSSTVTPSTWSPSETVTCNVAHPASSTKYDKKIVPRDSCGPGSEKSEINE----SGP---ISTINPCPKCE 252
QY 237 LRK--KSEIQGTALGNLKOIYYNSKAITSSSEKSAQDLTNTLLFKGFTFGHPHYNDLLV 294
Db 253 CHKCPAPNLEG--GPSVFIFPPNKDV-----LMI 280
QY 295 DLGSTAATSEYEGSSVDLYGAYVYQCAGTGNKTKACMYGGVTLHDNNRLTEKKVPINL 354
Db 281 SL-----TP----- 284
QY 355 WIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFLGSLNDSFGKVGQRLIVPHSS 414
Db 285 ----KVTGVVD-----VSEDDPDVQISWPNV-----VEVHTA 314
QY 415 EGSTVSYDLFDAQGYPTDLLRIYRNTTISSTLSLSLYLYTTSIVMTQPTSLLYSAG 474
Db 315 QTQTHREDY-----NSTIR-----VWSA- 332
QY 475 DRVTITCKASQSVSNDVAVYQKPGSKLLISYTSRVAGVDPDRFSGGYGDTFLTII 534
Db 333 -----LPIQHDWMSGKEFKCKVN 351
QY 535 SVOAEADAVYFCQDYNPSPTFGGKTKLEIKRADAAPTVSIFFPSEQLTSGGASVVCVF 594
Db 352 N-----KDLPSPIE---RTISKIKGLVRAPQVIVLPAPAEQLSRKDVSLTCLV 396
QY 595 NNFYPKIDINVKWKIDGSRQNGVLNSWTQDQSKDSTYSMSSTLTITLKDEYERHNS 649
Db 397 VGFNPGDISVETVTSNGHTTEENYKDTAPVLDS-----DGSYFIYSLDKDITKSKWEKTD 449
QY 650 YTCEATHK 657
Db 450 FSCNVRHE 457

RESULT 28
Q7TS98 MOUSE
ID Q7TS98_MOUSE PRELIMINARY; PRT; 236 AA.
AC Q7TS98;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-colorectal carcinoma light chain.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.

```

OX NCBI_TaxID=10090;
RN [1] NUCLEOTIDE SEQUENCE.
RX MEDLINE=9383497; PubMed=8372513;
RA Tonge D.W., Hennam J.F., Greene A.R., Lee I.D., Edge M.D.;
RT "Cloning and characterization of 116NS19.9 heavy and light chain
RT cDNAe and expression of antibody fragments in Escherichia coli.";
RL Year Immunol. 7:56-62(1993).
DR EMBL; S65921; AAB28160.1; -, mRNA.
DR HSP; P01837; IKB5.
DR SMR; Q7TS98; 23-236.
DR Ensemble; ENSMUSG0000061260; Mus musculus.
DR GO; GO:003823; F-antigen binding; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin domain.
SQ SEQUENCE 236 AA; 26455 MW; 2C586EBF5EA10F4C CRC64;

Query Match 25.2%; Score 886; DB 2; Length 236;
Best Local Similarity 79.2%; Pred. No. 4.4e-47;
Matches 168; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

QY 460 IVMTQPTTSLVSAGDRVTITCKASQSDNVAVYQKFGQSPKLLISTSYRYAGVDPDR 519
DB 24 IKWTQSPSMYASLGRVITITCKASQDINSYLFQKFGKSPKTLIYRANRLVDGVPSR 83

QY 520 FSGSGVGTDTLTITSSVQAEADAAYFCQDYNPPTFGGKTKLEIKRAAAPTTSIFPPS 579
DB 84 FSGSGQGDYSLTISSEYEDMGYICLYQDFPRTFGGKTKLEIKRAAAPTTSIFPPS 143

QY 580 SGLQTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLSWTDQSKDSTYSMSSTLT 639
DB 144 SGLQTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLSWTDQSKDSTYSMSSTLT 203

QY 640 TKDEYERHNSYTCEATHKTSPIVKSFNRE 671
DB 204 TKDEYERHNSYTCEATHKTSPIVKSFNRE 235

RESULT 29
Q569Y8 MOUSE Q569Y8 PRELIMINARY; PRT; 237 AA.
ID Q569Y8;
AC Q569Y8;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Igk-C protein.
GN Name=Igk-C;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1] NUCLEOTIDE SEQUENCE.
RP STRAIN=FVB/N; TISSUE=Kidney;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marudani K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Kidney;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC092251; AAB92251.1; -, mRNA.
DR SMR; Q569Y8; 23-237.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 237 AA; 25978 MW; A88596AA47FFB932 CRC64;

Query Match 25.0%; Score 880.5; DB 2; Length 237;
Best Local Similarity 75.9%; Pred. No. 9.7e-47;
Matches 170; Conservative 23; Mismatches 30; Indels 1; Gaps 1;

QY 449 LSIISLYTTSIVMTQPTTSLVSAGDRVTITCKASQSV-SNDVAVYQKFGQSPKLLIS 507
DB 13 ISVTILSGEIVLTQSPALMAASPGKVTITCSVSSSIDSSNLHWYQKSGTSPKAWY 72

QY 508 YTSRYAGVDPDRFSGSGVGTDTLTITSSVQAEADAAYFCQDYNPPTFGGKTKLEIKRA 567
DB 73 GTSNLASGVFPFRFSGSGGTSTSLTISSEADAATYTCQWNYPLTFGGTRLEIKRA 132

QY 568 DAAPTYSIFPPSPSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLSWTDQSK 627
DB 133 DAAPTYSIFPPSPSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLSWTDQSK 192

QY 628 DSTYSMSSTLTITKDEYERHNSYTCEATHKTSPIVKSFNRE 671
DB 193 DSTYSMSSTLTITKDEYERHNSYTCEATHKTSPIVKSFNRE 236

RESULT 30
Q58E08 MOUSE Q58E08 PRELIMINARY; PRT; 239 AA.
ID Q58E08;
AC Q58E08;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Igk-C protein.
GN Name=Igk-C;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1] NUCLEOTIDE SEQUENCE.
RP STRAIN=CZECH II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner F.S., Shenmen C.M., Schuler G.D.,
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitling M., Touchman J.W., Green E.D., Dickson M.C.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Marra M.A.,
 RA Schnierch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CECH II;
 RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.
 RC Expression driven by an MMTV-LTR enhancer.;
 RG NIH MGC Project;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR ENBL; BC091750; AAH91750.1; -; mRNA.
 DR SMR; Q58E08; 21-239.
 DR GO; GO:0003823; F:antigen binding; IEA.
 DR InterPro; IPR003599; Ig-like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 1.
 DR SMART; SM00409; IG1; 1.
 DR SMART; SM00407; IGcl; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
 SQ SEQUENCE 239 AA; 26302 MW; 98FCA8A8EB404215 CRC64;
 Query Match 25.0%; Score 879.5; DB 2; Length 239;
 Best Local Similarity 76.8%; Pred. No. 1.1e-46;
 Matches 175; Conservative 15; Mismatches 33; Indels 5; Gaps 2;
 QY 449 LSLSLVLTTSIVMTPTSLYSAGDRVTITCKASQSV--SND---VAVYQKPGQSPK 503
 DB 11 LVLSIQETNGDVMTQPLTSLVITGPASISCKSSQSLHSGKTYLWLLQRPQSPK 70
 QY 504 LLISYTSRRYAGVPDRFSGSGYGTDFLTITSSVQAEADAAVYFCQDYNSPPTFGGGTKLE 563
 DB 71 LLILVYSKLSGVPDRFSGSGSGTDFTLKISRVEADLVYVYCLQATHPRPTFGGGTKLE 130
 QY 564 IKRADAAPTYSIIPPSSEQLTSGGASVYVCFNNFYPKDINVKWKIDGSRQNGVLNSWTD 623
 DB 131 IKRADAAPTYSIIPPSSEQLTSGGASVYVCFNNFYPKDINVKWKIDGSRQNGVLNSWTD 190
 QY 624 QDSKDSYSSMSSTLTLLTKDYERHNSYTCETHKTSPIVKSFNNE 671
 DB 191 QDSKDSYSSMSSTLTLLTKDYERHNSYTCETHKTSPIVKSFNNE 238
 RESULT 31
 Q52L95_MOUSE PRELIMINARY; PRT; 236 AA.
 AC Q52L95_MOUSE
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitling M., Touchman J.W., Green E.D., Dickson M.C.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Marra M.A.,
 RA Schnierch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Kidney;
 RG NIH MGC Project;
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR ENBL; BC094013; AAH94013.1; -; mRNA.
 DR SMR; Q52L95; 23-236.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 1.
 DR SMART; SM00409; IG1; 1.
 DR SMART; SM00407; IGcl; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
 KW Hypothetical protein.
 SQ SEQUENCE 236 AA; 26446 MW; 570453C3B97CD655 CRC64;
 Query Match 24.7%; Score 871; DB 2; Length 236;
 Best Local Similarity 77.4%; Pred. No. 3.8e-46;
 Matches 164; Conservative 20; Mismatches 28; Indels 0; Gaps 0;
 QY 460 IVMTPTSLYSAGDRVTITCKASQSVSNDVAVYQKPGQSPKLLISYTSRRYAGVPDR 519
 DB 24 IKMTQSPSMYSVSLGSAVTITCKASQDIYSFLKWKFOKKFGPKPTLIYHTRDMDGVPSR 83
 QY 520 FSGSGYGTDFLTITSSVQAEADAAVYFCQDYNPPPTFGGGTKLEIKRADAAPTYSIIPPS 579
 DB 84 FSGSGGQDYSLTINSLECEDMGIIYVYCLQVDEPPLTFGGGKLELRADAAPTYSIIPPS 143
 QY 580 SEQLTSGGASVYVCFNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDSYSSMSSTLTLL 639
 DB 144 SEQLTSGGASVYVCFNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDSYSSMSSTLTLL 203
 QY 640 TKDEYERHNSYTCETHKTSPIVKSFNNE 671
 DB 204 TKDEYERHNSYTCETHKTSPIVKSFNNE 235
 RESULT 32
 Q5XFY8_MOUSE PRELIMINARY; PRT; 235 AA.
 ID Q5XFY8_MOUSE
 AC Q5XFY8_MOUSE
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)

```

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RG NIH MGC Project;
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC084683; AAH84683.1; -; mRNA.
DR SMR; Q5XPF8; 23-235.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25835 MW; 82859ED277FDC667 CRC64;

Query Match 24.7%; Score 870.5; DB 2; Length 235;
Best Local Similarity 76.2%; Pred. No. 4e-46;
Matches 170; Conservative 20; Mismatches 32; Indels 1; Gaps 1;

QY 449 LSISLYLYTTSIVMTQPTSLVSGADRVITTCASQSVNDVAVYQKQSPKLLISY 508
Db 13 ISASVIRSGQIVLTSQPAISGPGKVKVMTTCRASSV-NYMHVYQKPGSPKPWIYA 71

QY 509 TSSRYAGVDPFRSGSGYGTFTLTISVQAEADAAYVFCQDYNSPPTFGGTTKLEIKRAD 568
Db 72 TSKLASGVPARFSGSGSGTSYSLTIRVEAEDAATYCCQWSSNPLTFGAGTLEIKRAD 131

QY 569 AAPTIVFPFPSSQLTSGGASVVCFLNNFYKPDINVKWKIDGSRQGVLSNSTDQDSKD 628
Db 132 AAPTIVFPFPSSQLTSGGASVVCFLNNFYKPDINVKWKIDGSRQGVLSNSTDQDSKD 191

QY 629 STYSMSSTLTLTQDEYRNHSYTCETHTKTSTSPVKSFNRN 671
Db 192 STYSMSSTLTLTQDEYRNHSYTCETHTKTSTSPVKSFNRN 234
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RESULT 33
Q58EV6_MOUSE PRELIMINARY; PRT; 235 AA.
ID Q58EV6_MOUSE PRELIMINARY; PRT; 235 AA.
AC Q58EV6;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Igk-C protein.
GN Name=Igk-C;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC091736; AAH91736.1; -; mRNA.
DR SMR; Q58EV6; 23-235.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 235 AA; 25719 MW; BE4E4ABDD2578252 CRC64;
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Query Match 24.6%; Score 867.5; DB 2; Length 235;
Best Local Similarity 75.8%; Pred. No. 6.2e-46;
Matches 169; Conservative 20; Mismatches 33; Indels 1; Gaps 1;

QY 449 LSISLYLYTTSIVMTQPTSLVSGADRVITTCASQSVNDVAVYQKQSPKLLISY 508
Db 13 ISASVIRSGQIVLTSQPAISGPGKVKVMTTCRASSV-NYMHVYQKSGTSPKRWIYD 71

QY 509 TSSRYAGVDPFRSGSGYGTFTLTISVQAEADAAYVFCQDYNSPPTFGGTTKLEIKRAD 568
Db 72 TSKLASGVPARFSGSGSGTSYSLTISSEAEADAATYCCQWTSNPLTFGAGTKLDLKRAD 131
```

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QY 569 AAPTVPSPSSSEQLTSGGASVVCFLNFPKQINVKWKIDGSRQGVLSNWTDDQSKD 628
Db 132 AAPTVPSPSSSEQLTSGGASVVCFLNFPKQINVKWKIDGSRQGVLSNWTDDQSKD 191
QY 629 STYSMSSTLTITKDEYERHNSYTCETHKTSTSPVKSPNRNE 671
Db 192 STYSMSSTLTITKDEYERHNSYTCETHKTSTSPVKSPNRNE 234

RESULT 34
Q65ZQ1_HUMAN
ID Q65ZQ1_HUMAN PRELIMINARY; PRT; 458 AA.
AC Q65ZQ1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Anti-colorectal carcinoma heavy chain.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93383497; PubMed=8372513;
RA Tonge D.W., Hennam J.F., Greene A.R., Lee I.D., Edge M.D.;
RT "Cloning and characterization of 1116NS19.9 heavy and light chain
RT cDNAs and expression of antibody fragments in Escherichia coli.";
RL Year Immunol. 7:56-62(1993).
CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC histocompatibility complex class I molecules (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
DR EMBL; S65761; AAB28159.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR PFam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
KW Immunoglobulin domain.
SQ
SEQUENCE 458 AA; 50602 MW; 4AEA29F9981D8DFF CRC64;

Query Match 24.6%; Score 867.5; DB 2; Length 458;
Best Local Similarity 22.3%; Pred. No. 1.6e-45;
Matches 216; Conservative 69; Mismatches 126; Indels 257; Gaps 16;

QY 1 EVLQSQGPDVLRFGASVKISKASGYSTGYTMHWYKQSPGRGLEWIGRI--NPNNGV 58
Db 20 EVKLESGGGLVQPGGSMKLSAASGFTFSDAWMDWVRQSPKGLWVAEIGNKNNHAT 79
QY 59 LYNQKFKDATALVDKSSYATYMELRITSEDAVYICARSTMITNYMDYWGCGSTVT 118
Db 80 YYAESVKGRTFVRDSDSKSRVYLQMSLRVEDTGTYCT-----TRFA--YMGQGLTV 132
QY 119 SSAKTPPSVYPLAPGSAATNSMTVLGCLVKGVFPPEVTVTVNWSGLSSGVHTFPAVLQ 178
Db 133 SAAKTPPSVYPLAPGSAATNSMTVLGCLVKGVFPPEVTVTVNWSGLSSGVHTFPAVLQ 192
QY 179 SLDYTLSSSVTVPSSTWSPSTVTCNVAHPASSTKVDKKIYPRDSGGPSEKSEINEKDLR 238
Db 193 SLDYTLSSSVTVPSSTWSPSTVTCNVAHPASSTKVDKKIYPRDCG-----237
QY 239 KKSLEQGTALGNLKQIYYNYSKAITSSEKSAQDFLTWLLFKGFTTGHYPYNDLLVDLGS 298
Db 238 --CKPCICTVPEVSSVFIPFPK-----PKDVLATITL-----266
QY 299 TAATSEYEGSSVDLYGAYGVQCAGGTPTNCTACMYGGVTVLHDNNRLTEKKVPLNWLIDG 358
Db 267 -----TP-KVTCVVVDIS-----KDDPEVQSFVFD-291
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QY 359 KQTTVIDKVKTSKEV-----TYVELDLQARHYLHGK-FGL-YNSDSFGCKVQVRLI 409
Db 292 ---DVEVHTAQTPRBEQENSTFRSVELPFIHQDWLNGKEFKCRVNSAAPPAPIER-- 345
QY 410 VFHSSSGSTVSVDLPDAQGYPTDLLRIYRDNTTISTSTLSISLYLTITVTQTPTSL 469
Db 346 -----TISKT-----350
QY 470 LVSAGDRVTITCKASQSVSNDAWYQQKQPGSKLLISYTSRYAGVDPDRFSGSGYGTDF 529
Db 351 -----350
QY 530 TLTISVQAEADAAYVFCQDYNSPPTFGGKTLEIKRADAAPTVTFPPSSSEQLTSGAS 589
Db 351 -----KGRKPAQVQVYTIPTPPKQMAKDKVS 375
QY 590 VVCFLANFYPKDINVKWKIDGSRQGVLSNWTDDQSKDSTYSMSSTLTITKDEYERHNS 649
Db 376 LTCMTDFFEDITVWQWNGQPAEN-YKNTQIPMDT-DGSYFYVSKLVQKNWEAGNT 433
QY 650 YTCEATHK 657
Db 434 FTCSVLHE 441

RESULT 35
Q5XKG4_MOUSE
ID Q5XKG4_MOUSE PRELIMINARY; PRT; 234 AA.
AC Q5XKG4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426030999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Maman A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland;
RA Director MGC Project;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC01349; AAH31349.1; -; mRNA.
DR SNR; Q5XKG4; 16-234.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
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ID Q5M7V3_RAT PRELIMINARY; PRT; 461 AA.
AC Q5M7V3;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE LOC367586 protein.
DE Names=LOC367586;
GN Rattus norvegicus (Rat).
OS Mammalia; Eutheria; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosak S.A., Touchman J.W., Green E.D., Dickinson M.C.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RG NIH MGC Project;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC histocompatibility complex class I molecules (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
DR EMBL; BC088423; AAH8423.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGcl; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
KW Immunoglobulin domain; Repeat.
SQ SEQUENCE 461 AA; 50949 MW; 25EA4ECB6F0P5A9 CRC64;

Query Match 24.2%; Score 852; DB 2; Length 461;
Best Local Similarity 31.9%; Pred. No. 1.4e-44;
Matches 211; Conservative 78; Mismatches 131; Indels 242; Gaps 15;

QY 1 EVQLQGGPGLVKPGASVKISKASGYSTFTGYTHHWVKSPGKGLWIGRINPNNGVTLY 60
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 NQKFKDKATLVDSSTTAINELRSLTSEDSAVYICARSTMTINVDYWGQGTSTVTSV 120
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 80 RDSVKGRFTISRDAKSTLYLQMSLSRSEDATYICATNRWLLHLLHYDFYWGQGMVTVSS 139
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 AKTTPSPVYPLAGSAQNTSMVTLGCLVKGYFPEPVTVTVNSGSLSSGHTHPAVLQSD 180
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 140 AETAPSVYPLAPGALTKSNMVTGLCLVKGYFPEPVTVTVNSGALSSGVHTHPAVLQSG 199
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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QY 61 NQFKDKATLVKSGSTTAYMELSLTSDSAVYCARSTMTNY-----VMDYWGQGT 115
Db 80 VPKFQDKATLVKSGSTTAYMELSLTSDSAVYCARSTMTNY-----LFGYDGRDYFYWGQGT 135
QY 116 VVSSAKTTPSPVPLAPGAAQTNMVTGLGVKGYFPEPVTWNSGSLSSGVHTFPA 175
Db 136 ITVSSAKTTPSPVPLAPGCGDTTGGSTVGLGVKGYFPEPVTWNSGSLSSGVHTFPA 195
QY 176 VLQSDLYTLSSVTPSPSTWSETVTCNVAHPASSTKVDDKIVPRDGGPSEKSEELNE- 234
Db 196 LQSLGYTMSSVTPSPSTWSETVTCNVAHPASSTKVDDKIVPRDGGPSEKSEELNE- 249
QY 235 ---KDLRK--KSELQGTALGNLKOIYYNYSKAITSEKSDAQFLNTLLFKGFTGHPWY 289
Db 250 PPCKECHKCAPNLEG--GPSVFIFPPNIKDV----- 279
QY 290 NDLLVDLGSAAATSEYEGSSVDLYGAYGYQCAGGTENKTCACMYGGVTLHDNNRLTEKK 349
Db 280 --LMISL-----TP----- 286
QY 350 VPINLWIDGKQTTVPIDKVKTSKEVTVOBLDLOARHYLHGKFGLYNDSFGGKVORGLI 409
Db 287 -----KVCVVVD-----VSEDDPDVQISWFVN-----V 311
QY 410 VFHSSEGSTVSYDLFDAQGYQPTLLRIYRDNTTISSTLSISLYLTTISVMTQPTSL 469
Db 312 EVHTAQOTQTHREDY-----NSTIR----- 330
QY 470 LVSGADRVITCKASQSVSNDAVYQKQKPGQSKLLISYTSRYAGVDPFSGSGYGTDF 529
Db 331 VVSA-----LPIQHQMWSGKEF 348
QY 530 TLTISSVQAEADAAVYFCQDYNPPTFGGQTKLEIKRADAAPTVSIPPSPSEOLTSGGAS 589
Db 349 KCKVNN-----KDLPEPIE---RTISKIKGLVRAPQVYILPPAEQLSREDVS 393
QY 590 VVCFANFPKIDINVKKIDGSEKQN-----GVNLNWDQDSDKSTYSMSSTLTLDKDEY 644
Db 394 LTLGVGFPNGDISVETNSGHTENYKDTAPVLDS-----DGSFYIYKLDIKTSKW 446
QY 645 ERHNSYTCEATHK 657
Db 447 EKTDSFSCNVRHE 459

RESULT 40
Q5M842_RAT PRELIMINARY; PRT; 458 AA.
AC Q5M842;
DT 01-FEB-2005 (T-EMBLrel. 29, Created)
DT 01-FEB-2005 (T-EMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (T-EMBLrel. 29, Last annotation update)
DE Gamma-2a immunoglobulin heavy chain.
GN Name=IGG-2a;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Beta-2-microglobulin is the beta-chain of major
histocompatibility complex class I molecules (By similarity).
CC -I- SUBCELLULAR LOCATION: Secreted (By similarity).
DR EMBL; BC088240; AAH88240.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG1; 2.
DR SMART; SM00406; IG1; 1.
DR PROSITE; PS50835; IG LIKE; 4.
KW Immunoglobulin domain; Repeat.
SQ SEQUENCE 458 AA; 50268 MW; 0CB5AA613DD9439 CRC64;
Query Match 23.6%; Score 832.5; DB 2; Length 458;
Best Local Similarity 31.4%; Pred. No. 2,3e-43;
Matches 208; Conservative .77; Mismatches 132; Indels 245; Gaps 17;
QY 1 EVOLQSGDPLVKPGASVKISCKASGYSTFTGYMHVWKQSPGKLEWIGRINPNNGVTLY 60
Db 20 QVQLMESGPGLVQPSSETSLICTVSGFSLTSYNVHWVROPKPKGLEMMG-VMMSGGNTDY 78
QY 61 NQFKDKATLVKDSSTTAYMELSLTSDSAVYCARSTMTNYVMDYWGQGTSTVTS 120
Db 79 NSALKSRSLISRDTSKNQVFLKMSLQSEDAITTYCAREGY--PYFNYWGQGVMTVTS 136
QY 121 AKTTTPSPVPLAPGAAQTNMVTGLGVKGYFPEPVTWNSGSLSSGVHTTTPAVLQSD 180
Db 137 AETTAPSVPLAPGTALKNSMTVGLGVKGYFPEPVTWNSGSLSSGVHTTTPAVLQSG 196
QY 181 LYTSSSVTPSPSTWSETVTCNVAHPASSTKVDDKIVPRDGGPSEKSEINEKDLRKK 240
Db 197 LYTSSSVTPSPSTWSSQAVTCNVAHPASSTKVDDKIVPRE- 238
QY 241 SELQGTALGNLKOIYYNYSKAITSEKSDAQFLNTLLFKGFTGHPWYNDLVDLGSTA 300
Db 239 -----NPGCTGSEVSS-----VFIFPKTKDVL----- 262
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTENKTCACMYGGVTLHDNNRLTEKKVPINLWIDG-- 358
Db 263 -----ITL-----TP-KVTCVVVDISQND-----PEVRFSEWFDIDVE 294
QY 359 ---KQTTVPIDKVKTSKEVTVOBLDLOARHYLHGKFGLYNDSFGGKVORGLIVFHSSE 415
Db 295 VHTAQTHAPEKQSNSTLR--SVSELPVHRDNLNGK-----TFCKVNN----- 335
QY 416 GSTVSYDLFDAQGYQPTLLRIYRDNTTISSTLSISLYLTTISVMTQPTSLVLSAGD 475
Db 336 -----SGAFPAI----- 343
QY 476 RVITICKASQSVSNDAVYQKQKPGQSKLLISYTSRYAGVDPFSGSGYGTDFTLTIS 535
Db 344 -----EKSIS-----KEGTPTP----- 355
QY 536 VQAEADAAVYFCQDYNPPTFGGQTKLEIKRADAAPTVSIPPSPSEOLTSGGASVVCFLN 595

[3]
 RP NUCLEOTIDE SEQUENCE.
 RA PubMed=7498516; DOI=10.1016/0014-5793(95)01224-3;
 RX Takagi M., Kohda K., Hamuro T., Harada A., Yamaguchi H., Kamachi M.,
 Imanaka T.;
 RT "Thermostable peroxidase activity with a recombinant antibody L chain-
 RL porphyrin Fe(III) complex";
 DR EMBL; BC010327; AAH10327.1; -; mRNA.
 DR FIR; S68213; S68213.
 DR HSSP; P01783; 1IGC.
 DR SMR; Q91205; 20-469.
 DR MGI; MGI:2144967; AU044919.
 DR MGI; MGI:2144967; I9hg.
 DR GO:0003823; F:antigen binding; IEA.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; C1-aet; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Immunoglobulin domain.
 SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;
 Query Match 22.8%; Score 803; DB 2; Length 473;
 Best Local Similarity 32.0%; Pred. No. 1.7e-41;
 Matches 214; Conservative 74; Mismatches 138; Indels 242; Gaps 18;
 QY 1 EVQLQSGDPLVKPGASVKISKASGYSTGYVHWVKSPGKGLSWIGRIIPNNGVTLY 60
 DB 20 EVQLVPSGGLVAPGGRKSLKCAASGFTSDYGMHWVRQAPKGLWVAIVYNGSTIIY 79
 QY 61 NQKFKDKATLTVDKSSTTAYMELRSITSDSAVYCARSTMTITNYMDYMGQTSITVSS 120
 DB 80 ADTVKGRFTISRDAKNTLFLQMTLSRSDTAMYYCARELWLR--IDYWGQGTITVSS 137
 QY 121 AKTTPSVPLAPGSAQAQNSMTGLCLVKGYFPEVPTVWNSGSLSSGVHFPVAVLQSD 180
 DB 138 AKTTPSVPLAPGCGDGTGSSVTLGLVKGYFPESVTVWNSGSLSSGVHFPVAVLQSG 197
 QY 181 LYTLSSTVTPSTWPTSETVTCNVAHPASSTKYDKKIVPRDSGPGSEKSEELNE---KD 236
 DB 198 LVTMSSTVTPSTWPTSEVTVCSVAHPASSTVDDKLEP---SGP---ISTINCPCKE 251
 QY 237 LRK--KSELQGTALGNLKOIYYNSKAITSSSEKADQFLNTLLFKGFTTGHVPWYNDLIV 294
 DB 252 CHKCPAPNLEG---GPSVFIFPPNIKDV-----LMI 279
 QY 295 DLGSTAATSEYEGSSVDLYGAYGYOCAGGTNKTACMYGGVTLHNNRLTEKKVPINL 354
 DB 280 SL-----TP----- 283
 QY 355 WIDGKOTVPIDKVTSKKEVTVQELDLQARHVLHGKFGLYNSDSFGGKVGRLIVFHSS 414
 DB 284 ----KVTGVVD-----VSDDPDVQISFPVNN-----VEVHTA 313
 QY 415 EGSSTSYDLFDAQGGVPTLLRIYRNTTISSTLSLSLYLVTTSIVMTQTPTSLVAVSAG 474
 DB 314 QTQTHREDY-----NSTIR-----VISA- 331
 QY 475 DRVTITCKASQSVSNDAVYQKPGQSKLLISYTSRAGVDPDRPSGGYGTDFTLTIS 534
 DB 332 -----LPIQHDWMSGKEFKCKYN 350
 QY 535 SVQAEDAADVFCODYNSPPTFGGKLEIKRADAAPTYSIFPPSSEQLTSGGASVVCFL 594
 DB 351 N-----KDLPSPIE---RTSIKIKGLVRAPOVYILPPPAQLSRKDVSLTCLV 395
 QY 595 NNFPYKDIINVKWIDGSRQN-----GVLSMTDQDSKDSYMSSTLTLTDKDEYERHNS 649
 DB 396 VGFNPGDISVEMTSNGHTEENYKDTAPVLD-----DGSYFIYSKLDIKTSKWEKTD 448

QY 650 YTCETHK 657
 DB 449 FSCNVRHE 456
 RESULT 44
 Q4KM66 RAT PRELIMINARY; PRT; 234 AA.
 AC Q4KM66;
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Hypothetical protein.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Thymus;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vialalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Thymus;
 RG NIH MGC Project;
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC098746; AAH98746.1; -; mRNA.
 KW Hypothetical protein.
 SQ SEQUENCE 234 AA; 25692 MW; DPA12A3F8801666D CRC64;
 Query Match 22.5%; Score 791; DB 2; Length 234;
 Best Local Similarity 68.2%; Pred. No. 3.4e-41;
 Matches 152; Conservative 29; Mismatches 38; Indels 4; Gaps 1;
 QY 453 LVLYTT----SIVMTQTPTSLVAVSAGDRVTITCKASQSVSNDAVYQKPGQSKLLISY 508
 DB 11 LLLWTHAICIDRMQTQSPASLSASLGVTNIECLASDIYSLAWYQKPGKSPQLLIYN 70
 QY 509 TSSRYAGVDPDRPSGGYGTDFTLTISVQAEDAADVFCODYNSPPTFGGKLEIKRAD 568
 DB 71 ANSLQNGVPSRSGSGSGTQYSLKINSLOQSDVATYFCQYNNYPTWFGGKLEIKRAD 130
 QY 569 AAPTYSIFPPSSEQLTSGGASVVCFLNNFPYKDIINVKWIDGSRQNQVLSMTDQSDK 628
 DB 131 AAPTYSIFPPSTEQLATGASVVCFLNNFPYKDIINVKWIDGSRQNQVLSMTDQSDK 190
 QY 629 STYSMSSTLTLTDKDEYERHNSYTCETHKTSPIVKSFNRE 671
 DB 191 STYSMSSTLTLTADYESHNLITCEVVHKTSSPPVVKSFNRE 233


```
Matches 202; Conservative 73; Mismatches 202; Indels 185; Gaps 13;
QY 1 EVOLQSGDPLVKGASVKISCKASGYSTGYMHWVKQSPGKLEWIGRINPNNGVTLY 60
DB 20 QVHLVQSGAEVKKGASVKYCTASGYPTNFHFINWVRQAPGQSGLEWGWINTGNTKY 79
QY 61 NQPKDKATLTVDKSSTAYMELASLTSSESAVYICARSTM--ITNVYMDYWGQSTVTV 118
DB 80 SOKPQGRVTTTRDTWTMTAYMDLSLSESDTAVWCARDAPQGVTTTTFYFYWGQSTLTV 139
QY 119 SSATTPPSVYPLAPGSAQAQNSMTLGLVKGYFPEPVTWNSGSLGVTFFPAVLQ 178
DB 140 SSASTKGPSVFPPLAPCSRSTSGGTAALGCLVKDYFPEPVTWNSGALTSVGHVTFPAVLQ 199
QY 179 SD-LYTLSSSVTVPSSTWSPSETVTCNVAHPASSTKVDKIVPRDSGGPSEKSEINEKDL 237
DB 200 SSGLYSLSSVTVPSSSLGQTCTYCNVNHKPSNTKVDKRV----- 239
QY 238 RKXSELQGTALGNLQIYYNSKAITSSSEKSAQDLNTLLFKGFTTGHWPYNDLLVDLG 297
DB 240 -----ELKTPLG 246
QY 298 STAATSEYEGSSVDLYGAYGYQCAGGTPNKT--ACMYGGVTLLHNNRLTEEKVPINLW 355
DB 247 DTHTTCP-----RCPEPKPCDTPPC-----PRCEPKSC----- 276
QY 356 IDGKQTTVPIDKVKTSKKEVTVQBLDQARHYLHGKFGLYNSDSFGKGKVGRLIVHSE 415
DB 277 -----DTPEPCPEPKSCDTPPCPCPAPELLGGPSVF---LFPKPKDTLMISRTPE 329
QY 416 GSTVSVDLPAQGYPTLLRIYRDNNTTISLTSLSLYLYTTSIVMTQPTTSLLSAGD 475
DB 330 VTCV---VVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQVNSTFRVSVLTVLHQDLN 386
QY 476 RVITCKASQSVNDVAWYQKQPKQSKLLISYTSRYAGVDPDRFSGSGYGTDFTLTSS 535
DB 387 GKYEKKCVS-----NKALPAP---IEKTIKTKGP----- 414
QY 536 VQAEADAAYVFCQDYNPSPTFGGKTKLEIKRADAAPTVISFPSPSEQLTSGGASVVCFLN 595
DB 415 -----REPOVYTLPSREEMTKNQVSLTCLVK 441
QY 596 NFPVKDINVKWKIDGSRQNGVLNSWTDQDSKQSTYSMSSTLTLTKDYEYRHNSYTCAT 655
DB 442 GFYPSDIAVEWESSGQPENN--YNTTPMLDSDSGSFYLSKLTVDKSRWQGNIFSCVM 499
QY 656 HK 657
DB 500 HE 501

RESULT 50
Q727P5_HUMAN
ID Q727P5_HUMAN PRELIMINARY; PRT; 469 AA.
AC Q727P5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGH1 protein.
GN Name=IGH1;
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haefl F.,
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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051328; AAH51328.1; -; mRNA.
DR HSSP; P01857; IHZH.
DR SMK; Q7Z7P5; 20-469.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Immunoglobulin domain.
SQ SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;

Query Match 21.3%; Score 750; DB 2; Length 469;
Best Local Similarity 30.3%; Pred. No. 3.2e-38;
Matches 201; Conservative 70; Mismatches 156; Indels 236; Gaps 16;
QY 1 EVOLQSGDPLVKGASVKISCKASGYSTGYMHWVKQSPGKLEWIGRINPNNGVTLY 60
DB 20 QVHLVQSGAEVKKGASVKYCTASGYPTNFHFINWVRQAPGQSGLEWGWINTGNTKY 79
QY 61 NQPKDKATLTVDKSSTAYMELASLTSSESAVYICARSTMITNVYMDYWGQSTVTVSS 120
DB 80 ARKQGRVMTTDTSTATTSMYFSLRSDDTALFYCATKSRGQVDFDSGQGTLTVTSS 139
QY 121 AKTTPPSVYPLAPGSAQAQNSMTLGLVKGYFPEPVTWNSGSLGVTFFPAVLQSD 180
DB 140 ASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSVGHVTFPAVLQSS 199
QY 181 -LYTLSSSVTVPSSTWSPSETVTCNVAHPASSTKVDKIVPRDSGGPSEKSEINEKDLRK 239
DB 200 GLYSLSSVTVPSSSLGQTCTYCNVNHKPSNTKVDKKEVPKSC----- 242
QY 240 KSELQGTALGNLQIYYNSKAITSSSEKSAQDLNTLLFKGFTTGHWPYNDLLVDLGST 299
DB 243 -----DKHTTCPAPPELLGGPSVF--LFPKPK--KDTLM----- 274
QY 300 AATSEYEGSSVDLYGAYGYQCAGGTTPNKTACMYGGVTLLHNNRLTEEKVPINLMDGK 359
DB 275 -----ISRTPEVT--CVVVDVS-----HEDPEVKFNWYVDG-- 303
QY 360 QTTVPIDKVKTSKKEVTVQBLDQARHYLHGKFGLYNSDSFGKGKVGRLIVHSEGSTV 419
DB 304 ---VEVHNAKTKPREQ-----YNSTY---RVSVLTVLHQDWLNGK 339
QY 420 SYDLFDAQGYPTLLRIYRDNNTTISLTSLSLYLYTTSIVMTQPTTSLLSAGDRVTI 479
DB 340 EY----- 341
QY 480 TCASQSVSNDAWYQKQPKQSKLLISYTSRYAGVDPDRFSGSGYGTDFTLTSSVQAE 539
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Db 140 WGGQPTVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPPEVTVVSNWNGALTS 199
QY 170 VHTFPAVLQSD-LYTLSSSVTVSPSTWPTVCNVAHPASSTKDKKIVPRDSDGSPSEK 228
Db 200 VHTFPAVLQSSGLYSLSSVTVSPSSLGATQYICNVNHRKPSNTKDKRVEPKSC----- 253
QY 229 SEEINEKDLRKXSELQGTALGNLQIYYNNSKAITSSKSAQDFLNTLLEKGFTHGHPW 288
Db 254 -----DKHTCPCPAPPELLGGPSVF--LFPKP- 280
QY 289 YNDLLVLDGSTAATSEYEGSSVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLTEBK 348
Db 281 -KDTLM-----ISRTPEVT-CVVVDVS-----HEDP 304
QY 349 KVPINWIDGKQTVPIDKVKTSKEVTVQVELDLQARHYLHGKFLYNSDSFGGKVQGL 408
Db 305 EVKFNWYVDG---VEVHNAKTPREEQ-----YNSTY---RVVSVL 339
QY 409 IVFHSSEGTSVSDLPDAQOQYPTDLLRIYRDNTTISSTLSLSLYLTYTSIVMTQPTS 468
Db 340 TVLHQDWLNGKEY----- 352
QY 469 LLVSAGDRVTITCKASQSVNDVAMVQQKPGSPKLLISYTSRYAGVDPDRFSGGYGTD 528
Db 353 -----KCKVS-----NKALPAP---IEKTSKAGQP----- 376
QY 529 FTLTSSVQAEADAANYFCQDYNPSPTFGGTTKLEIKRADAPTYSIFPPSSEQLTSGGA 588
Db 377 -----REPQVYTLPPSREEMTKNOV 396
QY 589 SVVCFPLNYPKDVINVKWIDGSERON-----GVLSWTDQDSKDYTSMSSTLTITKDE 643
Db 397 STCLVKGYPSDIAVWESSNGQPNKYKTPPVLD-----DGSFFLYSKLTVDKSR 449
QY 644 YERHNSYTCETHK 657
Db 450 WQGNVFCVSMHE 463

RESULT 54
Q5EBM2 HUMAN PRELIMINARY; PRT; 519 AA.
AC Q5EBM2_HUMAN PRELIMINARY;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RA Director MGC Project;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC089421; RAH89421.1; -, mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 519 AA; 56813 MW; 988C5C2F9289E34C CRC64;
Query Match 21.0%; Score 741; DB 2; Length 519;
Best Local Similarity 30.1%; Pred. No. 1.3e-37;
Matches 199; Conservative 76; Mismatches 204; Indels 182; Gaps 14;
QY 1 EYQLQSQGPDLVKPGASVKISKASGYSTGYMHVVKSPGKLEWIGRIINPNNVTLY 60
Db 20 QVQLVQSGAEVKKPGASVKVSCVSGHTLTLSRHVRQAPGKLEWMMGGFDPEDGETVY 79
QY 61 NQKPKDKATLTVDKSTTAYMELRLSLTSDSAVYYCARST--MITNYV-MDYWGQSTSVT 117
Db 80 AQTQGRVMTEDTSTDTAYMDLSNLRSDDTAVYYCATGYDVLTCGYRFDYWGQGTQVT 139
QY 118 VSSASTKGPSVFLAPCSRSSTGGTAALGCLVKDYFPPEVTVVSNWNGALTS 177
Db 140 VSSASTKGPSVFLAPCSRSSTGGTAALGCLVKDYFPPEVTVVSNWNGALTS 199
QY 178 QSD-LYTLSSSVTVSPSTWPTVCNVAHPASSTKDKKIVPRDSDGSPSEKSEINEKD 236
Db 200 QSSGLYSLSSVTVSPSSLGATQYICNVNHRKPSNTKDKRVEPKSC----- 240
QY 237 LRKSELOQTALGNLQIYYNNSKAITSSKSAQDFLNTLLEKGFTHGHPWYNDLVDL 296
Db 241 -----ELKTP 246
QY 297 GSTAATSEYEGSSVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLTEKKVPINLWI 356
Db 247 GDTHTCP-----RC-----PEPKSC---DTPPCPCPCPEPKSC----- 277
QY 357 DGKQTTVPIDKVKTSKEVTVQVELDLQARHYLHGKFLYNSDSFGGKVQGLVHFSSEG 416
Db 278 ---DTPPCPCPCPEPKSCDTPPCPCPAPELLGGPSVF--LFPKPXDTLMISRTPEV 331
QY 417 STVSVDLFAQOQYPTDLLRIYRDNTTISSTLSLSLYLTYTSIVMTQPTSLVLSAGDR 476
Db 332 TCV---VVDVSHEDPEVQPKWYVDGVEVHNAKTPREEQYNSSTFRVSVLTVLHQDWLNG 388
QY 477 VIITCKASQSVNDVAMVQQKPGSPKLLISYTSRYAGVDPDRFSGGYGTDFTLTISV 536
Db 389 KKYKCKVS-----NKALPAP---IEKTSKTKGP----- 415
QY 537 QAEDAANYFCQDYNPSPTFGGTTKLEIKRADAPTYSIFPPSSEQLTSGGASVWVFLNN 596
Db 416 -----REPQVYTLPPSREEMTKNOVSLTCLVKG 443
QY 597 FYPKQINVKWIDGSRQNGVLSWTDQDSKDYTSMSSTLTITKDEYERHNSYTCETH 656
Db 444 FYPDSIAVWESSGQPNEN--YNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMH 501

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QY 657 K 657
Db 502 E 502

RESULT 55
Q6GMW1_HUMAN
ID Q6GMW1_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6GMW1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073791; AAH73791.1; -; mRNA.
DR SRR; Q6GMW1; 24-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PSS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25751 MW; 5BF6EA087AFAC437 CRC64;

Query Match 20.8%; Score 734; DB 2; Length 236;
Best Local Similarity 65.3%; Pred. No. 1.2e-37;
Matches 139; Conservative 27; Mismatches 47; Indels 0; Gaps 0;

QY 459 SIWMTPTSLVLSAGDRVTITCKASQSVSNDVAVYQKQKPGKLLIYSYRYAGVPD 518
Db 23 AIQMTQSPSLASVSGDRVTITCSQGISNDLIGWYQKQKPGKAPKLLIYAASLSQGVPS 82
QY 519 RFSGSGYGTDTLTITSSVQAEADAAYFCQDYNSPPTFGGGTKLEIKRADAPTVISIFPP 578
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QY	294	VDLGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLTEKKVPI	353
Db	280	M-----ISRTPEVT-CVVVDVS-----HEDPEVKFN	304
QY	354	LWIDGQTTVPIDKVKTSKEVTQVELDLQARHYLHGKFLYNSDSFGKGKVGQGLIVFHS	413
Db	305	WVDG---VEVHNAKTPREBQ-----YNSTY---RVSVLTVLHQ	339
QY	414	SEGSTVSYDLFDAQGOQYPTLLRIYRDNTTISSTLSISLYLYTTSIVMTQPTSLLSA	473
Db	340	DWLNKKEY-----	347
QY	474	GRVITTCASQSVSNDAVWYQKQKPGQSPKLLISYTSRYAGVDPFRFSGSGYGTDTLTI	533
Db	348	-----KCKVS-----NKALPAP---IEXTISKAKGP	371
QY	534	SSVQAEADAAYFCQQDYNSPPTFGGKTKLEIKRADAAPTIVSIPFSSSEQLTSGGASVWCF	593
Db	372	-----REPOVYTLPPSRDELTKNOVSLTCL	396
QY	594	LNNFPKIDINVKWIDGSRQN-----GYLNSWTDQDSKDYTSMSSTLTTLTKDEYERHN	648
Db	397	VKGFPDSIAVEVWSNGQPENNYKTPPVLDSE-----DGSFFLYSKLTVDKSRWQOQN	449
QY	649	SYTCEATHK 657	
Db	450	VFSCVMHE 458	
RESULT 57			
Q6N089 HUMAN			
ID	Q6N089_HUMAN	PRELIMINARY; PRT; 472 AA.	
AC	Q6N089;		
DT	05-JUL-2004 (TrEMBLrel. 27, Created)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)		
DE	Hypothetical protein DKFZp686P15220.		
GN	Name=DKFZp686P15220;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;		
OC	Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RC	NUCLEOTIDE SEQUENCE.		
RG	The German cDNA Consortium;		
RA	Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,		
RA	Fobo G., Han M., Wiemann S.;		
RL	Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BX640627; CAE45781.1; -; mRNA.		
DR	HSSP; P01861; IADO.		
DR	InterPro; IPR003599; Ig.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003597; Ig_c1.		
DR	InterPro; IPR003006; Ig_MHC.		
DR	Pfam; PF07654; C1-set; 3.		
DR	SMART; SM00409; IG; 2.		
DR	SMART; SM00407; IGc1; 3.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PS00835; IG_LIKE; 4.		
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_2.		
KW	Hypothetical protein.		
SQ	SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;		
Query Match 20.5%; Score 721.5; DB 2; Length 472;			
Best Local Similarity 29.3%; Pred. No. 1.9e-36;			
Matches 195; Conservative 71; Mismatches 161; Indels 239; Gaps 17;			
QY	1	EVQLQSGPDLVKPGASVKISCKASGYSTGYWMHWKQSPGKGLIEWIGRINPNNGVTLY	60
		: : : : : : : : : : : : : :	

Db	20	EVQLVESGGGLYQGRSLRLSCAASGFTEDDYAMHWVRQAPGKGLIEWSGISNGSIAY	79
QY	61	NQKFKDKATLTVDKASTTAYMELRLSLTSDSAVYYCARSTMITN---YMDYWGQGTSVT	117
Db	80	ADSVKGRFTISRDNKGNLSYLQMSLRADETALYYCAKEIGHNFYYYGNDVMGQGTIVT	139
QY	118	VSSAKTPPSVYPLAPGSAATNSMVTLCGLVKGPPEPVTWNSGSLSSSGVHTFPVAVL	177
Db	140	VSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDIPPEPVTVSWNSGALITSGVHTFPVAVL	199
QY	178	QSD-LYTTSSSVTFSPSTWPTVTCNVAPASSTKVDKKIVPRDSGGSPSEKSEENEXD	236
Db	200	QSSGLYSLSSVTVTFSSSLGTQYICNVNHKPSNTKVDKRVKPKSC-----	245
QY	237	LRKKSELOGTALGNLKOIYYNSKAITSEKSEADQLTNTLLFKGFTGHPWVNDLLVDL	296
Db	246	-----DKHTCTPCPAPELLGGPSVF--LFPKPK--KDTLM--	277
QY	297	GSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLTEKKVPI	356
Db	278	-----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYV	304
QY	357	DKQKQTTVPIDKVKTSKEVTQVELDLQARHYLHGKFLYNSDSFGKGKVGQGLIVFHS	416
Db	305	DG---VEVHNAKTPREBQ-----YNSTY---RVSVLTVLHQDWL	339
QY	417	STVSYDLFDAQGOYPTLLRIYRDNTTISSTLSISLYLYTTSIVMTQPTSLLSVAGDR	476
Db	340	NGKEY-----	344
QY	477	VITTCASQSVSNDAVWYQKQKPGQSPKLLISYTSRYAGVDPFRFSGSGYGTDTFTLTI	536
Db	345	---KCKVS-----NKALPAP---IEXTISKAKGP	368
QY	537	QAEDAAYFCQQDYNSPPTFGGKTKLEIKRADAAPTIVSIPFSSSEQLTSGGASVWCF	596
Db	369	-----REPOVYTLPPSRDELTKNOVSLTCLVKG	396
QY	597	FYPKIDINVKWIDGSRQN-----GYLNSWTDQDSKDYTSMSSTLTTLTKDEYERH	651
Db	397	FYPDSIAVEVWSNGQPENNYKTPPVLDSE-----DGSFFLYSKLTVDKSRWQO	449
QY	652	CEATHK 657	
Db	450	CSVMHE 455	
RESULT 58			
Q569F4 HUMAN			
ID	Q569F4_HUMAN	PRELIMINARY; PRT; 469 AA.	
AC	Q569F4;		
DT	10-MAY-2005 (TrEMBLrel. 30, Created)		
DT	10-MAY-2005 (TrEMBLrel. 30, Last sequence update)		
DT	10-MAY-2005 (TrEMBLrel. 30, Last annotation update)		
DE	IGHG1 protein.		
GN	Name=IGHG1.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;		
OC	Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Lymph;		
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klauser R.D., Collins F.S., Wagner L., Shenmen C.M., Schat N.K.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.G.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,		

```
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC092518; AAH92518.1; -, mRNA.
SQ SEQUENCE 469 AA; 51254 MW; AC13448E3047784F CRC64;

Query Match 20.4%; Score 719; DB 2; Length 469;
Best Local Similarity 29.3%; Pred. No. 2.7e-36;
Matches 194; Conservative 70; Mismatches 163; Indels 236; Gaps 16;

QY 1 EVLOQSGDPLVKPGASVKISKASGYFTGYVHWVKQSPGKLEWIGRINPNNGVTLY 60
DB 20 EVLVESGGVVPGGSLRLSCAASGFTFDYAHMWVRQAPGKLEWVLSLISWDGGSTY 79
QY 61 NQFKDKATLVDSKSTTAYMELRSLTSDSAVYCARSTMTINVMYDVGQSTVTS 120
DB 80 ADSVKGRFTISRDNKNSLYLQNSLRAEDTALYCATRGYTAGDYWGQGTTLVTS 139
QY 121 AKTTPSPVYPLAPGSAQTNSMTVGLVKGYPEPVTWVNSGSLSSGGVHTTTPAVLQSD 180
DB 140 ASTKGSPVPLAPGSKSTSGTALGCLVKDYPEPVTWVNSGALTSGVHTTTPAVLQSS 199
QY 181 -LYTLSSVTPGSTWPESTVTCNVHPASSTKVDKIVPRDSGGPSEKSEENKDLRK 239
DB 200 GLYSLSSVTPVPSGLTQTYICNVNKPSTKVDKKEPKSC----- 242
QY 240 KSELOGTALGNLQIYYNSKATSTSEKSAQDFLTNTLLFKGFTGHPWYNDLLVLDGST 299
DB 243 -----DKTHTCPCPAPPELLGGPSVF--LFPKPK--KDTLM----- 274
QY 300 AATSEYEGSDVLYGAYGYOCAGGTENKTCACMGVYTLHDNNRLTEKKVPINLWDGK 359
DB 275 -----ISRTPEVT-CVVVDV-----HEDPEVKFNWYDG- 303
QY 360 QTTVPIDKVKTSKEVTVBQLDQARHYLHKFGLYNSDSFGKQVQGLIVFHSSSGSTV 419
DB 304 ---VEVHNKTKPREEQ-----YNSTY---RVVSVLTVLHQDWLNGK 339
QY 420 SYDLFDAQGGYPTLLRIYRDNTTISTSLISLYLTTSTIVMTQPTSLLSAGDVTI 479
DB 340 EY----- 341
QY 480 TCKASQSVSDVAWYQKPGQSKLLISYTSRYAGVDPDRFGSGYGTDTLTATSSVQAE 539
DB 342 KCKVS-----NKALPAP---LEKTSIKAKGP----- 365
QY 540 DAAVYFCQDYNPGPTFGGKTKLEIKRADAAPTVSIPTSPSEQLTSGGASVWVCLANNFYP 599
DB 366 -----REPVYTLPPSRDELTKNQVSLTCLVKGFYF 396
QY 600 KDTNWKIKDGRQN-----GVLSNWTQDSKDSYSTMSSTLTTLTKDEYERHNSYTCEA 654
DB 397 SDIAVESNGQPNKYKTTTPVLDL-----DGSFFLYSKLTVDKSRWQQGNVPSCSV 449
QY 655 THK 657
DB 450 MHE 452
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RESULT 59
Q6PI81 HUMAN
ID Q6PI81 HUMAN PRELIMINARY; PRT; 478 AA.
AC Q6PI81;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE IGHM protein.
GN Name=IGHM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041037; AAH41037.1; -, mRNA.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGG1; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 478 AA; 52667 MW; 17BED38D917970D6 CRC64;

Query Match 20.4%; Score 717.5; DB 2; Length 478;
Best Local Similarity 29.0%; Pred. No. 3.4e-36;
Matches 195; Conservative 73; Mismatches 159; Indels 245; Gaps 18;

QY 1 EVLOQSGDPLVKPGASVKISKASGYFTGYVHWVKQSPGKLEWIGRINPNNGVTLY 60
DB 20 EVLVESGGVLPGGSLRLSCAASGFTTSSYVWVVRQAPGKLEWVNIKQDGSKEY 79
QY 61 NQFKDKATLVDSKSTTAYMELRSLTSDSAVYCARSTMTIT-----NYVMDYWG 111
DB 80 VDSVKGRFTISRDNKNSLYLQNSLRAEDTAVYCARFEFESTMTTNTVADYFYFMDVWG 139
QY 112 QGTSVTVSSNAKTTTPSPVYPLAPGSAQTNSMTVGLVKGYFPEPVTWVNSGSLSSGVH 171
DB 140 KGTTVTVSSASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSGVH 199
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QY 172 TPAVLQSD-LYTLSSSVTPSPWSETVTCNVAHPASSTKVKKIIVPRDGGPSEKSE 230
Db 200 TPAVLQSGLSLSSVTPSPSSLTQTYICNVNHPKNTKDKRVEPKSC----- 251
QY 231 EINEKDLKKSELQGTALGNLKKIYYNKAITSSEKSDAQFLTNLLFKGFFTGHPWYN 290
Db 252 -----DKTHTCPCPAPPELLGGPSVF--LFPKP--K 279
QY 291 DLLVDLGSTAATSEYEGSVLDLYGAYGYQCAGGTNKTACMYGGVTLHDNNRLTEKKV 350
Db 280 DTLM-----ISRTPEVT-CVVVDVS-----HEDPEV 304
QY 351 PINLWIDGKQTVPIDKVKTSKEVTVOELDLQARHYLHGKGLYNSDFGKGVQGLIV 410
Db 305 KFNWYVDG---VEVHNAKTPREEQ-----YNSTY---RVSVSLTV 339
QY 411 FHSSEGSTVSYDLFDAQGGVPTDLLRIYRDNTTISLSLSLYLTTISIVMTQTPTSL 470
Db 340 LHQDWLNGEY----- 350
QY 471 VSAGDRVTITCKASQSVSNDAWYQKPGQSPKLLISYTSRYAGVPDRFSGGYGTDFT 530
Db 351 -----KCKVS-----NKALPAP---IEKTISKAKGQP----- 374
QY 531 LTISSVQAEADAAYFCQDYNPPTFGGKTKLEIKRADAAPTIVISIPPSSEQLTSGGASV 590
Db 375 -----REPQVYTLPPSREEMTKNQVSL 396
QY 591 VCFNLNFPYKIDNVKWKIDGSRQN-----GVLSNMTDQDSKDYTSMSSTLTLTDEYE 645
Db 397 TCVLKGFSYSDIAVESNGQPNYKTPPVLDSE-----DGSFFLYSKLTVDKSRWQ 449
QY 646 RHNSYCEATHK 657
Db 450 QGNVFCVSMHE 461

RESULT 60
Q6GMX6 HUMAN
ID Q6GMX6 HUMAN PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McQuellan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
```

```
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBDJ databases.
DR EMBL, BC073766, AAH73766.1; -, mRNA.
DR GO; GO:0016022; C:integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match 20.3%; Score 715; DB 2; Length 465;
Best Local Similarity 29.7%; Pred. No. 4.7e-36;
Matches 197; Conservative 64; Mismatches 162; Indels 240; Gaps 18;

QY 1 EVQLQQSGDPLVKPGASVKISKASYSTGYMMHWKSPGKLEWIGRIINPNNGVTLY 60
Db 20 QVQLQESGPGLVKPSSETLSLTCTVSGGSIISGYIWSIRQAPAGKLEWIGRIY-TSGSTNY 78
QY 61 NQKPKDKATLTVDKSTTAYMELSLTSDSAVYTCARSTMITNYVMDYWGQSTSVTVSS 120
Db 79 NPSLSRVTVMSVDTSKNQPSLKSLSVTAADTAVIYCARGFT---YFDWGGQTLTVSS 135
QY 121 AKTTPSPVYPLAPGSAATNSMVTGLCLVKGYFPEPTVTWNSSGSLSSGVHTFPAYLQSD 180
Db 136 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 195
QY 181 -LYTLSSSVTPSPSTWPTVTCNVAHPASSTKVKKIIVPRDGGPSEKSEINEKDLRK 239
Db 196 GLYSLSVVTPSPSSLTGTYICNVNHPKNTKDKRVEPKSC----- 238
QY 240 KSELQGTALGNLKKIYYNKAITSSEKSDAQFLTNLLFKGFFTGHPWYNLDLVDLST 299
Db 239 -----DKTHTCPCPAPPELLGGPSVF--LFPKP--KDTLM----- 270
QY 300 AATSEYEGSVLDLYGAYGYQCAGGTNKTACMYGGVTLHDNNRLTEKKVPIINLWIDGK 359
Db 271 -----ISRTPEVT-CVVVDVS-----HEDPEVKNWYVDG- 299
QY 360 QTTVPIDKVKTSKEVTVOELDLQARHYLHGKGLYNSDFGKGVQGLIVFHSSEGSTV 419
Db 300 ---VEVHNAKTPREEQ-----YNSTY---RVSVSLTVLHQDWLNGK 335
QY 420 SYDLFDAQGGVPTDLLRIYRDNTTISLSLSLYLTTISIVMTQTPTSLVSGDRVTI 479
Db 336 EV----- 337
QY 480 TCKASQSVSNDAWYQKPGQSPKLLISYTSRYAGVPDRFSGGYGTDFTLTISVQAE 539
Db 338 KCKVS-----NKALPAP---IEKTISKAKGQP----- 361
QY 540 DAAVYFCQDYNPPTFGGKTKLEIKRADAAPTIVISIPPSSEQLTSGGASVVCFLNFPY 599
Db 362 -----REPQVYTLPPSREEMTKNQVSLTCLVKGFYYP 392
QY 600 KDINVKWKIDGSRQN-----GVLSNMTDQDSKDYTSMSSTLTLTDEYERHNSYTCFA 654
Db 393 SDLAWESENGQPNYKTPPVLDSE-----DGSFFLYSKLTVDKSRWQQGVNFCVSV 445
QY 655 THK 657
|:
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QY 579 SSEQLTSGASVVCFLNNFYPKDINVKWKIDGSRQGVNSWTDODSKDSTYSMSSTLT 638
DB 141 SDEQLKSGTASVVCLNNFYPREKQVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLT 200

QY 639 LTKDEYERHNSYTCEATHKTSTSPIVKSFNRNE 671
DB 201 LSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGE 233

RESULT 63
Q6PIH7 HUMAN
ID Q6PIH7_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6PIH7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.U.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RG NIH MGC Project;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034141; AAH34141.1; -; mRNA.
DR HSSP; P01607; 1AR2.
DR SMR; Q6PIH7; 23-236
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;

Query Match 20.2%; Score 710; DB 2; Length 236;
Best Local Similarity 63.2%; Pred. No. 3.7e-36;
Matches 134; Conservative 31; Mismatches 47; Indels 0; Gaps 0;
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QY 460 IVMOTPTSLVYAGDRVTTITCKASQSVNSDVAVYQOKGQSPKLLISYTSRYAGVPDR 519
DB 24 IQLTQSPFLSASGDRVTTITCRASQGISYLAWYQOKGKAPNLLIYAASTLQSGVPSR 83

QY 520 FSGSGYGTDFTLTISVQAEDAAYVFCQDYNSPPTFGGTTKLEIKRADAAPTVSIFPPS 579
DB 84 FSGSGGTFTLTISSLQPEDFATYVCCQLNSSPPTFGGTTKVEIKRTVAAPSVFIFPPS 143

QY 580 SEQLTSGASVVCFLNNFYPKDINVKWKIDGSRQGVNSWTDODSKDSTYSMSSTLT 639
DB 144 DEQLKSGTASVVCLNNFYPREKQVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLT 203

QY 640 TKDEYERHNSYTCEATHKTSTSPIVKSFNRNE 671
DB 204 SKADYEKKHKVYACEVTHQGLSSPVTKSFNRGE 235

RESULT 64
Q6GMW0 HUMAN
ID Q6GMW0_HUMAN PRELIMINARY; PRT; 235 AA.
AC Q6GMW0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE IGKV1-5 protein.
GN Name=IGKV1-5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.U.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Director MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073792; AAH73792.1; -; mRNA.
DR SMR; Q6GMW0; 21-233.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 2.
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DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 235 AA; 25765 MW; 4360C36B6D4133F5 CRC64;

Query Match 20.1%; Score 707.5; DB 2; Length 235;
Best Local Similarity 63.1%; Pred. No. 5.3e-36;
Matches 137; Conservative 33; Mismatches 45; Indels 3; Gaps 2;

457 TTSIVMTQTPTSLVLSAGDRVTITCKASQSVNDVAWYQQKPGQSPKLLISYSSRYAGV 516
TGIIVMTQSPATLSVSPGERATLSCRASQSIISNNLAWYQQRPGQAPRLLIYGASSRVTGI 78

517 PDRFSGSGYGTDTFTLTISISSVQAEADAAVYFCQDYNS--PPTFGGTYKLEIKRADAPTVS 574
79 PGRFSGSGSGTEFTLTISISLSQSEDFAVYFCQ-QYNDWLLYTFGGTKLEIKRTVAAPSVF 137

575 IFPPSSBQLTSGGASVVCFLNNFVKDINVKWKIDGSRQGVLSNMTDQSDKSTYSMS 634
138 IFPPSBQLTSGTASVVCFLNNFVKDINVKWKIDGSRQGVLSNMTDQSDKSTYSLS 197

635 STLTLDKDEYERHNSYTCEATHKTSTSPVKSFNRE 671
198 STLTLSKADYKHKVYACEVTHQGLSLSPVTKSFNRGE 234

RESULT. 65
Q6GMX0 HUMAN
ID Q6GMX0 HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6GMX0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073775; AAH73775.1; -; mRNA.
DR SRR; Q6GMX0; 23-236.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_CL.
DR InterPro; IPR003006; Ig_MHC.
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DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7B92BF8F CRC64;

Query Match 20.0%; Score 706; DB 2; Length 236;
Best Local Similarity 62.7%; Pred. No. 6.6e-36;
Matches 133; Conservative 30; Mismatches 49; Indels 0; Gaps 0;

460 IVMTQPTSLVLSAGDRVTITCKASQSVNDVAWYQQKPGQSPKLLISYSSRYAGV 519
IQMTQSPSSLSASVGRVTITCRASQINNNLWYQLKPGKAPNLLIYAASSLSQGVPSR 83

520 FSGSGYGTDTFTLTISISSVQAEADAAVYFCQDYNSPPTFGGTYKLEIKRADAPTVS 579
FSGSGSGTDTFTLTISISSLRPDDFATYYCQSYNIPLTFGGGTNVEIKRTVAAPSVF 143

580 SEQLTSGGASVVCFLNNFVKDINVKWKIDGSRQGVLSNMTDQSDKSTYSMSFTLT 639
144 DEQLKSGTASVVCFLNNFVKDINVKWKIDGSRQGVLSNMTDQSDKSTYSLSLTLL 203

640 TKDEYERHNSYTCEATHKTSTSPVKSFNRE 671
SKADYKHKVYACEVTHQGLSLSPVTKSFNRGE 235

NAME=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klaugner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL SUBMITTED (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073763; AAH73763.1; -; mRNA.
DR SMR; Q6GKX9; 23-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PR07654; Cl-set; 1.
DR SMART; SM00409; IG1; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25924 MW; FDE2093DC560CFF7 CRC64;

Query Match 19.8%; Score 699; DB 2; Length 236;
Best Local Similarity 63.7%; Pred. No. 1.8e-35;
Matches 135; Conservative 28; Mismatches 49; Indels 0; Gaps 0;

QY 460 IVMTOPTSLVAGDRVTITCKASQSVNDVAWYQKQSPKLIYSYSSRYAGVDP 519
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
24 IQMTQSPSSLSASVGRHVTITCRASQNSVRLAWYQORPEKAPKSLIYATSSLHSGVPS 83
QY 520 FSGSGYGTDFTLTISVQAEDAAVYFCQDYNPPTFGGQTKLEIKRADAAPTIVSIFPPS 579
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84 FSGSGYGTDFTLTISLQPEDFATYCYQNTYPLTFGGGTVKVEIKRTVAAPSVFIFPPS 143
QY 580 SEQLTSGGASVCFLLNFPKQINVKWIDGSRQNGVLNSWTDQSKOSTYMSSTLTL 639
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
144 DEQLKSGTASVCLNLFNFPREARVQWVDNALQSGNSQESVTEQDSKDSTYSLSSTL 203
QY 640 TKDEYERHNSYTCETHTKSTSPVKSFNRE 671
Db ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
204 SKADYEKHKVYACEVTHQGLSSPVTKSFNRGE 235

RESULT 69
Q6PJA4 HUMAN
ID Q6PJA4_HUMAN PRELIMINARY; PRT; 470 AA.
AC Q6PJA4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klaugner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL SUBMITTED (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; -; mRNA.
DR HSSP; P01861; 1ADQ.
DR SMR; Q6EJ44; 20-470.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PR07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 470 AA; 51716 MW; 7B39556A11FD7D99 CRC64;

Query Match 19.8%; Score 698.5; DB 2; Length 470;
Best Local Similarity 28.9%; Pred. No. 5e-35;
Matches 192; Conservative 72; Mismatches 162; Indels 239; Gaps 18;

QY 1 EVQLQSGDPLVKPGASVKISCKASGYSTGYMHVWVKSPGKLEWIGRINPNNGVTLY 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
20 EVQLVSGGGLVQPGGSLRLSCVSGFTSSYMWVRQAPGKLEWVANI KDGSEKY 79
QY 61 NQKFKDKATLVTDKSTTAYMELRLSITSDSAVYYCAR--STMTINVMYDMYQGQTSVTV 118
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
80 VDSVKGRTIISRDNAKNSLYLQNSLRAREDYAVYCARDGSSWYRDW-FDPWGQGLTVTV 138
QY 119 SSAKTTTPSPVYPLAPGSAAGTNSMTVTLGLVKVGFPEPVTVTWNSGSLSSGVHTFFAVLQ 178
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
139 SSASTKGPSVFFPLAPSSKSTSGTAAALGLVKDYFPPEPTVTSWNSGALTSGVHTFFAVLQ 198
QY 179 SD-LYTLSSSVTPSPSTWSETVTCNVAHPASTKVDKIKVIPRDSGGPSEKSEINEKDL 237
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
199 SSGLYSLSSVTPSPSSLTQTQYICNVNHPKSNTKVDKKVEPKSC----- 243
QY 238 RKKSELQGTALGNLKGIIYYNSKAITSSSEKSDQFLNTLLPKGFFTGHPWYNLLVDLG 297
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
244 -----DKTHCTPCCPAPELGGSPV--LPKPFP--KDTLM--- 275
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QY 298 STAATSEYEGSSVDLYGAYGYQCAGTGNKTAACMYGGVTLHDNNRLTEKKVPINLWID 357
Db 276 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVD 303
QY 358 GKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVGRLIVFHSSEGS 417
Db 304 G-----VEVHNKTKPREEQ-----YNSY-----RVSVSLTVLHQDWLN 338
QY 418 TVSYDLFDAQGGYPTDLLRIYRDNNTTISLSISLYLTTSIVMTQTPTSLLSVAGDRV 477
Db 339 GREY-----
QY 478 TITCKASQSVNDVAVYQKPGSKLLISYTSRVRAGVDPDRFSGSGYGTDFTLTISSVQ 537
Db 343 --KCKVS-----NKALPAP---TEKTSKAKGP----- 366
QY 538 AEDAAVYFCQDYNPPTFGGKLEIKRADAAFTVSIIPPSPSEQLTSGGASVVCFLNPF 597
Db 367 -----REPVYTLPPSRDELTKQVSLTCLVKGF 395
QY 598 YPKDINVKKIDGSRQN-----GVLSWTDQDSKDYMSSTLTLTDEYERHNSYTC 652
Db 396 YPSDIAVEWESNGQPNKYKTPPVLDSE-----DGSFFLYSKLTVDKSRWQOGNVFSC 448
QY 653 EATHK 657
Db 449 SVMHE 453

RESULT 70
Q6IN78 HUMAN
ID Q6IN78_HUMAN PRELIMINARY; PRT; 466 AA.
AC Q6IN78;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schumetz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072419; AAH72419.1; -; mRNA.
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DR HSSP; P01861; IAD0.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN 2.
SQ SEQUENCE 466 AA; 50854 MW; 53EB0BCED81076E CRC64;

Query Match 19.8%; Score 697.5; DB 2; Length 466;
Best Local Similarity 29.3%; Pred. No. 5.8e-35;
Matches 195; Conservative 67; Mismatches 160; Indels 243; Gaps 19;

QY 1 EVQLQSGDPLVKPGASVKISCKASGYSTGYMHVVKOSPGKLEWIGRINPNNGVTLY 60
Db 20 EVQLVESGGLIQPGSLTSCAASGLTVSSNMYHVRQAPGKLEWVS-VLYIGATYY 78
QY 61 NQKFKDKATLVYDKSSTTAYMELRLSLTSEDSAVYYCARSTMITNYMDY--WGQGSVTV 118
Db 79 ADSVKGRFTISRDNKNTLYLQMSLSRAEDTAVYYCARG----NYVVPAPMGQGLTVV 134
QY 119 SSAKTPPSVYPLAPGSAQAQTNMTVTLGCLVKGYPEPTVTMNSGLSSGSGVHTTFAVLQ 178
Db 135 SSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYPEPTVTSMNSGALTSGVHTTFAVLQ 194
QY 179 SD-LYTLSSSVTPSPSETVTCNVAHPASSTKVDKKIVPRDSGSPSEKSEINEKDL 237
Db 195 SSGLYSLSSVTVTPSSSLGTQYICNVNHPKNTKVDKEVEPKSC----- 239
QY 238 RKKSELQGTALGNLAKQIYYNYSKATTSSEKSDAQFTNTLLPKGFTGHPWINDLLVDLG 297
Db 240 -----DKTHTCPPCPAPELILGGPSVF--LPPPKP--KDTLM--- 271
QY 298 STAATSEYEGSSVDLYGAYGYQCAGTGNKTAACMYGGVTLHDNNRLTEKKVPINLWID 357
Db 272 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVD 299
QY 358 GKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVGRLIVFHSSEGS 417
Db 300 G-----VEVHNKTKPREEQ-----YNSY-----RVSVSLTVLHQDWLN 334
QY 418 TVSYDLFDAQGGYPTDLLRIYRDNNTTISLSISLYLTTSIVMTQTPTSLLSVAGDRV 477
Db 335 GREY----- 338
QY 478 TITCKASQSVNDVAVYQKPGSKLLISYTSRVRAGVDPDRFSGSGYGTDFTLTISSVQ 537
Db 339 --KCKVS-----NKALPAP---TEKTSKAKGP----- 362
QY 538 AEDAAVYFCQDYNPPTFGGKLEIKRADAAFTVSIIPPSPSEQLTSGGASVVCFLNPF 597
Db 363 -----REPVYTLPPSRDELTKQVSLTCLVKGF 391
QY 598 YPKDINVKKIDGSRQN-----GVLSWTDQDSKDYMSSTLTLTDEYERHNSYTC 652
Db 392 YPSDIAVEWESNGQPNKYKTPPVLDSE-----DGSFFLYSKLTVDKSRWQOGNVFSC 444
QY 653 EATHK 657
Db 445 SVMHE 449

RESULT 71
Q502W4 HUMAN
ID Q502W4_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q502W4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
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13-SEP-2005 (TReMBLrel. 31, Last annotation update)
IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Glandular pool- thyroid;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Glandular pool- thyroid;
RG NIH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC095489; AAH95489.1; -, mRNA.
DR SMR; Q502W4; 23-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig MHC.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25936 MW; E2DF79AC18756AA9 CRC64;
Query Match 19.8%; Score 696; DB 2; Length 236;
Best Local Similarity 63.4%; Pred. No. 2.8e-35;
Matches 135; Conservative 28; Mismatches 48; Indels 2; Gaps 2;
QY 460 IVMTQPTSLVLSAGDRVTITCKASQSVNDVAVYQKQSPKLLISYTSRRVAGVPDR 519
DB 24 IQMTQSPSSLSASVGDRTVTITCRASQGRINDLGYQKQPKAPKRLIFAASSLSQSGVPSR 83
QY 520 FSGSGYGTDFLTITSSVQAEADAAVYFCQQDYNS-PPTFGGQTKLEIKRADAAPTIVSIFFP 578
DB 84 FSGSGSGTEFTLTINSIQPEDFATYICLQ-YNSYPTFGGQTKVEIKRTVAAPSVFI 142
QY 579 SSEQLTSGGASVVCFLNFPKDNVWKIDGSRQNGVNLNSWTDQDSKOSTYSMSLT 638
DB 143 SDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKOSTYSLSLT 202
QY 639 LTKDEYRHNSYTCATHTKSTSPIVKSNRNE 671
DB 203 LSKADYEKKHYACEVTHQGLSSPVTKSFNRRG 235

RESULT 72
Q6GMV9 HUMAN
ID Q6GMV9 HUMAN PRELIMINARY; PRT; 235 AA.
AC Q6GMV9;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073793; AAH73793.1; -, mRNA.
DR SMR; Q6GMV9; 21-235.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig-v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25646 MW; DF32B580BAD19E4B CRC64;
Query Match 19.7%; Score 694.5; DB 2; Length 235;
Best Local Similarity 61.6%; Pred. No. 3.4e-35;
Matches 133; Conservative 33; Mismatches 49; Indels 1; Gaps 1;
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DB 19 TGBIVLTQSPGTTLSLSPGSRALASCRASQSVNSKYLAWYQKQPKAPRLMYAASIRATG 78
QY 516 VPRFSGSGYGTDFLTITSSVQAEADAAVYFCQQDYNS-PPTFGGQTKLEIKRADAAPTIVSI 575
DB 79 IPRFSGSGSGTDFLTITISPLESEDFALYFCQQYGTSPITFGGQTKVEIKRTVAAPSVFI 138
QY 576 FPPSSEQLTSGGASVVCFLNFPKDNVWKIDGSRQNGVNLNSWTDQDSKOSTYSMS 635


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DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Immunoglobulin domain.
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match 19.6%; Score 691; DB 2; Length 234;
Best Local Similarity 61.5%; Pred. No. 5.6e-35;
Matches 131; Conservative 32; Mismatches 50; Indels 0; Gaps 0;

QY 459 SIIVMTQPTSLVSGADRVITTCASQSVNDVAVYQOKPGQSPKLLISYTSRYAGVPD 518
DB 21 AIRMTQSPSFSASTGDRVITTCASQSIGSYLAWYQOKPGKAPQLLIYAASLTQSGVPS 80

QY 519 RFGSGYGTDTLTITISSVQAEAAVYFCQDYNPSPTFGGGTKLEIKRADAAPTVSIFPP 578
DB 81 RFGSGASGTDFTLSISCLQSEDFATYCYQQYVTPWTFGGTKVEIKRTVAAPSVFIAPP 140

QY 579 SSQLTSGGASVVCFLNFPKINVKWIKDGERQNGVLSNWTDDQSKDSTYSMSSTLT 638
DB 141 SDQLKSGTASVVCLLNFPYKAVQWKVDNALQSGNSQESVTEQDSKDSYLSSTLT 200

QY 639 LTKDEYERHNSYCEATHKTSPTIVKSFNRNE 671
DB 201 LSKADYEKKHYACEVTHQGLSSPVTKSFNRGE 233

RESULT 75
Q6P5S8 HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6P5S8 HUMAN PRELIMINARY;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Glandular pool- thyroid;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Glandular pool- thyroid;
RA Strausberg R.;
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Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC062704; AAH62704.1; -, mRNA.

DR HSSP; P01837; 1KCU.

DR SMR; Q6P5S8; 21-236.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig cl.

DR InterPro; IPR003006; Ig MHC.

DR InterPro; IPR003596; Ig v.

DR Pfam; PF07654; C1-set; 1.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGV; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG LIKE; 2.

DR PROSITE; PS00290; IG MHC; UNKNOWN_1.

KW Hypothetical protein.

SQ SEQUENCE 236 AA; 25773 MW; 953E37BEB4FF5F27 CRC64;

Query Match 19.6%; Score 689; DB 2; Length 236;

Best Local Similarity 61.3%; Pred. No. 7.5e-35;

Matches 133; Conservative 34; Mismatches 48; Indels 2; Gaps 2;

QY 457 TTSIVMTQPTSLVSGADRVITTCASQSV-SNDVAVYQOKPGQSPKLLISYTSRYAG 515

DB 19 TGEIVLTQSPGTLSPFSGERATLSCASQTVFSSHLAWYQORPGQAPRLLIYGAASRATG 78

QY 516 VDPFRFSGSGYGTDTLTITISSVQAEAAVYFCQDYNPSPTFGGGTKLEIKRADAAPTVS 574

DB 79 IPRFSGSGSGYGTDTLTITRLEPEDFAVYFCQYGTSPSLTFGGGTRVEIKRTVAAPSVF 138

QY 575 IPPPSSEQLTSGGASVVCFLNFPKINVKWIKDGERQNGVLSNWTDDQSKDSTYSMS 634

DB 139 IPPPSDEQLKSGTASVVCLLNFPYKAVQWKVDNALQSGNSQESVTEQDSKDSYLS 198

QY 635 STLTLTDEYERHNSYCEATHKTSPTIVKSFNRNE 671

DB 199 STLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGE 235

Search completed: February 15, 2006, 20:18:11

Job time : 239.277 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 15, 2006, 20:18:35 ; Search time 51.2354 Seconds
(without alignments)
1084.369 Million cell updates/sec

Title: US-09-900-766-1

Perfect score: 3522

Sequence: 1 EVQLQSGPDLVKPGASVKI.....EATHKTSPIVKSFRNRES 672

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1108.5	31.5	489	4	PCT-US95-11405-35
2	1107	31.4	233	2	US-08-695-692B-8
3	1107	31.4	257	2	US-08-486-099-112
4	1107	31.4	257	2	US-08-360-107A-122
5	1107	31.4	257	2	US-08-484-223B-112
6	1107	31.4	257	2	US-08-919-597-112
7	1107	31.4	257	2	US-08-475-668A-112
8	1107	31.4	257	2	US-08-485-551A-112
9	1107	31.4	257	2	US-08-471-913A-112
10	1107	31.4	257	2	US-08-485-264A-112
11	1107	31.4	257	2	US-08-474-349A-112
12	1107	31.4	257	2	US-08-470-896-112
13	1107	31.4	257	2	US-08-485-546A-112
14	1107	31.4	257	2	US-08-487-266A-112
15	1107	31.4	257	2	US-08-484-741-112
16	1071	30.4	254	2	US-09-350-841A-1598
17	1059.5	30.1	445	1	US-08-353-400-33
18	1059.5	30.1	464	1	US-08-353-400-36
19	1040	29.5	226	2	US-08-896-933-24
20	1040	29.5	226	2	US-09-314-235-24
21	1040	29.5	226	2	US-09-708-008B-24
22	980.5	27.8	711	2	US-09-485-737B-90
23	980.5	27.8	711	2	US-10-071-485-90
24	966	27.4	468	1	US-08-116-247-7
25	966	27.4	468	1	US-09-348-224-7
26	960	27.3	212	1	US-08-737-129A-2
27	957	27.2	468	1	US-08-303-569B-7

28	957	27.2	468	2	US-09-795-515-7	Sequence 7, Appli
29	953.5	27.1	223	4	PCT-US94-14106-51	Sequence 51, Appl
30	948	26.9	233	4	US-08-695-692B-7	Sequence 7, Appli
31	948	26.9	257	2	US-08-486-099-113	Sequence 113, App
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33	948	26.9	257	2	US-08-484-223B-113	Sequence 113, App
34	948	26.9	257	2	US-08-919-597-113	Sequence 113, App
35	948	26.9	257	2	US-08-475-668A-113	Sequence 113, App
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37	948	26.9	257	2	US-08-471-913A-113	Sequence 113, App
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43	948	26.9	257	2	US-08-484-741-113	Sequence 113, App
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45	944	26.8	233	1	US-08-446-918A-4	Sequence 4, Appli
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47	941.5	26.7	219	1	US-08-353-400-34	Sequence 34, Appl
48	933	26.5	222	1	US-08-737-129A-6	Sequence 6, Appli
49	931.5	26.4	232	2	US-08-896-933-23	Sequence 23, Appl
50	931.5	26.4	232	2	US-09-314-235-23	Sequence 23, Appl
51	931.5	26.4	232	2	US-09-708-008B-23	Sequence 23, Appl
52	925	26.3	257	2	US-09-144-776B-2	Sequence 2, Appli
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54	921	26.1	233	2	US-09-144-776B-4	Sequence 4, Appli
55	921	26.1	233	2	US-08-882-431B-4	Sequence 4, Appli
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58	915.5	26.0	254	1	US-08-792-824-10	Sequence 10, Appl
59	915.5	26.0	254	1	US-08-792-824-13	Sequence 13, Appl
60	909.5	25.8	254	1	US-08-792-824-4	Sequence 4, Appli
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63	903.5	25.7	447	6	5455030-1	Patent No. 5455030
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68	893.5	25.4	219	2	US-09-254-180C-131	Sequence 131, App
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73	889.5	25.3	235	2	US-09-011-769A-23	Sequence 23, Appl
74	885.5	25.1	216	2	US-09-254-180C-132	Sequence 132, App
75	885.5	25.1	216	2	US-09-254-180C-183	Sequence 183, App
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78	874	24.8	214	2	US-09-653-755A-5	Sequence 5, Appli
79	873	24.8	647	2	US-09-423-439-60	Sequence 60, Appl
80	872	24.8	236	1	US-08-792-824-3	Sequence 3, Appli
81	872	24.8	236	1	US-08-792-824-9	Sequence 9, Appli
82	872	24.8	236	1	US-08-792-824-12	Sequence 12, Appl
83	872	24.8	453	2	US-09-301-593-18	Sequence 18, Appl
84	870	24.7	234	2	US-09-770-916-4	Sequence 4, Appli
85	868.5	24.7	216	2	US-09-254-180C-182	Sequence 182, App
86	866.5	24.6	252	2	US-09-350-841A-1599	Sequence 1599, Ap
87	864	24.5	218	4	PCT-US94-14106-61	Sequence 61, Appl
88	863.5	24.5	472	2	US-09-301-593-30	Sequence 30, Appl
89	861	24.4	215	2	US-09-170-769A-4	Sequence 4, Appli
90	860.5	24.4	466	2	US-09-698-705-11	Sequence 11, Appl
91	858	24.4	234	4	PCT-US94-07659-4	Sequence 4, Appli
92	855.5	24.3	250	2	US-09-011-769A-21	Sequence 21, Appl
93	855.5	24.3	473	2	US-09-171-945-131	Sequence 131, App
94	855.5	24.3	473	2	US-09-910-059-131	Sequence 131, App
95	854.5	24.3	470	2	US-09-238-741-4	Sequence 4, Appli
96	852.5	24.2	235	1	US-08-303-569B-5	Sequence 5, Appli
97	852.5	24.2	235	1	US-08-116-247-5	Sequence 5, Appli
98	852.5	24.2	235	2	US-09-795-515-5	Sequence 5, Appli
99	852.5	24.2	235	2	US-09-348-224-5	Sequence 5, Appli
100	850.5	24.1	200	6	5189147-8	Patent No. 5189147

101	841	23.9	454	1	US-07-934-373C-22	Sequence 22, Appl	174	741.5	21.1	298	2	US-08-804-444A-60	Sequence 60, Appl
102	841	23.9	454	2	US-08-437-642B-22	Sequence 22, Appl	175	741.5	21.1	298	2	US-09-026-985-60	Sequence 60, Appl
103	841	23.9	454	2	US-08-146-206C-22	Sequence 22, Appl	176	741.5	21.1	298	2	US-09-121-952A-60	Sequence 60, Appl
104	841	23.9	454	2	US-09-705-686-22	Sequence 22, Appl	177	741.5	21.1	298	2	US-09-234-340A-60	Sequence 60, Appl
105	841	23.9	454	2	US-09-705-398A-22	Sequence 22, Appl	178	741.5	21.1	298	2	US-09-355-014-60	Sequence 7, Appl
106	841	23.9	454	2	US-09-705-398-22	Sequence 22, Appl	179	737	20.9	446	2	US-08-397-411-7	Sequence 52, Appl
107	841	23.9	454	4	PCR-US93-07832-22	Sequence 22, Appl	180	734.5	20.9	253	2	US-09-027-449-52	Sequence 52, Appl
108	840	23.9	206	6	5189147-9	Patent No. 5189147	181	734.5	20.9	253	2	US-09-027-449-55	Sequence 55, Appl
109	834.5	23.7	217	4	PCR-US94-14106-59	Sequence 59, Appl	182	734.5	20.9	253	2	US-08-804-444A-52	Sequence 52, Appl
110	831.5	23.6	247	4	PCR-US94-07659-2	Sequence 2, Appl	183	734.5	20.9	253	2	US-08-804-444A-55	Sequence 55, Appl
111	830	23.6	233	1	US-08-792-824-6	Sequence 6, Appl	184	734.5	20.9	253	2	US-09-026-985-52	Sequence 52, Appl
112	828.5	23.5	235	2	US-08-444-644-28	Sequence 28, Appl	185	734.5	20.9	253	2	US-09-026-985-55	Sequence 55, Appl
113	828.5	23.5	235	2	US-08-444-644-28	Sequence 28, Appl	186	734.5	20.9	253	2	US-09-121-952A-52	Sequence 52, Appl
114	827.5	23.5	215	6	5455030-3	Patent No. 5455030	187	734.5	20.9	253	2	US-09-121-952A-55	Sequence 55, Appl
115	826.5	23.5	235	2	US-08-444-644-42	Sequence 42, Appl	188	734.5	20.9	253	2	US-09-234-340A-52	Sequence 52, Appl
116	826.5	23.5	235	2	US-08-232-246A-42	Sequence 42, Appl	189	734.5	20.9	253	2	US-09-234-340A-55	Sequence 55, Appl
117	825.5	23.4	235	2	US-08-444-644-19	Sequence 19, Appl	190	734.5	20.9	253	2	US-09-355-014-52	Sequence 52, Appl
118	825.5	23.4	235	2	US-08-232-246A-19	Sequence 19, Appl	191	734.5	20.9	253	2	US-09-355-014-55	Sequence 55, Appl
119	821.5	23.3	232	1	US-09-698-705-13	Sequence 13, Appl	192	734.5	20.9	256	2	US-09-027-449-70	Sequence 70, Appl
120	819	23.3	234	1	US-07-690-192-2	Sequence 2, Appl	193	734.5	20.9	256	2	US-09-026-985-70	Sequence 70, Appl
121	818.5	23.2	472	2	US-09-301-593-43	Sequence 43, Appl	194	734.5	20.9	256	2	US-09-121-952A-70	Sequence 70, Appl
122	812	23.1	467	1	US-07-916-098A-45	Sequence 45, Appl	195	734.5	20.9	256	2	US-09-234-340A-70	Sequence 70, Appl
123	811.5	23.0	233	2	US-08-444-644-33	Sequence 33, Appl	196	734.5	20.9	256	2	US-09-355-014-70	Sequence 70, Appl
124	811.5	23.0	233	2	US-08-232-246A-33	Sequence 33, Appl	197	731	20.8	233	1	US-07-934-373C-25	Sequence 25, Appl
125	803.5	22.8	478	2	US-09-770-916-2	Sequence 2, Appl	198	731	20.8	233	2	US-08-437-642B-25	Sequence 25, Appl
126	802	22.8	255	1	US-07-690-192-4	Sequence 4, Appl	199	731	20.8	233	2	US-08-146-206C-25	Sequence 25, Appl
127	802	22.8	452	2	US-09-027-449-71	Sequence 71, Appl	200	731	20.8	233	2	US-09-705-686-25	Sequence 25, Appl
128	802	22.8	452	2	US-09-026-985-71	Sequence 71, Appl	201	731	20.8	233	2	US-09-705-398A-25	Sequence 25, Appl
129	802	22.8	452	2	US-09-121-952A-71	Sequence 71, Appl	202	731	20.8	233	2	US-09-705-398-25	Sequence 25, Appl
130	802	22.8	452	2	US-09-234-340A-71	Sequence 71, Appl	203	731	20.8	233	4	PCR-US93-07832-25	Sequence 25, Appl
131	802	22.8	452	1	US-09-355-014-71	Sequence 71, Appl	204	730.5	20.7	232	1	US-07-934-373C-34	Sequence 34, Appl
132	794.5	22.6	449	1	US-08-458-516-13	Sequence 13, Appl	205	730.5	20.7	232	2	US-08-437-642B-34	Sequence 34, Appl
133	789	22.4	473	2	US-09-828-995B-20	Sequence 20, Appl	206	730.5	20.7	232	4	PCR-US93-07832-34	Sequence 34, Appl
134	785.5	22.3	470	2	US-09-859-053-28	Sequence 28, Appl	207	729	20.7	240	2	US-09-301-593-36	Sequence 36, Appl
135	782.5	22.2	462	2	US-09-627-896B-24	Sequence 24, Appl	208	728	20.7	222	1	US-08-458-516-22	Sequence 22, Appl
136	781.5	22.2	279	2	US-08-397-411-13	Sequence 13, Appl	209	728	20.7	235	1	US-08-458-516-23	Sequence 23, Appl
137	780	22.1	230	2	US-08-952-235-2	Sequence 2, Appl	210	728	20.7	237	1	US-08-463-587A-25	Sequence 25, Appl
138	780	22.1	230	2	US-09-669-971-2	Sequence 2, Appl	211	728	20.7	237	1	US-08-463-667A-3	Sequence 3, Appl
139	778.5	22.1	253	1	US-08-398-613A-58	Sequence 58, Appl	212	728	20.7	237	2	US-08-923-854-25	Sequence 25, Appl
140	778.5	22.1	253	1	US-08-398-612A-58	Sequence 58, Appl	213	728	20.7	237	2	US-09-097-303-6	Sequence 6, Appl
141	778.5	22.1	253	1	US-08-398-611A-58	Sequence 58, Appl	214	728	20.7	237	2	US-09-097-171A-10	Sequence 10, Appl
142	778.5	22.1	253	1	US-08-491-334A-58	Sequence 58, Appl	215	728	20.7	237	2	US-09-422-712B-2	Sequence 2, Appl
143	778.5	22.1	253	2	US-09-027-449-44	Sequence 44, Appl	216	728	20.7	237	2	US-09-607-756-2	Sequence 2, Appl
144	778.5	22.1	253	2	US-08-804-444A-44	Sequence 44, Appl	217	728	20.7	237	2	US-09-460-587-6	Sequence 6, Appl
145	778.5	22.1	253	2	US-09-026-985-44	Sequence 44, Appl	218	728	20.7	237	2	US-09-940-166A-6	Sequence 6, Appl
146	778.5	22.1	253	2	US-09-121-952A-44	Sequence 44, Appl	219	728	20.7	237	4	PCR-US91-09133-26	Sequence 26, Appl
147	778.5	22.1	253	2	US-09-234-340A-44	Sequence 44, Appl	220	727.5	20.7	451	2	US-09-247-352-3	Sequence 3, Appl
148	778.5	22.1	253	2	US-09-355-014-44	Sequence 44, Appl	221	727.5	20.7	451	2	US-09-466-635-3	Sequence 3, Appl
149	776.5	22.0	232	1	US-08-425-763-2	Sequence 2, Appl	222	727.5	20.7	476	1	US-08-378-939-10	Sequence 10, Appl
150	776.5	22.0	232	2	US-08-811-757-2	Sequence 2, Appl	223	727	20.6	224	2	US-09-456-090A-46	Sequence 46, Appl
151	776.5	22.0	232	2	US-09-249-230-2	Sequence 2, Appl	224	727	20.6	224	2	US-09-453-234-46	Sequence 46, Appl
152	776.5	22.0	468	2	US-09-828-995B-5	Sequence 5, Appl	225	726	20.6	214	2	US-07-934-373C-40	Sequence 40, Appl
153	775	22.0	215	2	US-09-170-769A-6	Sequence 6, Appl	226	726	20.6	214	1	US-08-788-800-11	Sequence 11, Appl
154	774	22.0	552	4	PCR-US93-07832-23	Sequence 23, Appl	227	726	20.6	214	2	US-08-437-642B-40	Sequence 40, Appl
155	759.5	21.6	470	2	US-09-828-995B-11	Sequence 11, Appl	228	726	20.6	214	2	US-09-097-309-2	Sequence 2, Appl
156	759	21.6	449	2	US-09-679-397-2	Sequence 2, Appl	229	726	20.6	214	2	US-09-097-171A-2	Sequence 2, Appl
157	759	21.6	449	2	US-09-680-148-2	Sequence 2, Appl	230	726	20.6	214	2	US-09-460-587-2	Sequence 2, Appl
158	759	21.6	449	2	US-09-304-465A-2	Sequence 2, Appl	231	726	20.6	214	2	US-09-679-397-1	Sequence 1, Appl
159	759	21.6	449	2	US-10-356-974-2	Sequence 2, Appl	232	726	20.6	214	2	US-09-680-148-1	Sequence 1, Appl
160	757	21.5	468	2	US-10-104-047-3329	Sequence 3329, Ap	233	726	20.6	214	2	US-09-304-465A-1	Sequence 1, Appl
161	756.5	21.5	468	2	US-09-485-737B-67	Sequence 67, Appl	234	726	20.6	214	2	US-09-940-166A-2	Sequence 2, Appl
162	756.5	21.5	468	2	US-10-071-485-67	Sequence 67, Appl	235	726	20.6	214	4	US-10-356-974-1	Sequence 1, Appl
163	756	21.5	450	1	US-08-788-800-12	Sequence 12, Appl	236	726	20.6	214	2	PCR-US93-07832-40	Sequence 40, Appl
164	756	21.5	469	1	US-07-934-373C-23	Sequence 23, Appl	237	726	20.6	220	2	US-08-952-235-1	Sequence 1, Appl
165	756	21.5	469	2	US-08-437-642B-23	Sequence 23, Appl	238	726	20.6	220	2	US-09-669-971-1	Sequence 1, Appl
166	756	21.5	469	2	US-08-146-206C-23	Sequence 23, Appl	239	726	20.6	553	1	US-08-263-911-9	Sequence 9, Appl
167	756	21.5	469	2	US-09-705-686-23	Sequence 23, Appl	240	725.5	20.6	300	2	US-09-097-309-7	Sequence 7, Appl
168	756	21.5	469	2	US-09-705-398A-23	Sequence 23, Appl	241	725.5	20.6	300	2	US-09-097-171A-11	Sequence 11, Appl
169	756	21.5	469	2	US-09-705-398-23	Sequence 23, Appl	242	725.5	20.6	300	2	US-09-422-712B-3	Sequence 3, Appl
170	752.5	21.4	213	2	US-09-170-769A-2	Sequence 2, Appl	243	725.5	20.6	300	2	US-09-607-756-3	Sequence 3, Appl
171	748	21.2	467	2	US-09-049-672A-8	Sequence 8, Appl	244	725.5	20.6	300	2	US-09-460-587-7	Sequence 7, Appl
172	743.5	21.1	642	2	US-09-423-439-26	Sequence 26, Appl	245	725.5	20.6	300	2	US-09-940-166A-7	Sequence 7, Appl
173	741.5	21.1	298	2	US-09-027-449-60	Sequence 60, Appl	246	722	20.5	214	1	US-07-934-373C-39	Sequence 39, Appl

Db 417 REAKVQKVDNALQSGNSQESVTEQDSKDSYSLSSLTLSKADYEKHKVYACEVTHOGL 476
QY 660 TSPVKSFNRE 671
Db 477 SSPVKSFNRE 488
RESULT 2
US-08-695-692B-8
; Sequence 8, Application US/08695692B
; Patent No. 6514498
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
; APPLICANT: Johan Hansson, Terje Kalland, Lars
; APPLICANT: Abrahamson and Goran Forsberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
; TITLE OF INVENTION: AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,692B
; FILING DATE: August 12, 1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9601245-5
; FILING DATE: March 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Krieger, Paul E.
; REGISTRATION NUMBER: 25,886
; REFERENCE/DOCKET NUMBER: 41986/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-695-692B-8
Query Match 31.4%; Score 1107; DB 2; Length 233;
Best Local Similarity 89.7%; Pred. No. 2.4e-69;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNYSKAITSEKSAOFLNTLLFKGFFTG 285
Db 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNYSKAITSEKSAOFLNTLLFKGFFTG 60
QY 286 HPWYNDLLVDLGSATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLT 345
Db 61 HPWYNDLLVDLGSATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLT 120
QY 346 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 405
Db 121 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
QY 406 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTSSLSISLYTT 458
Db 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTSSLSISLYTT 233

RESULT 3
US-08-486-099-112
; Sequence 112, Application US/08486099
; Patent No. 6013283
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
; TITLE OF INVENTION: B VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,099
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-486-099-112
Query Match 31.4%; Score 1107; DB 2; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.8e-69;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNYSKAITSEKSAOFLNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNYSKAITSEKSAOFLNTLLFKGFFTG 84
QY 286 HPWYNDLLVDLGSATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLT 345
Db 85 HPWYNDLLVDLGSATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLT 144
QY 346 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 405
Db 145 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTSSLSISLYTT 458
Db 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTSSLSISLYTT 257
RESULT 4
US-08-360-107A-122

; Sequence 122, Application US/08360107A
; Patent No. 6017536
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 149
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,107A
; FILING DATE: 20-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 122:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-360-107A-122

Query Match 31.4%; Score 1107; DB 2; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.8e-69;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSEKSDAQPLTNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQPLENTLLFKGFFTG 84

QY 286 HPWYNLLVDLGSSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
Db 85 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 346 EEKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 405
Db 145 EEKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204

QY 406 RGLIVFHSSEGSTSVSYDLFDAQGYPTLLRIYRDNTTISSTLSISLYLYTT 458
Db 205 RGLIVFHSSEGSTSVSYDLFDAQGYPTLLRIYRDNTTINSENHLDLYLYTT 257

RESULT 5
US-08-484-223B-112
; Sequence 112, Application US/08484223B
; Patent No. 6020459
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.

; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 245
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-484-223B-112

Query Match 31.4%; Score 1107; DB 2; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.8e-69;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSEKSDAQPLTNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQPLENTLLFKGFFTG 84

QY 286 HPWYNLLVDLGSSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
Db 85 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 346 EEKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 405
Db 145 EEKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204

QY 406 RGLIVFHSSEGSTSVSYDLFDAQGYPTLLRIYRDNTTISSTLSISLYLYTT 458
Db 205 RGLIVFHSSEGSTSVSYDLFDAQGYPTLLRIYRDNTTINSENHLDLYLYTT 257

RESULT 6
US-08-919-597-112
; Sequence 112, Application US/08919597
; Patent No. 6054265
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,597
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-919-597-112

Query Match 31.4%; Score 1107; DB 2; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.8e-69;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELQGTALGNLKOIYYNSKAITSEKSADQFLNTLLFKGFFTG 285
DB 25 SEKSEINEKDLRKSELQGNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84

QY 286 HPWYNDLLVDLGSATSTSEYEGSSVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 345
DB 85 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 144

QY 346 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
DB 145 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204

QY 406 RGLIVFHSSEGSTSVSYDLFDAQGYQPDTLRIYRDNNTTSSSTLSLSLYTT 458
DB 205 RGLIVFHSSEGSTSVSYDLFDAQGYQPDTLRIYRDNNTTSENHLDLYTT 257

RESULT 7
US-08-475-668A-112
Sequence 112, Application US/08475668A
Patent No. 6060065
GENERAL INFORMATION:
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-026
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-475-668A-112

Query Match 31.4%; Score 1107; DB 2; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.8e-69;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELQGTALGNLKOIYYNSKAITSEKSADQFLNTLLFKGFFTG 285
DB 25 SEKSEINEKDLRKSELQGNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84

QY 286 HPWYNDLLVDLGSATSTSEYEGSSVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 345
DB 85 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 144

QY 346 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
DB 145 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204

QY 406 RGLIVFHSSEGSTSVSYDLFDAQGYQPDTLRIYRDNNTTSSSTLSLSLYTT 458
DB 205 RGLIVFHSSEGSTSVSYDLFDAQGYQPDTLRIYRDNNTTSENHLDLYTT 257

RESULT 8
US-08-485-551A-112
Sequence 112, Application US/08485551A
Patent No. 6068973
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION

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/ NUMBER OF SEQUENCES: 211
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds LLP
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/485,551A
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7872-023
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ INFORMATION FOR SEQ ID NO: 112:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 257 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ US-08-485-551A-112

Query Match 31.4%; Score 1107; DB 2; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.8e-69;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSEKSAQDQFLTNLLFKGFFTG 285
DB 25 SEKSEINEKDLRKSELOQNALSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 286 HPWYNLLVDLGSATSEYEGSSVDLYGAYGYQCAGGTPNKTACWYGGVTLHDNNRLT 345
DB 85 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACWYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 405
DB 145 EEKVPINLWIDGKQTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204
QY 406 RGLIVFHSSEGSTSVSYDLFDAQOQYPTLLRIYRDNTTISSTLSISLYLYTT 458
DB 205 RGLIVFHSSEGSTSVSYDLFDAQOQYPTLLRIYRDNTTINSENHLDLYLYTT 257

RESULT 9
US-08-471-913A-112
/ Sequence 112, Application US/08471913A
/ Patent No. 6093794
/ GENERAL INFORMATION:
/ APPLICANT: Bolognesi, Dani P.
/ APPLICANT: Matthews, Thomas J.
/ APPLICANT: Wild, Carl T.
/ APPLICANT: Barney, Shawn O.
/ APPLICANT: Lambert, Dennis M.
/ APPLICANT: Petteway, Stephen R.
/ APPLICANT: Langlois, Alphonse J.
/ TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
/ TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
/ NUMBER OF SEQUENCES: 214
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds LLP

/ NUMBER OF SEQUENCES: 211
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds LLP
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/485,551A
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7872-023
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ INFORMATION FOR SEQ ID NO: 112:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 257 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ US-08-485-551A-112

Query Match 31.4%; Score 1107; DB 2; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.8e-69;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSEKSAQDQFLTNLLFKGFFTG 285
DB 25 SEKSEINEKDLRKSELOQNALSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 286 HPWYNLLVDLGSATSEYEGSSVDLYGAYGYQCAGGTPNKTACWYGGVTLHDNNRLT 345
DB 85 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACWYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 405
DB 145 EEKVPINLWIDGKQTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204
QY 406 RGLIVFHSSEGSTSVSYDLFDAQOQYPTLLRIYRDNTTISSTLSISLYLYTT 458
DB 205 RGLIVFHSSEGSTSVSYDLFDAQOQYPTLLRIYRDNTTINSENHLDLYLYTT 257

RESULT 10
US-08-485-264A-112
/ Sequence 112, Application US/08485264A
/ Patent No. 6228983
/ GENERAL INFORMATION:
/ APPLICANT: Bolognesi, Dani P.
/ APPLICANT: Matthews, Thomas J.
/ APPLICANT: Wild, Carl T.
/ APPLICANT: Barney, Shawn O.
/ APPLICANT: Lambert, Dennis M.
/ APPLICANT: Petteway, Stephen R.
/ APPLICANT: Langlois, Alphonse J.
/ TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
/ TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
/ TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
/ NUMBER OF SEQUENCES: 232
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds LLP
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
```

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; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US/08/485,264A
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-485-264A-112

Query Match 31.4%; Score 1107; DB 2; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.8e-69;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELTGALGNLKOIYYNSKAITSEKSDQFLNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELTGALGNLKOIYYNSKAITSEKSDQFLNTLLFKGFFTG 84
QY 286 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 345
Db 85 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVFHSSEGSTSVSYDLFDAQGYPTLLRIYRDNTTSSLSISLYTT 458
Db 205 RGLIVFHSSEGSTSVSYDLFDAQGYPTLLRIYRDNTTSSLSISLYTT 257

RESULT 11
US-08-474-349A-112
; Sequence 112, Application US/08474349A
; Patent No. 6333395
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
; NUMBER OF SEQUENCES: 517
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US/08/485,264A
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-485-264A-112
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-474-349A-112

Query Match 31.4%; Score 1107; DB 2; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.8e-69;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELTGALGNLKOIYYNSKAITSEKSDQFLNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELTGALGNLKOIYYNSKAITSEKSDQFLNTLLFKGFFTG 84
QY 286 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 345
Db 85 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVFHSSEGSTSVSYDLFDAQGYPTLLRIYRDNTTSSLSISLYTT 458
Db 205 RGLIVFHSSEGSTSVSYDLFDAQGYPTLLRIYRDNTTSSLSISLYTT 257

RESULT 12
US-08-470-896-112
; Sequence 112, Application US/08470896
; Patent No. 6479055
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-474-349A-112
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; SOFTWARE: PatentIn Release #1.0, Version #1.3.0
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,896
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-470-896-112

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	Query Match	31.4%	Score 1107;	DB 2;	Length 257;
	Best Local Similarity	89.7%	Pred. No. 2.8e-69;		
	Matches 209;	Conservative	9;	Mismatches 15;	Indels 0; Gaps 0;
Qy	226	SEKSEENEKDLRKKSELQGTALGNLQIYYYNKSKAITSEKSKADQFLTNTLLFKGFFTG	285		
Db	25	SEKSEENEKDLRKKSELQALNLRQIYYYNKSKAITENKESDDQFLNTLLFKGFFTG	84		
Qy	286	HPWYNDLLVDLGGSTAATSEYEGSSVDLYGAYYGQCAGGTENKTACMYGGVTLHDNNRLT	345		
Db	85	HPWYNDLLVDLGGSDATNKYKGGKVDLYGAYYGQCAGGTENKTACMYGGVTLHDNNRLT	144		
Qy	346	EKKVPINLMTDGGKQTTVPIDKVTSKSEVTVQELDQARHYLHGKFGCLYNSDSFGGKVQ	405		
Db	145	EKKVPINLMTDGGKQTTVPIDKVTSKSEVTVQELDQARHYLHGKFGCLYNSDSFGGKVQ	204		
Qy	406	RGLVTFHSSSEGSTVSYDLFDAQQGYPTDTLRIYRDNNTTISSTLSISLYLTT	458		
Db	205	RGLVTFHSSSEGSTVSYDLFDAQQGYPTDTLRIYRDNKTINSENLIDLILYTT	257		

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RESULT 13
US-08-485-546A-112
; Sequence 112, Application US/08485546A
; Patent No. 6518013
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Peteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,546A

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; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-485-546A-112

Query Match      31.4%; Score 1107; DB 2; Length 257;
Best Local Similarity 89.7%; Pred.No. 2.8e-69;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0

QY   226 SEKSEETNEKDLRKSKELQGTALGNLKQIYYYNASKAITSSSEKSADQFLTNTLLFKGFPTG 285
DB   |||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
QY   286 HPWYNDLLVDLGSTAAATSEYGSGSDLYGYAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 345
DB   |||||:|||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
QY   85 HPWYNDLLVDLGSKDATNKYKGKVLDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 144
DB   |||||:|||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
QY   346 EEKKVPINLMIDGKTTPVIDPKVKTSKEVTVOQLDLOARHYLHGKFGLYNSDSFGGKVQ 405
DB   |||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
QY   145 EEKKVPINLMIDGKTTPVIDPKVKTSKEVTVOQLDLOARHYLHGKFGLYNSDSFGGKVQ 204
DB   |||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
QY   406 RGLIVFHSSSGSTVSVDLPDAQOYPDTILRIYRDNNTISTSLISLSLYLT 458
DB   |||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:
QY   205 RGLIVFHSSSGSTVSVDLPDAQOYPDTILRIYRDNNTINSNLHIDLPLYTT 257
DB   |||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:

RESULT 14
US-08-487-266A-112
; Sequence 112, Application US/08487266A
; Patent No. 6824783
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUNCTION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,266A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
```

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; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; MOLECULE TYPE: protein
; US-08-487-266A-112

Query Match 31.4%; Score 1107; DB 2; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.8e-69;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELQGTALGNLKOIYYYNKAITSSSEKSDQFLNTLLFKGFPTG 285
DB 25 SEKSEINEKDLRKSELQGNALSRLRQIYYYNKAITENKESDDQFLENTLLFKGFPTG 84
QY 286 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYYGQCAGTGNKTCACMYGGVTLHDNNRLT 345
DB 85 HPWYNDLLVDLGSKDATNKYKGKVDLYGAYYGQCAGTGNKTCACMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVTSSKEVTQVELDQARHYLHGKFGLYNSDSFGGKVQ 405
DB 145 EEKVPINLWIDGKQTTVPIDKVTSSKEVTQVELDQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVFHSSEGSTVSYDLFDAQGGVPTLLRIYRDNNTTISSTLSISLYLYTT 458
DB 205 RGLIVFHSSEGSTVSYDLFDAQGGVPTLLRIYRDNKTINSENHLIDLYLYTT 257

RESULT 15
US-08-484-741-112
; Sequence 112, Application US/08484741
; Patent No. 6951717
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,741
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; MOLECULE TYPE: protein
; US-08-487-266A-112

Query Match 31.4%; Score 1107; DB 2; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.8e-69;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELQGTALGNLKOIYYYNKAITSSSEKSDQFLNTLLFKGFPTG 285
DB 25 SEKSEINEKDLRKSELQGNALSRLRQIYYYNKAITENKESDDQFLENTLLFKGFPTG 84
QY 286 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYYGQCAGTGNKTCACMYGGVTLHDNNRLT 345
DB 85 HPWYNDLLVDLGSKDATNKYKGKVDLYGAYYGQCAGTGNKTCACMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVTSSKEVTQVELDQARHYLHGKFGLYNSDSFGGKVQ 405
DB 145 EEKVPINLWIDGKQTTVPIDKVTSSKEVTQVELDQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVFHSSEGSTVSYDLFDAQGGVPTLLRIYRDNNTTISSTLSISLYLYTT 458
DB 205 RGLIVFHSSEGSTVSYDLFDAQGGVPTLLRIYRDNKTINSENHLIDLYLYTT 257

RESULT 16
US-09-350-841A-1598
; Sequence 1598, Application US/09350841A
; Patent No. 6750008
; GENERAL INFORMATION:
; APPLICANT: Jeffs, Peter;
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
; FILE REFERENCE: 7872-066-999
; CURRENT APPLICATION NUMBER: US/09/350,841A
; NUMBER OF SEQ ID NOS: 1946
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1598
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; US-09-350-841A-1598

Query Match 30.4%; Score 1071; DB 2; Length 254;
Best Local Similarity 88.0%; Pred. No. 8.7e-67;
Matches 206; Conservative 9; Mismatches 17; Indels 2; Gaps 2;

QY 226 SEKSEINEKDLRKSELQGTALGNLKOIYYYNKAITSSSEKSDQFLNTLLFKGFPTG 285
DB 22 SEKSEINEKDLRKSELQGNALSRLRQIYYYNKAITENKESDDQFLENTLLFKGFPTG 81
QY 286 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYYGQCAGTGNKTCACMYGGVTLHDNNRLT 345
DB 82 HPWYNDLLVDLGSKDATNKYKGKVDLYGAYYGQCAGTGNKTCACMYGGVTLHDNNRLT 141
QY 346 EEKVPINLWIDGKQTTVPIDKVTSSKEVTQVELDQARHYLHGKFGLYNSDSFGGKVQ 405
DB 142 EEKVPINLWID-KQTTVPIDKVTSSKEVTQVELDQARHYLHGKFGLYNSDSFGGKVQ 200
QY 406 RGLIVFHSSEGSTVSYDLFDAQGGVPTLLRIYRDNNTTISSTLSISLYLYTT 458
DB 201 RGLIVFHSSEGSTVSYDLFDAQGGVPTLLRIYRDNKTINSENHLIDLYLYTT 254

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Qy	551	LISSVQAEADRAVIFCQDINSIFPGGATLRLKADAAPIVSIPIFSSSGLTSSGGNSV	399
Db	338	-----KGRPKAPQVVYTIPIPPKEQMAKDKVSL	363
Qy	591	VFLLNFPYKDIINVKWKIDGSEKQGVLSWTDQDSKDSITYSMSSTLTLTKEDEYERHNSY	650
Db	364	TCMITDFPEDITVEWQNGQPAEN-YKNTQPMIDT-DGSYFVYVSKLVQKSNWEAGNTF	421
Qy	651	TCEATHK 657	
Db	422	TCSVLHE 428	
RESULT 18			
US-08-353-400-36			
; Sequence 36, Application US/08353400			
; Patent No. 5665357			
; GENERAL INFORMATION:			
; APPLICANT:			
; TITLE OF INVENTION: PROTEINS			
; NUMBER OF SEQUENCES: 37			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/353,400			
; FILING DATE:			
; CLASSIFICATION: 424			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: GB 9324819.3			
; FILING DATE: 03-DEC-1993			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: GB 9411089.7			
; FILING DATE: 03-JUN-1994			
; INFORMATION FOR SEQ ID NO: 36:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 464 amino acids			
; TYPE: amino acid			
; STRANDEDNESS: single			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
; US-08-353-400-36			
Query Match 30.1%; Score 1059.5; DB 1; Length 464;			
Best Local Similarity 37.5%; Pred. No. 1.2e-65;			
Matches 250; Conservative 61; Mismatches 107; Indels 249; Gaps 14;			
Qy	1	EVQLQSGPDLVKPGASVKISCKASGYFRTGYMHVWVKQSPGKLEWIGRIINPNNGVTLY	60
Db	20	QVQLQPGAEIVKPGASVQLSCKASGYFTFGYIHWVKRPGQGLEWIGEVNPSGTGRSDY	79
Qy	61	NRKPKDKATLVTKSSSTTAWEIIRSLTSEDSAVYICARSTMV-TNYVMDYKQGQGTSTVTS	119
Db	80	NEKPKDKATLVTKSSSTTAWEIIRSLTSEDSAVYICARERAYGDDMDTWQGQGTSTVTS	139
Qy	120	SAKTTTPSVYPLAPGAAQNTSMVTGLCLVKGYFPEPVTVTWNSGSLSSGVHTTFAVLQS	179
Db	140	SAKTTTPSVYPLAPGAAQNTSMVTGLCLVKGYFPEPVTVTWNSGSLSSGVHTTFAVLQS	199
Qy	180	DLTYLSSVTVPSSTWPSSETVTCNVAHPASTKVDKKIVPRDSGGPSEKSEEINEKDLRK	239
Db	200	DLTYLSSVTVPSSTWPSSETVTCNVAHPASTKVDKKIVPRDCG-----	243
Qy	240	KSELQGLTGLNLRKQIVVYNSKAITSEKSDQFLNTLTLPKGFPTGHPMYNDLLVLDLGS	299
Db	244	-KPEICTVPEVSSVIFPPK-----PKDVLITLT-----	272
Qy	300	AATSEYEGSSVDLYAGYGYQCAGGTPTNCTACMYGGVTLHNNRLTEKKVPIINLWDGK	359
Db	273	-----TP-KVTCVVVDIS-----KDDPEVQFSWFDV--	297

QY 229 SEBINEKDLKKSELOQTALGNLKOIYYNSKAITSEKSAQOFLNTLLFKGFFTGHPW 288
Db 1 SEBINEKDLKKSELOQTALGNLKOIYYNEKAITENKESDDOQFLENTLLFKGFFTGHPW 60
QY 289 YNDLLVDLGSSTAATSEYEGSSVDLYGAYYGCAGGTPNKTCWYGVTLHDNNRLTEEK 348
Db 61 YNDLLVDKSKDATNKFKKVDLYGAYYGTGAGGTPNKTCWYGVTLHDNNRLTEZ- 119
QY 349 KVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGKVGQRL 408
Db 120 ---VBRKIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGKVGQRL 176
QY 409 IVPHSSEGSTSVYDLFDAQOQYPTLLRIYRDNTTSSLSLSLYTT 458
Db 177 IVPHSSEGSTSVYDLFDAQOQYPTLLRIYRDNTTSSLSLSLYTT 226
RESULT 22
US-09-485-737B-90
; Sequence 90, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 988701139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-09-485-737B-90
Query Match 27.8%; Score 980.5; DB 2; Length 711;
Best Local Similarity 35.3%; Pred. No. 6.8e-60;
Matches 254; Conservative 103; Mismatches 180; Indels 183; Gaps 23;
QY 1 EVLOQSGDPLVKPGASVKISKASGYFTGYTHMHWKQSPKGLEWIGRINPNNGVTLY 60
Db 21 QVQLVQSGSELKPGASVKISKASGYFTFDYGMNWKQAPGQGLKWMGWINTYTGESTY 80
QY 61 NQKPKDKATLVTKSSTAYMELRSLTSEDSAVYCARSTMTINYVDYMGQGTSTVSS 120
Db 81 VDDFKGRFVPSLDTSSAAQLQISSLKAEATATYFCARRGF---YAMDYMGQGTSTVSS 137
QY 121 AKTTTPSVPLAPGSAQTNSMTLGLCVKGYPEPVTVTWNSGSLSSGVTTPAVLQSD 180
Db 138 ASTKGSVPLAPSSKTSGGTAALGCLVKDYPEPVTVSNWSGALTSGVHTTTPAVLQSS 197
QY 181 -LYTLSSSVTPSPSTPSETVTCNVAHPASSTKVDKKIVPRDS-----GG 224
Db 198 GLYLSLSSVTPSPSSLTQITVINCNVNKPNTKVDKRVKPSCKDKTHCTPCPAPELLGG 257
QY 225 PS-----EKSEI-----NEKDLRKKSELGGTALGNLK---QIYYN 258
Db 258 PSVELFPKPKDILMSRTPEVTICVVDVSHEDPEVKFNWYVDGVEVHNAKTPREBQYN 317
QY 259 S-----KAITSS-EK-----SADQ 271
Db 318 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPASIETKISKAKGQPREPOVYTLPPSRRE 377

QY 272 FLTN-----TLLFKGFTGHPWINDLLVDLGSTA-ATSEYEGSS--VDLYGAYYGCAGG 324
Db 378 MTKNQVSLTCLVKGYF-----SDIAVWESNQPENNYKTTTPVLDSDSGSFLLYSLK-- 430
QY 325 TPNTKATCMYGGV-----TLHD--NNRLTEEK-----KVPINLWIDGKQTTVPIDKV 368
Db 431 TVDKSRWQGNVPSVCSVMEALHNHYTQKSLSLSPKLGSGSQVLVOSSELEKPGASV 490
QY 369 KTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKVGQRLIVPHSSEGSTSVYDLFDAQO 428
Db 491 KISK-----ASGYTFTDYGMNWKQAPGQGLKWMGWINTYTGESTYVD--DFKG 538
QY 429 QYPTDLLRIYRDNTTSSLSLS-----LYLYT----- 457
Db 539 RF-----VPSLDTSSAAQLQISSLKAEATATYFCARRGFYAMDYMGQGTSTVSSGGG 592
QY 458 -----TSIVMTQPTSLVSGADRVTTICKASQSVSNDVAVYQKPGQSPKLLI 506
Db 593 GSGGGSGGGGSDIVLTQSPATMSAASGERVTITCSASSISY-MFWYHQRPGQSPRLLI 651
QY 507 SYTSSRYAGVPRFSGSGYGTDFTLTISVQAEDAAVYFCQDYNSPPTFGGQTKLEIKR 566
Db 652 YDTSNLASGVPARFSGSGGSGTSYSLTISRMEPEDPATYFCHQSSSYPTFTGQGTKLEIKR 711
RESULT 23
US-10-071-485-90
; Sequence 90, Application US/10071485
; Patent No. 6830752
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; TITLE OF INVENTION: SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 988701139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-10-071-485-90
Query Match 27.8%; Score 980.5; DB 2; Length 711;
Best Local Similarity 35.3%; Pred. No. 6.8e-60;
Matches 254; Conservative 103; Mismatches 180; Indels 183; Gaps 23;
QY 1 EVLOQSGDPLVKPGASVKISKASGYFTGYTHMHWKQSPKGLEWIGRINPNNGVTLY 60
Db 21 QVQLVQSGSELKPGASVKISKASGYFTFDYGMNWKQAPGQGLKWMGWINTYTGESTY 80
QY 61 NQKPKDKATLVTKSSTAYMELRSLTSEDSAVYCARSTMTINYVDYMGQGTSTVSS 120
Db 81 VDDFKGRFVPSLDTSSAAQLQISSLKAEATATYFCARRGF---YAMDYMGQGTSTVSS 137
QY 121 AKTTTPSVPLAPGSAQTNSMTLGLCVKGYPEPVTVTWNSGSLSSGVTTPAVLQSD 180
Db 138 ASTKGSVPLAPSSKTSGGTAALGCLVKDYPEPVTVSNWSGALTSGVHTTTPAVLQSS 197
QY 181 -LYTLSSSVTPSPSTPSETVTCNVAHPASSTKVDKKIVPRDS-----GG 224

Db 198 GYLSLVVVTVSSSLGTOTYICNVNHNKFSNTKYDKRVEPKSCDKTHTCPPCPAPPELLGG 257
QY 225 PS-----EKSEI-----NEKOLRKSEIQGTALGNLK---QIYYYN 258
Db 258 PSVFLPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 317
QY 259 S-----KATSS-EK-----SADQ 271
Db 318 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIETISKAKGQPRFPQVYTLPPSRBE 377
QY 272 FLTN-----TLLPKGFTGHPWYNDLLDVLGSTA-ATSEYEGSS--VDLYGAYGYQCAGG 324
Db 378 MYKNQVSLTCLVKGFY-----SDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSKL-- 430
QY 325 TPNTKACMYGGV-----TLHD--NNRLTEK-----KVPINLWIDGKQTTPVIDKV 368
Db 431 TVDKSRWQGNVFCSCVMHEALHNHYTKSLSLSPGKLGGSQVQLVQSGSELKPKGASV 490
QY 369 KTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQORGLIVFHSSEGSTVSVDLFLDAQ 428
Db 491 KISK-----ASGTYFTDYGMNVKQAPQGQLKWMGINTYTGSTYVD--DFKG 538
QY 429 QYPTDLLRIYRDNNTTSSLSLS-----LYLYT----- 457
Db 539 RP-----VPSLDTVSAAYLQISSLKAEATATYFCARRGFAMDYWGQTTTVYSSGG 592
QY 458 -----TSIVMTQPTSLLSVAGDRVTITCKASQSVNDVAVYQKPGQSPKLLI 506
Db 593 GSGGGSGGGSDIVLTQSPATMSAASGERVLTITCSASSISY-MFWYHQRPGQSPRLLI 651
QY 507 SVTSSRYAGVPRFSSGSGTQFTLTISVQAEADAAYVFCQDYNSTPFGGQTKLEIKR 566
Db 652 YDTSNLASGVAPARFSGSGSTSYSLTISRMEPEDFATYFCHOSSSYPTFGGQTKLEIKR 711

RESULT 24
US-08-116-247-7
; Sequence 7, Application US/08116247
; Patent No. 5929212
; GENERAL INFORMATION:
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Zivin, Robert A.
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; TITLE OF INVENTION: CD3 Specific Recombinant Antibody
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Wasburn Kurtz Mackiewicz & No. 5929212ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,247
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/743,377
; FILING DATE: 10-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Paintin, Francis A.
; REGISTRATION NUMBER: 19,386
; REFERENCE/DOCKET NUMBER: CARP-0011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439

; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-116-247-7

Query Match 27.4%; Score 966; DB 1; Length 468;
Best Local Similarity 34.9%; Pred. No. 3.9e-59;
Matches 241; Conservative 56; Mismatches 126; Indels 268; Gaps 14;

QY 1 EVQLQSGDILVKPGASVKISKASGYSPTGYMHWVKOSPGKGLFWIGRIINPNNGVTLY 60
Db 20 QVQLQSGDELARPASVMSKASGYTFRITMHWKORPGQGLEWIGIINPSRGTNY 79
QY 61 NQKFKDKATLTVDKSTTAYMELRLSLSSEDSAVYYCARSTMITNYVMDYWGQTSYTVSS 120
Db 80 NQKFKDKATLTVDKSSSTAYMQLSLSLSEDSAVYYCAR-YYDDHYCLDYWGQGTTLTVSS 138
QY 121 AKTTPPSVYPLAPGAAQTNSMTLGLVKGYFPPEVTVTWNSGSLSSGVHTFPAYLQSD 180
Db 139 AKTTPPSVYPLAPVCGDTTSSVTLGLVKGYFPPEVTVTWNSGSLSSGVHTFPAYLQSD 198
QY 181 LYTLSSTVTPSSVTPSETVTCNVAPASSTKVDKIVPRDSGGPSEKSEINEKDLRKK 240
Db 199 LYTLSSTVTPSSVTPSQSITCNVAPASSTKVDKIEPR---GPIKPCP----- 246
QY 241 SELQGTALGNLKOIYYYNKAITSEKSAQDQFLTNTLLFKGFTGHPWYNDLLVDLGSTA 300
Db 247 ----- 246
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKACMYGGVTLHDNNRLTEKKVPIINLWIDGKQ 360
Db 247 -----PCKCPAPN-----LLGSPSVF----- 262
QY 361 TTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQORGLIVFHSSEGSTVS 420
Db 263 -----IFPKIKDVLMI---SLSPVIT 281
QY 421 YDLFDAQGYPTLLRIYRDNNTTISLSISLYLYTTSIVMTQPTSLLSVAGDRVTIT 480
Db 282 CVVDVSEDDPD-----VQISWFWNVNVEVHTAQITQ----- 312
QY 481 CKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVPRFSSGSGYCTDFTLTISVQAE 540
Db 313 -----HREDYNSLTRVV----- 324
QY 541 AAVYFCQDYNSTPPTFGGQTKLEIKRAD-----AAPTVSIFPPSSSEQLT 584
Db 325 SALPIQHQQDWMSSGKEF---CKVNNKDLPAPIERTISKPGSVRAPQVYVLPPEEEMT 380
QY 585 SGGASVVCFLNNFYPKDINVKWKIDGSEKQN-----GVLSNWTDDQSKDSTYSMSSTLTLL 639
Db 381 KKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTPEVLDS-----DGSYFMYSKLRV 433
QY 640 TKDEYERHNSYTCETHK--TSTSPIVKSFNR 669
Db 434 EKKNWVERNSYSCSVVHGLNHNHTTKSFNR 464

RESULT 25
US-09-348-224-7
; Sequence 7, Application US/09348224
; Patent No. 6750325
; GENERAL INFORMATION:
; APPLICANT: Jolliffe, Linda Kay
; APPLICANT: Zivin, Robert Allan
; APPLICANT: Adair, John Robert
; APPLICANT: Achwal, Diljeet Singh
; TITLE OF INVENTION: CD3 Specific Recombinant Antibody
; FILE REFERENCE: CARP0066
; CURRENT APPLICATION NUMBER: US/09/348,224

; CURRENT FILING DATE: 1999-07-06
; EARLIER APPLICATION NUMBER: 08/116,247
; EARLIER FILING DATE: 1993-09-03
; EARLIER APPLICATION NUMBER: 07/743,377
; EARLIER FILING DATE: 1991-10-04
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 7
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Mouse
US-09-348-224-7

Query Match 27.4%; Score 966; DB 2; Length 468;
Best Local Similarity 34.9%; Pred. No. 3.9e-59;
Matches 241; Conservative 56; Mismatches 126; Indels 268; Gaps 14;

QY 1 EVQLQQSGDPLVKGASVKISCKASGYSFTGYMHVWQSPGKLEWIGRINPNNGVTLY 60
DB 20 QVQLQQSGDGLRPGASVKMSCKASGYTFRTYTHHWYKQRPQGQLEWIGVINSRGYTN 79
QY 61 NQKPKDKATLTVKSSFTAYMELSLTSEDSSAVYVCARSTMTITNVMYDYGQGTSTVSS 120
DB 80 NQKPKDKATLTVKSSFTAYMELSLTSEDSSAVYVCARSTMTITNVMYDYGQGTSTVSS 138
QY 121 AKTTPSVYPLAPGSAQAOTNSMTLGLCLVKGYPPEPVTVTNWNSGSLSSGGVHTFPVQLQSD 180
DB 139 AKTTPSVYPLAPGSAQAOTNSMTLGLCLVKGYPPEPVTVTNWNSGSLSSGGVHTFPVQLQSD 198
QY 181 LYTLSSTVTPSPSTWPSSTETVCNVAHPASSTKVDKIKVPRDGGPSEKSEINEKDLRKK 240
DB 199 LYTLSSTVTPSPSTWPSSTETVCNVAHPASSTKVDKIKVPRDGGPSEKSEINEKDLRKK 246
QY 241 SELQGTALGNLKIYYNNSKAITSSSEKSAQDLTNTLLPKGFTGHPWYNDLLVLDGSTA 300
DB 247 ----- 246
QY 301 ATSEYEGSVLDYGAAYGYQAGTGNKTAQMGVTLHDNRLTEKKVPINLWIDGKQ 360
DB 247 -----PCKCPAPN-----LLGGPSVF----- 262
QY 361 TTVPIDKVKTSKEVTVQELDLQARHYLHCKFGLYNSDSFGGKVGRLIVFHSSEGSTVS 420
DB 263 -----IFPKIKDVLMT---SLSPIT 281
QY 421 YDLFDAQGGVPTLLRIYRDNMTTSSLSGLYLTSTVMTQTPTSLLSVAGDRVTIT 480
DB 282 CVVDVSEDDPD-----VQISFVNNVEVHTAQQT----- 312
QY 481 CKASQSVSNDAVYQKPGQSPKLLISYTSRYAGVDPDRFGSGYGTDTFTLTSSVQAE 540
DB 313 -----HREDYNSTLRVV--- 324
QY 541 AAVYFCQDYNPPTFGGKLEIKRAD-----AAPTGISFPSSBOLT 584
DB 325 SALPIQHDWMSGKEF-----KCKVNNKDLPAPIERTISKPGSVRAPQVTVLPPEEEMT 380
QY 585 SGASVVCFLNNFVKDINVKWIKKIDGSERON-----GVLSNWTDDQDSKSTYSMSSTLT 639
DB 381 KKQVTLTCMTDMPEDIVYEWNTNGKTELNYKNTPEVLDS-----DGSYFMYSLRV 433
QY 640 TKDEYERHNSYTCETHK-TSTSPVKSFN 669
DB 434 EKKWVERNYSVCSVHVEGLHNHHTTKFSR 464

RESULT 26
US-08-737-129A-2
; Sequence 2, Application US/08737129A
; Patent No. 5885816
; GENERAL INFORMATION:
; APPLICANT: Ikuo FUJII et al.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES ENANTIOSELECTIVELY

; TITLE OF INVENTION: HYDROLYSING AMINO ACID ESTER DERIVATIVES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,129A
; FILING DATE: No. 5885816ember 15, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-737-129A-2

Query Match 27.3%; Score 960; DB 1; Length 212;
Best Local Similarity 84.7%; Pred. No. 3.6e-59;
Matches 193; Conservative 11; Mismatches 14; Indels 8; Gaps 1;

QY 6 QSGPDLVKGASVKISCKASGYSFTGYMHVWQSPGKLEWIGRINPNNGVTLYNQKFK 65
DB 2 ESGTELAKPGASVKMSCKASGYTFTSYTHHWKVRQPGQGLEWIGYINPSTDYTEYIQKFK 61
QY 66 DKATLTVDKSSFTAYMELSLTSEDSSAVYVCARSTMTITNVMYDYGQGTSTVSSAKTTP 125
DB 62 DKATLTADKSSFTAYMELSLTSEDSSAVYVCARSTMTITNVMYDYGQGTSTVSSAKTTP 113
QY 126 PSYVPLAPGSAQAOTNSMTLGLCLVKGYPPEPVTVTNWNSGSLSSGGVHTFPVQLQSDLYLS 185
DB 114 PSYVPLAPGSAQAOTNSMTLGLCLVKGYPPEPVTVTNWNSGSLSSGGVHTFPVQLQSDLYLS 173
QY 186 SSVTPSPSTWPSSTETVCNVAHPASSTKVDKIKVPRD 221
DB 174 SSVTPSPSTWPSSTETVCNVAHPASSTKVDKIKVPRD 209

RESULT 27
US-08-303-569B-7
; Sequence 7, Application US/08303569B
; Patent No. 5859205
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia

Db 247 ----- 246
QY 301 ATSEYEGSSVDLYGAYGYQACGTPNKTACTMYGGVTLHDNNRLTEKVKPINLWIDGKQ 360
Db 247 -----PCKCPAPN-----LLGGPSVF----- 262
QY 361 TTPIDKVTSSKEVTVOELDLQARHYLHGKFLGYNLSDSGGKQVQGLIVFHSSEGSTVS 420
Db 263 -----IPFPKIKOVLMT---SLSPIVT 281
QY 421 YDLFDAQGVDPDILLRIYRDNNTTSSLSLSLYLYTTSIVMTQTPTPSLLVASGRVIT 480
Db 282 CVVDVSEDDPD-----VQISFWNNVEVHTAQOT----- 312
QY 481 CKASQSVNDVAVYQKPGQSKLLISYTSRYAGVDPDRFSGYGTDFTLTSSVQAE 540
Db 313 -----HREDYNSTLRVV----- 324
QY 541 AAVYFCQDYNPPTFGGTYKLEIKRAD-----AAPTVISFPPSSEQLT 584
Db 325 SALPIQHQMWSGKEF-----CKVNNKDLPAPIERTISKPGSVRAPQVYVLPPEEEMT 380
QY 585 SGCASVVCFLNNFVPKDINVKWKIDGSERON-----GVLSNWDQDQSKDSTYSMSSTLTL 639
Db 381 KKQVTLTCMTDMPEDIVVENTNGKTELYNKNTEPVLDS-----DGSYFMYSKLRV 433
QY 640 TKDEYERHNSYTCETHK-TSTSPIVKSFNR 669
Db 434 EKNWVERNYSYSCSVWHEGLNHHHTTKSFSR 464

RESULT 29
PCT-US94-14106-51
; Sequence 51, Application PC/TUS9414106
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Process for Generating Specific Antibodies
; NUMBER OF SEQUENCES: 61
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14106
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 223 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-14106-51

Query Match 27.1%; Score 953.5; DB 4; Length 223;
Best Local Similarity 83.0%; Pred. No. 1.1e-58;
Matches 185; Conservative 12; Mismatches 23; Indels 3; Gaps 2;

QY 1 EVOLQSGPDLVKPGASVKISCKASGYSFTGYVHWVWKQSPGKLEWIGINFNNGVTLY 60
Db 1 EVOLQSGPELMPGASVKISCKATGYTLSSYVLEWYKQSPGKLEWIGILFGSGSAHY 60
QY 61 NQFKDKATLVTKSSFTAYMELRSITSEDSAVVYCARSTMITNY--VMDYWGQGTSTVTV 118
Db 61 NEFKGKATFTVDTSSNTAYMQLSSLTSEDSAVVYCARGP-YGNYGDYFYWGQGTTLTV 119
QY 119 SSAKTTPPSVYPLAPGAAQTNSMTGLCIVKGVFPPEVTVTWNSGSLSSGVHTFFAVLQ 178
Db 120 SSAKTTPPSVYPLAPGAAQTNSMTGLCIVKGVFPPEVTVTWNSGSLSSGVHTFFAVLQ 179
QY 179 SDLYTLSSSVTPSPSTWPSSTVTCNVAHPASSTKVKDKIIVPRD 221
; |||||

Db 180 SDLYTLSSSVTPSPSTWPSSTVTCNVAHPASSTKVKDKIIVPRD 222

RESULT 30
US-08-695-692B-7
; Sequence 7, Application US/08695692B
; Patent No. 6514498
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlisten,
; APPLICANT: Johan Hansson, Terje Kalland, Lars
; APPLICANT: Abrahamson and Goran Foreberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
; TITLE OF INVENTION: AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,692B
; FILING DATE: August 12, 1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9601245-5
; FILING DATE: March 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Krieger, Paul E.
; REGISTRATION NUMBER: 25,886
; REFERENCE/DOCKET NUMBER: 41986/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-695-692B-7

Query Match 26.9%; Score 948; DB 2; Length 233;
Best Local Similarity 76.4%; Pred. No. 2.8e-58;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKKSELOGTALGNLKOIYYVNSKAITSEKSDAQDFTLTLPKGFFTG 285
Db 1 SEKSEINEKDLRKKSELOGTALGNLKOIYYNEKAKTENKESHQDQLQTLILFKGFFTD 60
QY 286 HPWYNLLVDLGSSTAATSEYEGSSVDLYGAYGYQACGTPNKTACTMYGGVTLHDNNRLT 345
Db 61 HSWYNLLVDFDSKDIDVYKGGKVDLYGAYGYQACGTPNKTACTMYGGVTLHDNNRLT 120
QY 346 EEKKVPINLWIDGKQTPIDKVTSSKEVTVOELDLQARHYLHGKFLGYNLSDSGGKQV 405
Db 121 EEKKVPINLWIDGKQTPLETVTNKNQNTVOELDLQARRYLQEKYNLNSVDFDGKVQ 180
QY 406 RGLIVFHSSEGSTVSVDLFDQAQGVDPDILLRIYRDNNTTSSLSLSLYLYTT 458
Db 181 RGLIVFTSTPEPSVNYDLFQAQGVDPDILLRIYRDNNTINSENHIDILYTS 233

RESULT 31
US-08-486-099-113
; Sequence 113, Application US/08486099
; Patent No. 6013263

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/
;
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
; TITLE OF INVENTION: B VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,099
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-486-099-113

Query Match 26.9%; Score 948; DB 2; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.2e-58;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKQIYYNSKAITSEKSADQFLNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELOGTALGNLKQIYYNEKAKTENKESHDLQHTILFKGFFTD 84

QY 286 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 345
Db 85 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144

QY 346 EEKVPINLWIDGKQTTPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGCKVQ 405
Db 145 EEKVPINLWLDGKQNTVPLETVTKNKQNTVQELDLQARRYLQEKYLYNSDVFQGVQ 204

QY 406 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNTTISSTLSLSLYTT 458
Db 205 RGLIVFHTSTEPSVNYDLFGAQGYQSYNTLLRIYRDKNKTINSENMHIDVLYTS 257

RESULT 32
US-08-360-107A-123
; Sequence 123, Application US/08360107A
; Patent No. 6017536
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
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;
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 149
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,107A
; FILING DATE: 20-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-360-107A-123

Query Match 26.9%; Score 948; DB 2; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.2e-58;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKQIYYNSKAITSEKSADQFLNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELOGTALGNLKQIYYNEKAKTENKESHDLQHTILFKGFFTD 84

QY 286 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 345
Db 85 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144

QY 346 EEKVPINLWIDGKQTTPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGCKVQ 405
Db 145 EEKVPINLWLDGKQNTVPLETVTKNKQNTVQELDLQARRYLQEKYLYNSDVFQGVQ 204

QY 406 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNTTISSTLSLSLYTT 458
Db 205 RGLIVFHTSTEPSVNYDLFGAQGYQSYNTLLRIYRDKNKTINSENMHIDVLYTS 257

RESULT 33
US-08-484-223B-113
; Sequence 113, Application US/08484223B
; Patent No. 6020459
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
```

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; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 245
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-484-223B-113

Query Match 26.9%; Score 948; DB 2; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.2e-58;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLKIYYNKAITSSEKSAQDLTNTLLFKGFTG 285
Db 25 SEKSEINEKDLRKSELOQTALGNLKIYYNEKAKTENKESHQDLQHTILFKGFTD 84

QY 286 HPWYNLLVDLGSSTAATSEYSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
Db 85 HSWYNLLVDFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGKVQ 405
Db 145 EEKVPINLWIDGKQNTVPLETVKTNKGNVTVOELDLQARRYLQEKYLNYSNDFDGVQ 204

QY 406 RGLIVFHSSEGSTVSYDLFDAQOQYPTLLRIYRDNTTISTSLISLYLYTT 458
Db 205 RGLIVFHTSTEPSVNYDLFGAQOQYNTLLRIYRDNTKNTINSENHHDILYLYTS 257

RESULT 34
US-08-919-597-113
; Sequence 113, Application US/08919597
; Patent No. 6054265
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
```

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; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/919,597
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,896
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-919-597-113

Query Match 26.9%; Score 948; DB 2; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.2e-58;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLKIYYNKAITSSEKSAQDLTNTLLFKGFTG 285
Db 25 SEKSEINEKDLRKSELOQTALGNLKIYYNEKAKTENKESHQDLQHTILFKGFTD 84

QY 286 HPWYNLLVDLGSSTAATSEYSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
Db 85 HSWYNLLVDFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGKVQ 405
Db 145 EEKVPINLWIDGKQNTVPLETVKTNKGNVTVOELDLQARRYLQEKYLNYSNDFDGVQ 204

QY 406 RGLIVFHSSEGSTVSYDLFDAQOQYPTLLRIYRDNTTISTSLISLYLYTT 458
Db 205 RGLIVFHTSTEPSVNYDLFGAQOQYNTLLRIYRDNTKNTINSENHHDILYLYTS 257

RESULT 35
US-08-475-668A-113
; Sequence 113, Application US/08475668A
; Patent No. 6060065
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,668A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-026
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-475-668A-113

Query Match 26.9%; Score 948; DB 2; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.2e-58;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKQIYYNYSKAITSEKSADQFLNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELOGTALGNLKQIYYNEKAKTENKESHDQFLQHTILFKGFFTD 84
QY 286 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 345
Db 85 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTTPIDKVTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKQVQ 405
Db 145 EEKVPINLWLDGKQNTVPLETVKTKNKNVTVOELDLQARRYLQEKYNYNSDVDFGKQVQ 204
QY 406 RGLIVPHSSEGSTVSYDLFDAQGYPDTLRLRYRDNNTTSSLSLSLYTT 458
Db 205 RGLIVFHTSTEPSVNYDLFQAQGYQNTLLRLRYRDNKNTINSENMHIDIYLYTS 257

RESULT 37
US-08-471-913A-113
; Sequence 113, Application US/08471913A
; Patent No. 6093794
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711

; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,668A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-026
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-475-668A-113

Query Match 26.9%; Score 948; DB 2; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.2e-58;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKQIYYNYSKAITSEKSADQFLNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELOGTALGNLKQIYYNEKAKTENKESHDQFLQHTILFKGFFTD 84
QY 286 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 345
Db 85 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTTPIDKVTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKQVQ 405
Db 145 EEKVPINLWLDGKQNTVPLETVKTKNKNVTVOELDLQARRYLQEKYNYNSDVDFGKQVQ 204
QY 406 RGLIVPHSSEGSTVSYDLFDAQGYPDTLRLRYRDNNTTSSLSLSLYTT 458
Db 205 RGLIVFHTSTEPSVNYDLFQAQGYQNTLLRLRYRDNKNTINSENMHIDIYLYTS 257

RESULT 36
US-08-485-551A-113
; Sequence 113, Application US/08485551A
; Patent No. 6068973
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; STREET: 1155 Avenue of the Americas
; CITY: New York
```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-471-913A-113

Query Match 26.9%; Score 948; DB 2; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.2e-58;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLKKSELOQTALGNLKQIYYVNSKAITSEKSAQDQFLNTLLFKGFFTG 285
DB 25 SEKSEINEKDLKKSELOQTALGNLKQIYYNEKAKTENKESHQDQLQHTILFKGFFTD 84
QY 286 HPWYNLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
DB 85 HSWYNLLVDLFDSDKIDVRYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGVNSDFGKVQ 405
DB 145 EEKVPINLWLDGKQNTVPLETKNKNVTQVQELDLQARRYLQEKYNLYNSDVFQKVQ 204
QY 406 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNTTISSTLSLSLYTT 458
DB 205 RGLIVFHTSTEPSVNYDLFQAQGYNTLLRIYRDNTKNTSENHHDIIYLYTS 257

RESULT 38
US-08-485-264A-113
Sequence 113, Application US/08485264A
Patent No. 6228983
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Pettaway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,264A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-021
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-264A-113

Query Match 26.9%; Score 948; DB 2; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.2e-58;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLKKSELOQTALGNLKQIYYVNSKAITSEKSAQDQFLNTLLFKGFFTG 285
DB 25 SEKSEINEKDLKKSELOQTALGNLKQIYYNEKAKTENKESHQDQLQHTILFKGFFTD 84
QY 286 HPWYNLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
DB 85 HSWYNLLVDLFDSDKIDVRYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGVNSDFGKVQ 405
DB 145 EEKVPINLWLDGKQNTVPLETKNKNVTQVQELDLQARRYLQEKYNLYNSDVFQKVQ 204
QY 406 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNTTISSTLSLSLYTT 458
DB 205 RGLIVFHTSTEPSVNYDLFQAQGYNTLLRIYRDNTKNTSENHHDIIYLYTS 257

RESULT 39
US-08-474-349A-113
Sequence 113, Application US/08474349A
Patent No. 6333395
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Pettaway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
NUMBER OF SEQUENCES: 517
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

```

, APPLICATION NUMBER: US/08/474,349A
, FILING DATE: 07-JUN-1995
, CLASSIFICATION:
, ATTORNEY/AGENT INFORMATION:
, NAME: Coruzzi, Laura A.
, REGISTRATION NUMBER: 30,742
, REFERENCE/DOCKET NUMBER: 7872-024
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: (212) 790-9090
, TELEFAX: (212) 869-9741/8864
, TELEX: 66141 PENNIE
, INFORMATION FOR SEQ ID NO: 113:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 257 amino acids
, TYPE: amino acid
, STRANDEDNESS:
, TOPOLOGY: unknown
, MOLECULE TYPE: protein
US-08-474-349A-113

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	Query Match	26.9%	Score 948;	DB 2;	Length 257;
	Best Local Similarity	76.4%;	Pred. No. 3.2e-58;		
	Matches	178;	Conservative	21;	Mismatches 34; Indels 0; Gaps 0;
Qy	226	SEKSEENEKDLRKS	LOGTALGNL	KQIYYVNS	KAITSSEKSADQFLTNTLFLKGFPGFTG 285
Db	25	SEKSEENEKDLRKS	LOGTALGNL	KQIYYNEKAKTEN	KESHDFLOHTILEFKGFFTD 84
Qy	286	HPWYNDLLVDLG	STAATSEYEG	SVDIYGAYGYQC	AGGTPNKTCAMYGVTVLHDNNRLT 345
Db	85	HSWYNDLLVDP	DSKDI	VDKYKGKVDLY	GAYGYQCAGGTPNKTCAMYGVTVLHDNNRLT 144
Qy	346	BEKKVPINLMD	KGQTTVPID	KVKTSKKEVT	VQELDQARHYLHGKGLYNSDSFGKVKQ 405
Db	145	BEKKVPINLMD	KGQNTVPIET	VTKNKNVT	VQELDQARLYOEKYNLNSDVFDEKVKQ 204
Qy	406	RLGIVFHSS	SGSTSVSYDL	FDAGQGYPTL	LRIYRDNNTTISTSLISLYLTT 458
Db	205	RLGIVFHT	STEPSVNYDL	FDAGQGYSTL	LRIYRDNKTINSNNHDIYLYTS 257

RESULT 40
US-08-470-896-113
; Sequence 113, Application US/08470896
; Patent No. 6479055
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,896
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-470-896-113

Query Match 26.9%; Score 948; DB 2; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.2e-58;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

Qy 226 SEKSEINEKDLRKSELOGTALGNLKQIYYYNKAITSSSEKSADQFLNTLLFKGFFTG 285
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 226 SEKSEINEKDLRKSELOGTALGNLKQIYYYNKAKTENKESHQOFLQHTLLFKGFFTD 84
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 286 HPWYNLLVLDGASTAATSEYSGSSVDLYGAYYGQCAGTGNKTKACMGVTVLHDNNRLT 345
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 346 EEKVPINLWIDGKQTTPIDIKVTKTSKEVTVQELDLQARHYLHGKFLGYNLSDSGGKQV 405
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 145 EEKVPINLWIDGKQNTVPLETVKTNKMTVQELDLQARRYLQEKYNLYNSDVPDGKQV 204
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 406 RGLIVFHSSEGSVSYDLFDAQGYPDTLRLIYRDNNTTISSTLSLSLYLYTT 458
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 205 RGLIVFHTSTEPSVNDLFLGAQGYQNTLLRIYRDNKNTINSENMHIDIYLYTS 257
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 41
US-08-485-546A-113
; Sequence 113, Application US/08485546A
; Patent No. 6518013
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER:
; APPLICATION NUMBER: US/08/485,546A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742

```


;
;
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS: <unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-08-484-741-113

Query Match 26.9%; Score 948; DB 2; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.2e-58;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDKRKSELOGTALGNLKQIYYNKAITSSEKSAOQFLNTLLFKGFFTG 285
DB 25 SEKSEINEKDKRKSELOGTALGNLKQIYYNEKAKTENKESHDFLOHTILFKGFFTD 84

QY 286 HPWYNDLLVDLSTAASTSEYEGSSVDLYGAYGYQCAGGTPNKTKACMYGGVTLHNNRLT 345
DB 85 HSWYNDLLVDFSDKDIVKYKGGKVDLYGAYGYQCAGGTPNKTKACMYGGVTLHNNRLT 144

QY 346 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
DB 145 BEKKVPINLWIDGKQNTVPLETVTKNKNVTVOELDLQARRYLQEKYINLYNSDVFQKQV 204

QY 406 RGLIVPHSSEGSTVSYDLFDAOGQYDPTLLRIYRDNNTTISSTLSLSLYLYTT 458
DB 205 RGLIVHTSTEPSVNYDLFQAQGYQNTLLRIYRDNKTINSENMHIDIYLYTS 257

RESULT 44
US-08-353-400-37
; Sequence 37, Application US/08353400
; Patent No. 5665357
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 37
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,400
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9324819.3
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411089.7
; FILING DATE: 03-JUN-1994
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-353-400-37

Query Match 26.8%; Score 944.5; DB 1; Length 239;
Best Local Similarity 78.1%; Pred. No. 5e-58;
Matches 185; Conservative 22; Mismatches 19; Indels 11; Gaps 3;

QY 445 SSTLSLSLYLYTT-----STVMTQTPTSLVSAAGDRVTITCKASQSVND-----VAVY 494
DB 3 SQAQVILLLLWVSGTCGDIVMSQSPSSLAVSAGEKVTWSCSKSQSLNLSRTERKNLAWY 62

QY 495 QKPGQSPKLLISYTSGRVAGVDPDRSGSGYGTDFTLTITSSVQAEAAVYFCQDYNSSPP 554
DB 63 QKPGQSPKLLIYWASTRTSGVDPDRFTGSGSGYGTDFTLTITSSVQAEADLAIVYCKQSY-TLR 121

QY 555 TFGGKTKLEIKRADAAPTVSIFPPPSSEQLTSGASVVCFLNNFYPKDINVKKIDGSEKQ 614
DB 122 TFGGKTKLEIKRADAAPTVSIFPPPSSEQLTSGASVVCFLNNFYPKDINVKKIDGSEKQ 181

QY 615 NGVLNSWTDQDSKDYSTYSMSSTLTITKDEYERHNSYTCATHKTSTSPIVKGFNRNE 671
DB 182 NGVLNSWTDQDSKDYSTYSMSSTLTITKDEYERHNSYTCATHKTSTSPIVKGFNRNE 238

RESULT 45
US-08-446-918A-4
; Sequence 4, Application US/08446918A
; Patent No. 5705151
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,918A
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 552
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2879-29
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-918A-4

Query Match 26.8%; Score 944; DB 1; Length 233;
Best Local Similarity 76.3%; Pred. No. 5.3e-58;
Matches 177; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 227 EKSEINEKDLRKSELOGTALGNLKQIYYNKAITSSEKSAOQFLNTLLPKGPFTH 286
DB 2 EKSEINEKDLRKSELOGTALGNLKQIYYNEKAKTENKESHDFLOHTILFKGFFTDH 61

QY 287 PWYNDLLVDLSTAASTSEYEGSSVDLYGAYGYQCAGGTPNKTKACMYGGVTLHNNRLTE 346
DB 62 SWYNDLLVDFDSKDIVKYKGGKVDLYGAYGYQCAGGTPNKTKACMYGGVTLHNNRLTE 121

QY 347 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 406
DB 122 BEKKVPINLWIDGKQNTVPLETVTKNKNVTVOELDLQARRYLQEKYINLYNSDVFQKQV 181

QY 407 GLIVPHSSEGSTVSYDLFDAOGQYDPTLLRIYRDNNTTISSTLSLSLYLYTT 458
DB 182 GLIVHTSTEPSVNYDLFQAQGYQNTLLRIYRDNKTINSENMHIDIYLYTS 233

RESULT 46
US-08-580-806-4
; Sequence 4, Application US/08580806


```
; Patent No. 5935568
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmslie, Robyn E.
; APPLICANT: Potter, Terence A.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,806
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-29-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-580-806-4

Query Match 26.8%; Score 944; DB 1; Length 233;
Best Local Similarity 76.3%; Pred. No. 5.3e-58;
Matches 177; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 227 EKSEINEKDLRKKELOGTALGNLKOIYYNKAITSSEKSDAQFNTTLKPGFPTH 286
Db 2 EKSEINEKDLRKKELOGTALGNLKOIYYNKAITSSEKSDAQFNTTLKPGFPTH 61
QY 287 PWNLDLLVDLGSATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTE 346
Db 62 SWYNDLLVDLGSATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTE 121
QY 347 EKKVPINLWDGKQTTVPIDKVTSKKEVTVOELDLQARHVLHGKFLYNSDSFGGKVQR 406
Db 122 EKKVPINLWDGKQNTVPLETVTKNKQNTVQELDLQARHVLHGKFLYNSDSFGGKVQR 181
QY 407 GLIVFHSSGTSVSYDLFDAGQGVPTDLLRIYRDNNTTISSTLSISLYTT 458
Db 182 GLIVFHTSTSPSVNYDLFGAGQVSNLLAIYRDNKNTINSENHIDIYLT 233

RESULT 47
US-08-353-400-34
; Sequence 34, Application US/08353400
; Patent No. 5665357
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 37
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (BFO)
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/353,400
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9324819.3
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411089.7
; FILING DATE: 03-JUN-1994
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 219 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-353-400-34

Query Match 26.7%; Score 941.5; DB 1; Length 219;
Best Local Similarity 83.0%; Pred. No. 7.2e-58;
Matches 181; Conservative 19; Mismatches 11; Indels 7; Gaps 2;

QY 460 IVMTOTPTSLVVSAGDRVTITCKASQSVND-----VANYQKPGQSPKLLISYTSRY 513
Db 2 IVNQSPSSLVVSAGEKVTMCKSSQSLNSTRKKNYLAWYQQRPGQSPKLLIYWASTRT 61
QY 514 AGVPDRFSGSGYGTDFLTITISSVQADAAVYFCQDYNSPPTFGGGTKLEIKRADAAPT 573
Db 62 SGVPDRFSGSGYGTDFLTITISSVQADAAVYFCQDYNSPPTFGGGTKLEIKRADAAPT 120
QY 574 SIFFPSSEQLTSGASVVCFLNNFYPKDINVKWKIDGSEQRQNGVLNSWTQDSDKSTYSM 633
Db 121 SIFFPSSEQLTSGASVVCFLNNFYPKDINVKWKIDGSEQRQNGVLNSWTQDSDKSTYSM 180
QY 634 SSTLTLTQDEYERHNSYTCETHKTSTSPIVKSFNRNE 671
Db 181 SSTLTLTQDEYERHNSYTCETHKTSTSPIVKSFNRNE 218

RESULT 48
US-08-737-129A-6
; Sequence 6, Application US/08737129A
; Patent No. 5885816
; GENERAL INFORMATION:
; APPLICANT: Ikuo FUJII et al.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES ENANTIOSELECTIVELY
; TITLE OF INVENTION: HYDROLYSING AMINO ACID ESTER DERIVATIVES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,129A
; FILING DATE: No. 5885816member 15, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
```

```
;
; TELEFAX:
;
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-737-129A-6

Query Match      26.5%; Score 933; DB 1; Length 222;
Best Local Similarity 82.6%; Pred. No. 2.9e-57;
Matches 180; Conservative 12; Mismatches 24; Indels 2; Gaps 1;

QY 6 QSGPDLVKGASVKISCKASGYSFTGYMHVWKQSPKGLEWIGRINPNNGVTLNKKPK 65
Db 2 ESGPELVKPGSVTISCKASGYGFTTSMWNVQRPGQGLEWIGRIYPGSGDNVYNGKPK 61
QY 66 DKATLTVDKSSITAYMELSLTSEDASVYCAR--STMITNYVMDYMGOGTSVTYSSAKT 123
Db 62 VKATLTAEKSSITVYLHLSSLTSVDSAVYFCARFHYDYSVAMDYMGOGTSVTYSSAKT 121
QY 124 TTPSVVPLAPGSAAGTNSMVTLGCLVKGYPFPBPVTVTNWNSGSLSSGVHTFPVAVLQSDLYT 183
Db 122 TTPSVVPLAPGSAAGTNSMVTLGCLVKGYPFPBPVTVTNWNSGSLSSGVHTFPVAVLQSDLYT 181
QY 184 LSSSVTPSSTWPSSTVTCNVAHPASSTKVDKIVPRD 221
Db 182 LSSSVTPSSTWPSSTVTCNVAHPASSTKVDKIVPRD 219
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RESULT 49
US-08-896-933-23
; Sequence 23, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
;
US-08-896-933-23
```

```
Query Match      26.4%; Score 931.5; DB 2; Length 232;
Best Local Similarity 76.0%; Pred. No. 3.9e-57;
Matches 177; Conservative 21; Mismatches 34; Indels 1; Gaps 1;

QY 226 SEKSEINEKDLRKSELOQTALGNLKQIYYNSKAITSEKSADQFLNTLLFKGFFTG 285
Db 1 SEKSEINEKDLRKSELOQTALGNLKQIYYNEKAKTENKESHDQFL-HTILFKGFFTD 59
QY 286 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 345
Db 60 HSWYNDLLVDFDSKQIVDKYKGVKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 119
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKQV 405
Db 120 EEKVPINLWIDGKQNTVPLETVTKNKNVTVOELDPQARRYLOEKYXLYNSDVDFGKQV 179
QY 406 RGLIVPHSSEGSTVSYDLFDAQQYPTDLLRIYRDNNTTSSLSISLYTT 458
Db 180 RGLIVPHSTPEPSVNYDLFGAQQGYGNTLLRIYRDNKNTINSENMHIDIYLYTS 232
```

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RESULT 50
US-09-314-235-23
; Sequence 23, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; EARLIER FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
;
US-09-314-235-23
```

```
Query Match      26.4%; Score 931.5; DB 2; Length 232;
Best Local Similarity 76.0%; Pred. No. 3.9e-57;
Matches 177; Conservative 21; Mismatches 34; Indels 1; Gaps 1;

QY 226 SEKSEINEKDLRKSELOQTALGNLKQIYYNSKAITSEKSADQFLNTLLFKGFFTG 285
Db 1 SEKSEINEKDLRKSELOQTALGNLKQIYYNEKAKTENKESHDQFL-HTILFKGFFTD 59
QY 286 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 345
Db 60 HSWYNDLLVDFDSKQIVDKYKGVKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 119
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKQV 405
Db 120 EEKVPINLWIDGKQNTVPLETVTKNKNVTVOELDPQARRYLOEKYXLYNSDVDFGKQV 179
QY 406 RGLIVPHSSEGSTVSYDLFDAQQYPTDLLRIYRDNNTTSSLSISLYTT 458
Db 180 RGLIVPHSTPEPSVNYDLFGAQQGYGNTLLRIYRDNKNTINSENMHIDIYLYTS 232
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RESULT 51
US-09-708-008B-23
; Sequence 23, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978
; PRIOR FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 232
; TYPE: PRT
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ORGANISM: Staphylococcus aureus
US-09-708-008B-23

Query Match 26.4%; Score 931.5; DB 2; Length 232;
Best Local Similarity 76.0%; Pred. No. 3.9e-57;
Matches 177; Conservative 21; Mismatches 34; Indels 1; Gaps 1;
QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSEKADQPLTNTLLFKGFFTG 285
DB 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESHQPL-HTILFKGFFTD 59
QY 286 HPWYNLLVLDGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
DB 60 HSWYNLLVDFDSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 119
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 405
DB 120 EEKVPINLWLDGKQNTVPLETKNKNVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 179
QY 406 RGLIVHSSSEGSTVSYDLFDAQGYPTLLRIYRDNTTISSTLSLSLYLYTT 458
DB 180 RGLIVHTSTEPSVNYDLFQAQGYQNTLLRIYRDNTTISSTLSLSLYLYTS 232

RESULT 52
US-09-144-776B-2
Sequence 2, Application US/09144776B
Patent No. 6399332
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
Vaccines
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Charles H. Harris
STREET: US Army MRC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
Acty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-Sep-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/882,431
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 257
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Query Match 26.3%; Score 925; DB 2; Length 257;
Best Local Similarity 75.1%; Pred. No. 1.3e-56;
Matches 175; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSEKADQPLTNTLLFKGFFTG 285
DB 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESHQDQFQHTILFKGFFTD 84
QY 286 HPWYNLLVLDGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
DB 85 HSWYNLLVDFDSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 405
DB 145 EEKVPINLWLDGKQNTVPLETKNKNVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 204
QY 406 RGLIVHSSSEGSTVSYDLFDAQGYPTLLRIYRDNTTISSTLSLSLYLYTT 458
DB 205 RGLIVHTSTEPSVNYDLFQAQGYQNTLLRIYRDNTTISSTLSLSLYLYTS 257

RESULT 53
US-08-882-431B-2
Sequence 2, Application US/08882431B
Patent No. 6713284
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
Vaccines
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Charles H. Harris
STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431B
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 257
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431B-2

Query Match 26.3%; Score 925; DB 2; Length 257;
Best Local Similarity 75.1%; Pred. No. 1.3e-56;
Matches 175; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSEKADQPLTNTLLFKGFFTG 285

Db 25 SEKSEINEKDLRKKSELOQTALGNLKQIYYVNEKAKTENKESHDOFRQHTILFKGFSTD 84
QY 286 HPWYNLLVDLGGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
Db 85 HSWYNLLVRFDSKDIDVRYKGGKVDLYGAYAGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 346 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGGKVQ 405
Db 145 EKKVPINLWIDGKQNTVPLETVTKNKNVTVOELDQARHYLHGKFGLYNSDSVDFGKVQ 204
QY 406 RGLIVFHSSEGSTSVSYDLFDAQOQYPTTLRIYRDNTTISSTLSLSLYTT 458
Db 205 RGLIVFHTSTEPSVNDLFGAQOQYNTLLRIYRDNTINSENHDIYLYTS 257

RESULT 54
US-09-144-776B-4
; Sequence 4, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MPMC -504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-144-776B-4

Query Match 26.1%; Score 921; DB 2; Length 233;
Best Local Similarity 75.0%; Pred. No. 2.1e-56;
Matches 174; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
QY 227 EKSEINEKDLRKKSELOQTALGNLKQIYYVNEKAKTENKESHDOFRQHTILFKGFSTD 286
Db 2 EKSEINEKDLRKKSELOQTALGNLKQIYYVNEKAKTENKESHDOFRQHTILFKGFSTD 61
QY 287 PWNVDLLVLDGKQNTVPLETVTKNKNVTVOELDQARHYLHGKFGLYNSDSFGGKVQ 346

Db 62 SWYNLLVRFDSKDIDVRYKGGKVDLYGAYAGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
QY 347 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGGKVQ 406
Db 122 EKKVPINLWIDGKQNTVPLETVTKNKNVTVOELDQARHYLHGKFGLYNSDSVDFGKVQ 181
QY 407 GLIVFHSSEGSTSVSYDLFDAQOQYPTTLRIYRDNTTISSTLSLSLYTT 458
Db 182 GLIVFHTSTEPSVNDLFGAQOQYNTLLRIYRDNTINSENHDIYLYTS 233

RESULT 55
US-08-882-431B-4
; Sequence 4, Application US/08882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MPMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431B-4

Query Match 26.1%; Score 921; DB 2; Length 233;
Best Local Similarity 75.0%; Pred. No. 2.1e-56;
Matches 174; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
QY 227 EKSEINEKDLRKKSELOQTALGNLKQIYYVNEKAKTENKESHDOFRQHTILFKGFSTD 286
Db 2 EKSEINEKDLRKKSELOQTALGNLKQIYYVNEKAKTENKESHDOFRQHTILFKGFSTD 61
QY 287 PWNVDLLVLDGKQNTVPLETVTKNKNVTVOELDQARHYLHGKFGLYNSDSFGGKVQ 346
Db 62 SWYNLLVRFDSKDIDVRYKGGKVDLYGAYAGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
QY 347 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGGKVQ 406
Db 122 EKKVPINLWIDGKQNTVPLETVTKNKNVTVOELDQARHYLHGKFGLYNSDSVDFGKVQ 181


```
QY 475 DRVTITKASQSVNDVAMVQKPGQPKLLISYTSRVRAGVDPDRFGSGGYGDTFLTLIS 534
Db 312 -----TLP1Q 316
QY 535 SVOAEDAAVYFCQDYNSPPTFGGKLEIKRADAAPTYSIFPPSSEQLTSGGASVVCFL 594
Db 317 HQDWSGKEFKCKVNNKDLPSPIERTISKIGLVRAPQVYVILPPPAEQLSRKDVSLTCLV 376
QY 595 NNFYPKDINVWKIDGSRQN-----GVLNWTQDQSKDSTYSMSSTLTTLTKDEYERHNS 649
Db 377 VGFNPGDISVWETSNGHTEENYKDTAPVLDS-----DGSFYISKLNKMTSKWEKTD 429
QY 650 YTCEATHK 657
Db 430 FSCNVRHE 437

RESULT 58
US-08-792-824-10
; Sequence 10, Application US/08792824
; Patent No. 5932449
; GENERAL INFORMATION:
; APPLICANT: EMANUEL, PETER A.
; APPLICANT: BURANS, JAMES P.
; APPLICANT: VALDES, JAMES J.
; APPLICANT: MOHYEE, ELDEFRAWI E.
; TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: U.S. Army Chemical and Biological Defense
; STREET: Office of the Chief Counsel, Bldg E4435
; CITY: Aberdeen Proving Ground
; STATE: MD
; COUNTRY: U.S.
; ZIP: 21010-5423
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,824
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Biffoni, U. J.
; REGISTRATION NUMBER: 39,908
; REFERENCE/DOCKET NUMBER: DAM 431-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 410-671-1158
; TELEFAX: 410-671-2534
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-792-824-10

Query Match 26.0%; Score 915.5; DB 1; Length 254;
Best Local Similarity 79.2%; Pred. No. 5.7e-56;
Matches 179; Conservative 15; Mismatches 27; Indels 5; Gaps 2;

QY 1 EVOLQSQGPDLPKPGASVKISCKASGYSTGYMHVVKSPGKLEWIGRINPNNGVTL 60
Db 23 EVOLQSQGAEVLKPGASVKLSCTASGNFKDTFMHVKORPEQGLEWIGRIDPANGTEY 82
QY 61 NQKFKDKATLTVDKSTTAYMELRLSTSDSAVYYCARSTMITNYMDYWGQGSTVTSS 120
Db 83 DPKFQKGATITADTSSNTVNLQSLSTSDTAYYCASSGELG---FPYWGQGLTVTVA 139
QY 121 AKTTTPSVYPLAPGSAQAQNSMTVLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPVQLSD 180
Db 140 AKTTTPSVYPLAPGSAQAQNSMTVLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPVQLSD 199
QY 181 LYTLSSTVTPSSTWPSSETVTCNVAHPASSTKVDKKIVPRD--SGG 224
Db 200 LYTLSSTVTPSSTWPSSETVTCNVAHPASSTKVDKKIVPRDCTSGG 245

RESULT 60
US-08-792-824-10
; Sequence 10, Application US/08792824
; Patent No. 5932449
; GENERAL INFORMATION:
; APPLICANT: EMANUEL, PETER A.
; APPLICANT: BURANS, JAMES P.
; APPLICANT: VALDES, JAMES J.
; APPLICANT: MOHYEE, ELDEFRAWI E.
; TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: U.S. Army Chemical and Biological Defense
; STREET: Office of the Chief Counsel, Bldg E4435
; CITY: Aberdeen Proving Ground
; STATE: MD
; COUNTRY: U.S.
; ZIP: 21010-5423
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,824
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Biffoni, U. J.
; REGISTRATION NUMBER: 39,908
; REFERENCE/DOCKET NUMBER: DAM 431-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 410-671-1158
; TELEFAX: 410-671-2534
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-792-824-10

Query Match 26.0%; Score 915.5; DB 1; Length 254;
Best Local Similarity 79.2%; Pred. No. 5.7e-56;
Matches 179; Conservative 15; Mismatches 27; Indels 5; Gaps 2;

QY 1 EVOLQSQGPDLPKPGASVKISCKASGYSTGYMHVVKSPGKLEWIGRINPNNGVTL 60
Db 23 EVOLQSQGAEVLKPGASVKLSCTASGNFKDTFMHVKORPEQGLEWIGRIDPANGTEY 82
QY 61 NQKFKDKATLTVDKSTTAYMELRLSTSDSAVYYCARSTMITNYMDYWGQGSTVTSS 120
Db 83 DPKFQKGATITADTSSNTVNLQSLSTSDTAYYCASSGELG---FPYWGQGLTVTVA 139
QY 121 AKTTTPSVYPLAPGSAQAQNSMTVLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPVQLSD 180
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Db 140 AKTTTPSVYPLAPGSAQAQNSMTVLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPVQLSD 199
QY 181 LYTLSSTVTPSSTWPSSETVTCNVAHPASSTKVDKKIVPRD--SGG 224
Db 200 LYTLSSTVTPSSTWPSSETVTCNVAHPASSTKVDKKIVPRDCTSGG 245

RESULT 59
US-08-792-824-13
; Sequence 13, Application US/08792824
; Patent No. 5932449
; GENERAL INFORMATION:
; APPLICANT: EMANUEL, PETER A.
; APPLICANT: BURANS, JAMES P.
; APPLICANT: VALDES, JAMES J.
; APPLICANT: MOHYEE, ELDEFRAWI E.
; TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: U.S. Army Chemical and Biological Defense
; STREET: Office of the Chief Counsel, Bldg E4435
; CITY: Aberdeen Proving Ground
; STATE: MD
; COUNTRY: U.S.
; ZIP: 21010-5423
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,824
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Biffoni, U. J.
; REGISTRATION NUMBER: 39,908
; REFERENCE/DOCKET NUMBER: DAM 431-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 410-671-1158
; TELEFAX: 410-671-2534
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-792-824-13

Query Match 26.0%; Score 915.5; DB 1; Length 254;
Best Local Similarity 79.2%; Pred. No. 5.7e-56;
Matches 179; Conservative 15; Mismatches 27; Indels 5; Gaps 2;

QY 1 EVOLQSQGPDLPKPGASVKISCKASGYSTGYMHVVKSPGKLEWIGRINPNNGVTL 60
Db 23 EVOLQSQGAEVLKPGASVKLSCTASGNFKDTFMHVKORPEQGLEWIGRIDPANGTEY 82
QY 61 NQKFKDKATLTVDKSTTAYMELRLSTSDSAVYYCARSTMITNYMDYWGQGSTVTSS 120
Db 83 DPKFQKGATITADTSSNTVNLQSLSTSDTAYYCASSGELG---FPYWGQGLTVTVA 139
QY 121 AKTTTPSVYPLAPGSAQAQNSMTVLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPVQLSD 180
Db 140 AKTTTPSVYPLAPGSAQAQNSMTVLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPVQLSD 199
QY 181 LYTLSSTVTPSSTWPSSETVTCNVAHPASSTKVDKKIVPRD--SGG 224
Db 200 LYTLSSTVTPSSTWPSSETVTCNVAHPASSTKVDKKIVPRDCTSGG 245

RESULT 60
```



```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence: Designed heavy
US-09-192-545-4

Query Match      25.7%; Score 904.5; DB 2; Length 238;
Best Local Similarity 79.5%; Pred. No. 3e-55;
Matches 175; Conservative 18; Mismatches 22; Indels 5; Gaps 2;

QY 457 TTSIVMTQPTSLVAGDRVTITCKASQSV--SND---VAMYQKPGQSPKLLISYTS 511
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 18 SSDVLMTQPTSLPVLGDAQSISCRSSQSIHVSNGNTYLEWYLPKPGQSPKLLIYKVN 77
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 512 RVAGVDPDRSGSGYGTDFLTITSSVQAEDAAVYFCQDYNSPPTFGGCTKLEIKRADAAP 571
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 78 RFGVDPDRSGSGYGTDFLTILSRVBAEDLVYVYCFQGSHPVLTFGAGTKLEIKRADAAP 137
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 572 TVSIFFPSSEQLTSGGASVVCFLNNFPKIDINVKWKIDGSEKQVGLNSWTQDQSKDSTY 631
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 138 TVSIFFPSSEQLTSGGASVVCFLNNFPKIDINVKWKIDGSEKQVGLNSWTQDQSKDSTY 197
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 632 SMSSTLTLTCKDEYERHNSYTCEATHKTSTSPIVKSFRNE 671
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 198 SMSSTLTLTCKDEYERHNSYTCEATHKTSTSPIVKSFRNE 237
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 63
5455030-1
; Patent No. 5455030
; APPLICANT: LADNER, ROBERT C.; BIRD, ROBERT E.; HARDMAN, KARL
; TITLE OF INVENTION: IMMUNOTHERAPY USING SINGLE CHAIN
; POLYPEPTIDE BINDING MOLECULES
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/04,440
; FILING DATE: 1-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 512,910
; FILING DATE: 25-APR-1990
; APPLICATION NUMBER: 299,617
; FILING DATE: 19-JAN-1989
; APPLICATION NUMBER: 92,110
; FILING DATE: 02-SEP-1987
; APPLICATION NUMBER: 902,971
; FILING DATE: 01-SEP-1986
; SEQ ID NO: 1:
; LENGTH: 447
5455030-1

Query Match      25.7%; Score 903.5; DB 6; Length 447;
Best Local Similarity 32.9%; Pred. No. 8.2e-55;
Matches 222; Conservative 69; Mismatches 121; Indels 263; Gaps 15;

QY 1 EVQLQSGDPLVKPGASVKISCKASGYFTGYMHVVKQSPGKLEWIGRINPNNGVTLY 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 EVQLVESGDDLKPG-SLKLSCAASFTTISYCMVWRQTPDKRLEWATISGSGTYTY 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 NQKFKDKATLTVDKSTTAYMELRSLTSEDSAVYYCAR---SPMTITN-YVMIDYWGQTSV 116
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 60 PDSVKGRTISRDNAXNTLYLQMSGLKSEDTAMYCARITTVLTIDYAMDYWGQTSV 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 117 TVSSAKTTPPVYPLAPGAAQTNSMTLGLCVKGFPEPVTVTWNSGLSSGVHTFPFV 176
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 120 TVSSAKTTPPVYPLAPGAAQTNSMTLGLCVKGFPEPVTVTWNSGLSSGVHTFPFV 179
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 177 LQSDLYTLSSSVTPSPSTWPESEITCNVAHPASSTKVDKKIIPRDSGGPSEKSEINEKD 236
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 180 LQSDLYTLSSSVTPSPSTWPESEITCNVAHPASSTKVDKKIIPRDCG----- 226
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 237 LRKKSLEQGTALGNLKOIYYNSKATTSSEKSAQQLTWTLLPKGFTHPWYNDLLVDL 296
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 227 -----CKPCICTVPEVSSVIFPPK-----PKDVLITLT----- 255
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

PCT-US94-14106-57
; Sequence 57, Application PC/TUS9414106
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Process for Generating Specific Antibodies
; NUMBER OF SEQUENCES: 61
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14106
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-14106-57

Query Match      25.6%; Score 901; DB 4; Length 218;
Best Local Similarity 80.6%; Pred. No. 4.7e-55;
Matches 174; Conservative 9; Mismatches 29; Indels 4; Gaps 1;

QY 460 IVMOTPTSLVAGDRVTITCKASQSVND----VAMYQKPGQSPKLLISYTSRYAG 515
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2 IVMOTSPASLAVSLGORATISCRVRSVSTSHSYMHYQKPGQPKLLIKYASNLSEG 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 516 VPDRESGSGYGTDFLTITSSVQAEDAAVYFCQDYNSPPTFGGCTKLEIKRADAAPTISI 575
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 VPARSGSGSGYGTDFLTINHPVSEEDATYTCQHSWEIPTFGGCTKLEIKRADAAPTISI 121
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 576 FPPSSEQLTSGGASVVCFLNNFPKIDINVKWKIDGSEKQVGLNSWTQDQSKDSTYSMS 635
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 122 FPPSSEQLTSGGASVVCFLNNFPKIDINVKWKIDGSEKQVGLNSWTQDQSKDSTYSRS 181
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 636 TLTLTCKDEYERHNSYTCEATHKTSTSPIVKSFRNE 671
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 182 TLTLTCKDEYERHNSYTCEATHKTSTSPIVKSFRNE 217
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

PCT-US94-14106-57
; Sequence 57, Application PC/TUS9414106
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Process for Generating Specific Antibodies
; NUMBER OF SEQUENCES: 61
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14106
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-14106-57
```



```

Qy 1 EVOLQSGPDLVKPGASVKLSCKASGYSFRTGYMHVWVKQSPGKGLEWIGRINPNNGVTLY 60
Db 1 EVOLQSGAELMMPGASVKLSCKATGYTLSSSLWEVWKQSPGHGLEWIGILFGSGSAHY 60
Qy 61 NQPKDKATLTVDKSSPTAYMELRSLTSEDSAVYVCARSTMITNY--VMDYWGQGTSTVY 118
Db 61 NEAPKGAFTVDTSSNTAYMQLSLTSEDSAVYVCARGD-YNGYGDYFDYWGQQAALT 119
Qy 119 SSAKTTPPSYVPLAPGSAQTSMVTLGCLVKGYFPEPVTVTVWNSGSLSSGVHTFPAVLQ 178
Db 120 FSAKTPSSVYPLAAGSAAQTSMVTLGCLVKGYLPEPVTVTVWNSGSLSSGVHTFPAVLQ 179
Qy 179 SDLYTLSSSVTVPSSTWPSSTVTCNVAHPASSTKVDKKIIVPRD 221
Db 180 SDLYTLRSVTVPSSTWPSSTVTCNVAHPASSTKVDKKIIVPRD 222

RESULT 67
US-08-737-129A-8
; Sequence 8, Application US/08737129A
; Patent No. 5885816
; GENERAL INFORMATION:
; APPLICANT: Ikuo FUJII et al.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES ENANTIOSELECTIVELY
; TITLE OF INVENTION: HYDROLYSING AMINO ACID ESTER DERIVATIVES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,129A
; FILING DATE: No. 5885816ember 15, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-737-129A-8

Query Match 25.4%; Score 895; DB 1; Length 215;
Best Local Similarity 80.2%; Pred.No.1.2e-54;
Matches 170; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

Qy 460 IVMTQPTSLLSVAGDRVTITCKASQSVSNDAVYQKQSPKLLISYTSRYAGVPDR 519
Db 2 LVMTQPTSSMYASLGERVITCKASQDINILYLSFWQKQSPKALYRTNGLVDGVPDR 61
Qy 520 FSGSGYGTDFTLTISVVQAEAAVYFCQDYNSPPTFGGQTKLEIKRADAAPTVSIPPS 579

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Db 62 FSGSGQDYSLTISSEYEDMGIYCYQVDFPPYTFGGTKLEIKRAADAAPTVSIFPPS 121
QY 580 SSQLTSGGASVVCFLNFPKQINVKWKIDGSRQGVLSNWTDDQSDKSTYSMSSTLTL 639
Db 122 SSQLTSGGASVVCFLNFPKQINVKWKIDGSRQGVLSNWTDDQSDKSTYSMSSTLTL 181
QY 640 TKDEYERHNSYCEATHKSTSTPIVKSFRNE 671
Db 182 TKDEYERHNSYCEATHKSTSTPIVKSFRNE 213
RESULT 68
US-09-254-180C-131
; Sequence 131, Application US/09254180C
; Patent No. 6777540
; GENERAL INFORMATION:
; APPLICANT: OKUMURA, Ko
; APPLICANT: EDA, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: USHIO, Yoshitaka
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or
; FILE REFERENCE: 050006-0055
; CURRENT APPLICATION NUMBER: US/09/254,180C
; PRIOR FILING DATE: 1999-04-15
; PRIOR FILING DATE: 1997-08-27
; PRIOR FILING DATE: 1996-09-20
; PRIOR FILING DATE: 1996-09-02
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 131
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Mouse
US-09-254-180C-131
Query Match 25.4%; Score 893.5; DB 2; Length 219;
Best Local Similarity 78.9%; Pred. No. 1.6e-54;
Matches 172; Conservative 17; Mismatches 28; Indels 1; Gaps 1;
QY 3 QLQSQGPDLVKPGASVKISKASGYSTGYNMHWKQSPGKLEWIGRINPNNGVTLNQ 62
Db 3 QLQSQGAELVRPGSSVKISKASGYAFSFWNMVKRPGQGLEWIGQIYPGDDNKYNG 62
QY 63 KFKDKATLTVDKSSSTAYMELSLTSEDSAVYVCARSTMTITNVMYDYGQGTSTVTSSAK 122
Db 63 KFKGKATLTADKSSSTAYMQLYSLTSEDSAVYFCARSGNYP-YAMDYWGQGTSTVTSSAK 121
QY 123 TTPPSVYPLAPGSAQTNSMTVLGCLVKGYFPEPTVTWNSGSLSGSVHTFFAVLQSDLY 182
Db 122 TTAPSVYPLAPVCGGTGSSVTLGCLVKGYFPEPTVLTWNSGSLSGSVHTFFAVLQSGLY 181
QY 183 TLSSSVTVPSSTWPSQTTCNVAHPASSTKVDKKIVPR 220
Db 182 TLSSSVTVTSSTWPSQTTCNVAHPASSTKVDKKIEPR 219
RESULT 69
US-09-254-180C-181
; Sequence 181, Application US/09254180C
; Patent No. 6777540
; GENERAL INFORMATION:
; APPLICANT: OKUMURA, Ko
; APPLICANT: EDA, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: USHIO, Yoshitaka
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: NAKATA, Motomi

; TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or
; FILE REFERENCE: 050006-0055
; CURRENT APPLICATION NUMBER: US/09/254,180C
; PRIOR FILING DATE: 1999-04-15
; PRIOR FILING DATE: 1997-08-27
; PRIOR FILING DATE: 1996-09-20
; PRIOR FILING DATE: 1996-09-02
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 181
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-254-180C-181
Query Match 25.4%; Score 893.5; DB 2; Length 219;
Best Local Similarity 78.9%; Pred. No. 1.6e-54;
Matches 172; Conservative 17; Mismatches 28; Indels 1; Gaps 1;
QY 3 QLQSQGPDLVKPGASVKISKASGYSTGYNMHWKQSPGKLEWIGRINPNNGVTLNQ 62
Db 3 QLQSQGAELVRPGSSVKISKASGYAFSFWNMVKRPGQGLEWIGQIYPGDDNKYNG 62
QY 63 KFKDKATLTVDKSSSTAYMELSLTSEDSAVYVCARSTMTITNVMYDYGQGTSTVTSSAK 122
Db 63 KFKGKATLTADKSSSTAYMQLYSLTSEDSAVYFCARSGNYP-YAMDYWGQGTSTVTSSAK 121
QY 123 TTPPSVYPLAPGSAQTNSMTVLGCLVKGYFPEPTVTWNSGSLSGSVHTFFAVLQSDLY 182
Db 122 TTAPSVYPLAPVCGGTGSSVTLGCLVKGYFPEPTVLTWNSGSLSGSVHTFFAVLQSGLY 181
QY 183 TLSSSVTVPSSTWPSQTTCNVAHPASSTKVDKKIVPR 220
Db 182 TLSSSVTVTSSTWPSQTTCNVAHPASSTKVDKKIEPR 219
RESULT 70
US-08-442-542-18
; Sequence 18, Application US/08442542
; Patent No. 5686600
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine B.
; APPLICANT: Koziel, Michael G.
; TITLE OF INVENTION: Antibodies which Bind to Insect Gut
; TITLE OF INVENTION: Proteins and their Use
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,542
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/267,641
; FILING DATE: 28-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: CGC 1750

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8615
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 599 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-442-542-18

Query Match      25.3%; Score 892.5; DB 1; Length 599;
Best Local Similarity 32.4%; Pred. No. 7.1e-54;
Matches 219; Conservative 73; Mismatches 118; Indels 265; Gaps 16;

QY 1 EVLOQSGDPLVKPGASVKISCKASGVFTGYVMHWKQSPGKGLWIGRI--NPNGVT 58
Db 155 QVKLQSGGGVLQPKGSLKLSKAASGFTFNFMNFWVRQAPGKLEWVARIRKSNYAT 214

QY 59 LYNQKPKDKATLVKDSSTTAYMELSLTSEDSAVYYCARSTMTITNYVMDYWGQGSVTV 118
Db 215 SYGDSVKDRFTVSRDSDSQSMFYLMNNLKTEDTAMYYCYR---VVYGMADYWGQGSVTV 271

QY 119 SSAKTTTPSPVYPLAPG--SAAQTNNSMVTGLCLVKGYFPEPVPTVITWNSGSLSSGVHTFPVAV 176
Db 272 SSAKTTTPSPVYPLAPGSRSAQTNSMVTGLCLVKGYFPEPVPTVITWNSGSLSSGVHTFPVAV 331

QY 177 LQSDLYTLSSSVTPSPSTWPESETVTCNVAHPASSTKVDDKIVPRDGGPSEKSEINEKD 236
Db 332 LQSDLYTLSSSVTPSPSTWPESETVTCNVAHPASSTKVDDKIVPRDCG----- 378

QY 237 LRKKSLEQGTALGNLQIYYNSKAITSEKSAQDLTNTLFLPKGFTGHPWYNDLLVDL 296
Db 379 -----CKPCTCTPEVSSVFIFPPK-----PKDVLITL----- 407

QY 297 GSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLLHNNRLTTEKKVPINLWI 356
Db 408 -----TP-KVTCVVVDIS-----KDDPEVQFSWFV 431

QY 357 DGKQTTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVQRG 407
Db 432 D-----DVEVHTAQTPREEQFNSTFRSVSELPIMHQDLNGKFKCKRVNSAAPAPIEK- 486

QY 408 LIVFHSSEGSTVSYDLFDAQGYPDTLRLIYRDNTTISSTLSISLYLTTISVMTQTPT 467
Db 487 -----TISKI----- 491

QY 468 SLLVSAGDRVTITCKASQSVSNVDVAVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGT 527
Db 492 ----- 491

QY 528 DFTLTISVQAEAAVYFCQDYNSPPTFGGTTKLEIKRADAAPTYSIRPPSSEQLTSGG 587
Db 492 -----KGRPKAPQVVTIPPPKEQWAKDK 514

QY 588 ASVVCFLNFPYKIDINVKWIDGSEKQN-----GVLSNWTDOBSKDSYMSSTLTITKD 642
Db 515 VSLTCMTIDTFEPDIIVQWQNGQPAENYKNTQPINMT-----NGSYFVYSKLVNQS 567

QY 643 EYERHNSYTCETHK 657
Db 568 NWEAGNTFTCSVLHE 582

RESULT 71
US-08-765-469-18
; Sequence 18, Application US/08765469
; Patent No. 6069301
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine B.
; APPLICANT: Koziel, Michael G.
; TITLE OF INVENTION: Antibodies which Bind to Insect Gut
; TITLE OF INVENTION: Proteins and their Use
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; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,469
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/267,641
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: CGC 1750
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8615
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 599 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-765-469-18

Query Match      25.3%; Score 892.5; DB 2; Length 599;
Best Local Similarity 32.4%; Pred. No. 7.1e-54;
Matches 219; Conservative 73; Mismatches 118; Indels 265; Gaps 16;

QY 1 EVLOQSGDPLVKPGASVKISCKASGVFTGYVMHWKQSPGKGLWIGRI--NPNGVT 58
Db 155 QVKLQSGGGVLQPKGSLKLSKAASGFTFNFMNFWVRQAPGKLEWVARIRKSNYAT 214

QY 59 LYNQKPKDKATLVKDSSTTAYMELSLTSEDSAVYYCARSTMTITNYVMDYWGQGSVTV 118
Db 215 SYGDSVKDRFTVSRDSDSQSMFYLMNNLKTEDTAMYYCYR---VVYGMADYWGQGSVTV 271

QY 119 SSAKTTTPSPVYPLAPG--SAAQTNNSMVTGLCLVKGYFPEPVPTVITWNSGSLSSGVHTFPVAV 176
Db 272 SSAKTTTPSPVYPLAPGSRSAQTNSMVTGLCLVKGYFPEPVPTVITWNSGSLSSGVHTFPVAV 331

QY 177 LQSDLYTLSSSVTPSPSTWPESETVTCNVAHPASSTKVDDKIVPRDGGPSEKSEINEKD 236
Db 332 LQSDLYTLSSSVTPSPSTWPESETVTCNVAHPASSTKVDDKIVPRDCG----- 378

QY 237 LRKKSLEQGTALGNLQIYYNSKAITSEKSAQDLTNTLFLPKGFTGHPWYNDLLVDL 296
Db 379 -----CKPCTCTPEVSSVFIFPPK-----PKDVLITL----- 407

QY 297 GSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLLHNNRLTTEKKVPINLWI 356
Db 408 -----TP-KVTCVVVDIS-----KDDPEVQFSWFV 431

QY 357 DGKQTTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVQRG 407
Db 432 D-----DVEVHTAQTPREEQFNSTFRSVSELPIMHQDLNGKFKCKRVNSAAPAPIEK- 486

QY 408 LIVFHSSEGSTVSYDLFDAQGYPDTLRLIYRDNTTISSTLSISLYLTTISVMTQTPT 467
Db 487 -----TISKI----- 491

QY 468 SLLVSAGDRVTITCKASQSVSNVDVAVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGT 527
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Db 492 ----- 491
QY 528 DFTLTSSVOAEDAAYFCQDYNSPPTFGGKLEIKRADAAPTYSIIPPSPSEQLTSGG 587
Db 492 -----KGRPKAPQVYTTIPPKQEQMAKDK 514
QY 588 ASVVCFLNFPYKIDNVKMKIDSERQ-----GVLSNWTDDQSKDSTYSMSSTLTLT KD 642
Db 515 VSLTCMIDTFEPEDITVEQWNGQPAENYKNTQPIWMT-----NGSYFVYSKLVNQKS 567
QY 643 EVERHNSYTCETHK 657
Db 568 NWEAGNTFTCSVLHE 582

RESULT 72
US-09-423-439-58
; Sequence 58, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
; BLAKEY, David Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS word
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APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-No. 6339070-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 58:

US-09-423-439-58
Query Match 25.3%; Score 889.5; DB 2; Length 235;
Best Local Similarity 77.1%; Pred. No. 3.3e-54;
Matches 172; Conservative 19; Mismatches 31; Indels 1; Gaps 1;
QY 449 LGISLYLYTTSIVMTQTPTSLVLSAGDRVITTCASQSVNDVAMVYQKPGQSPKLLISY 508
Db 13 ISASVIMSGQTVLSQSPAILSASPGKVTMTCRASSVTY-IHWYQKPGSSPKSWIYA 71
QY 509 TSSRYAGVDRFRSGSGYGTDFTLTSSVOAEDAAYFCQDYNSPPTFGGKLEIKRAD 568
Db 72 TSNLASGVPARFSGSGSGTSYSLTISRVAEDAATYICQHWSSKPTFGGKLEIKRAD 131
QY 569 AAPTYSIIPPSSQLTSGGASVVCFLNFPKIDNVKMKIDGERQGVLSNWTDDQSKD 628
Db 132 AAPTYSIIPPSSQLTSGGASVVCFLNFPKIDNVKMKIDGERQGVLSNWTDDQSKD 191
QY 629 STYSMSSTLTLTKDEYERHNSYTCETHKSTSTSPIVKSFNRNE 671
Db 192 STYSMSSTLTLTKDEYERHNSYTCETHKSTSTSPIVKSFNRNE 234

RESULT 73
US-09-011-769A-23
; Sequence 23, Application US/09011769A
; Patent No. 6436691
; GENERAL INFORMATION:
; APPLICANT: SLATER, Anthony M.
; BLAKEY, David C.
; DAVIES, David H.
; HENNAM, John F.
; HENNEQUIN, Laurent F.A.
; MARSHAM, Peter R.
; DOWELL, Robert I.
; TITLE OF INVENTION: Chemical Compounds
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, LLP
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,769A
FILING DATE: 13-Feb-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/01975
FILING DATE: 13-AUG-1996
APPLICATION NUMBER: GB 9612295.7
FILING DATE: 12-JUN-1996
APPLICATION NUMBER: GB 9611019.2
FILING DATE: 25-MAY-1996
APPLICATION NUMBER: GB 9516810.0
FILING DATE: 16-AUG-1995
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:

US-09-011-769A-23
Query Match 25.3%; Score 889.5; DB 2; Length 235;
Best Local Similarity 77.1%; Pred. No. 3.3e-54;
Matches 172; Conservative 19; Mismatches 31; Indels 1; Gaps 1;
QY 449 LGISLYLYTTSIVMTQTPTSLVLSAGDRVITTCASQSVNDVAMVYQKPGQSPKLLISY 508
Db 13 ISASVIMSGQTVLSQSPAILSASPGKVTMTCRASSVTY-IHWYQKPGSSPKSWIYA 71
QY 509 TSSRYAGVDRFRSGSGYGTDFTLTSSVOAEDAAYFCQDYNSPPTFGGKLEIKRAD 568
Db 72 TSNLASGVPARFSGSGSGTSYSLTISRVAEDAATYICQHWSSKPTFGGKLEIKRAD 131
QY 569 AAPTYSIIPPSSQLTSGGASVVCFLNFPKIDNVKMKIDGERQGVLSNWTDDQSKD 628
Db 132 AAPTYSIIPPSSQLTSGGASVVCFLNFPKIDNVKMKIDGERQGVLSNWTDDQSKD 191
QY 629 STYSMSSTLTLTKDEYERHNSYTCETHKSTSTSPIVKSFNRNE 671
Db 192 STYSMSSTLTLTKDEYERHNSYTCETHKSTSTSPIVKSFNRNE 234
RESULT 74
US-09-254-180C-132

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; Sequence 132, Application US/09254180C
; Patent No. 6777540
; GENERAL INFORMATION:
; APPLICANT: OKUMURA, Ko
; APPLICANT: EDA, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: USHIO, Yoshitaka
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or
; FILE OF INVENTION: Fragments Thereof, and Apoptosis-Induced Site From Fas Ligand
; FILE REFERENCE: 050006-0055
; CURRENT APPLICATION NUMBER: US/09/254,180C
; CURRENT FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: PCT/JP97/02983
; PRIOR FILING DATE: 1997-08-27
; PRIOR APPLICATION NUMBER: 271546/1996
; PRIOR FILING DATE: 1996-09-20
; PRIOR APPLICATION NUMBER: 231472/1996
; PRIOR FILING DATE: 1996-09-02
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 132
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Mouse
US-09-254-180C-132

Query Match      25.1%; Score 885.5; DB 2; Length 216;
Best Local Similarity 80.0%; Pred. No. 5.6e-54;
Matches 172; Conservative 14; Mismatches 24; Indels 5; Gaps 1;

QY 460 IVMTQPTSLVLSAGDRVTITCKASQSVSND-----VAVYQKPGQSPKLLISYTSRYA 514
Db 2 VLMTQPLSLPVLGDAQSISCKSSQSIHSSGNTYFEWYLPQPGSPKLLIYKVSNRFS 61
QY 515 GVPDRFSGSGYGTDFLTITSSVQAEAAVYFCQDYNSPPTFGGGTKLEIKRADAAPTVS 574
Db 62 GVPDRFSGSGGTDFLTIKISRVEAEDLGYYVYCFQGSHPPTFGSGTKLEIKRADAAPTVS 121
QY 575 IPPPSSEQLTSGGASVVCFLNNFPKDIINVKWIDGSRQNGVLNSWTDQDSKDYYSMS 634
Db 122 IPPPSSEQLTSGGASVVCFLNNFPKDIINVKWIDGSRQNGVLNSWTDQDSKDYYSMS 181
QY 635 STLTLTCKDEYERHNSYTCEATHKTSPIVKSFNR 669
Db 182 STLTLTCKDEYEWNSYTCEATHKTSPIVKSFNR 216

Search completed: February 15, 2006, 20:20:13
Job time : 60.2354 secs
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; Sequence 132, Application US/09254180C
; Patent No. 6777540
; GENERAL INFORMATION:
; APPLICANT: OKUMURA, Ko
; APPLICANT: EDA, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: USHIO, Yoshitaka
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or
; FILE OF INVENTION: Fragments Thereof, and Apoptosis-Induced Site From Fas Ligand
; FILE REFERENCE: 050006-0055
; CURRENT APPLICATION NUMBER: US/09/254,180C
; CURRENT FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: PCT/JP97/02983
; PRIOR FILING DATE: 1997-08-27
; PRIOR APPLICATION NUMBER: 271546/1996
; PRIOR FILING DATE: 1996-09-20
; PRIOR APPLICATION NUMBER: 231472/1996
; PRIOR FILING DATE: 1996-09-02
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 132
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Mouse
US-09-254-180C-132

Query Match      25.1%; Score 885.5; DB 2; Length 216;
Best Local Similarity 80.0%; Pred. No. 5.6e-54;
Matches 172; Conservative 14; Mismatches 24; Indels 5; Gaps 1;

QY 460 IVMTQPTSLVLSAGDRVTITCKASQSVSND-----VAVYQKPGQSPKLLISYTSRYA 514
Db 2 VLMTQPLSLPVLGDAQSISCKSSQSIHSSGNTYFEWYLPQPGSPKLLIYKVSNRFS 61
QY 515 GVPDRFSGSGYGTDFLTITSSVQAEAAVYFCQDYNSPPTFGGGTKLEIKRADAAPTVS 574
Db 62 GVPDRFSGSGGTDFLTIKISRVEAEDLGYYVYCFQGSHPPTFGSGTKLEIKRADAAPTVS 121
QY 575 IPPPSSEQLTSGGASVVCFLNNFPKDIINVKWIDGSRQNGVLNSWTDQDSKDYYSMS 634
Db 122 IPPPSSEQLTSGGASVVCFLNNFPKDIINVKWIDGSRQNGVLNSWTDQDSKDYYSMS 181
QY 635 STLTLTCKDEYERHNSYTCEATHKTSPIVKSFNR 669
Db 182 STLTLTCKDEYEWNSYTCEATHKTSPIVKSFNR 216

RESULT 75
US-09-254-180C-183
; Sequence 183, Application US/09254180C
; Patent No. 6777540
; GENERAL INFORMATION:
; APPLICANT: OKUMURA, Ko
; APPLICANT: EDA, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: USHIO, Yoshitaka
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or
; FILE OF INVENTION: Fragments Thereof, and Apoptosis-Induced Site From Fas Ligand
; FILE REFERENCE: 050006-0055
; CURRENT APPLICATION NUMBER: US/09/254,180C
; CURRENT FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: PCT/JP97/02983
; PRIOR FILING DATE: 1997-08-27
; PRIOR APPLICATION NUMBER: 271546/1996
; PRIOR FILING DATE: 1996-09-20
; PRIOR APPLICATION NUMBER: 231472/1996
; PRIOR FILING DATE: 1996-09-02
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn version 3.1
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101	903	25.6	233	2	US-08-882-431-4	Sequence 4, Appl1	174	832.5	23.6	468	6	US-11-004-639-12	Sequence 12, Appl1
102	901.5	25.6	219	4	US-10-683-815-10	Sequence 10, Appl1	175	832.5	23.6	624	5	US-10-723-003-30	Sequence 30, Appl1
103	900.5	25.6	462	4	US-10-281-479A-23	Sequence 23, Appl1	176	832.5	23.6	624	6	US-11-004-639-30	Sequence 30, Appl1
104	900.5	25.6	462	4	US-10-286-132A-23	Sequence 23, Appl1	177	832.5	23.6	639	5	US-10-723-003-32	Sequence 32, Appl1
105	900.5	25.6	464	4	US-10-275-180A-23	Sequence 23, Appl1	178	832.5	23.6	639	6	US-11-004-639-32	Sequence 32, Appl1
106	895	25.4	214	5	US-10-488-074-69	Sequence 69, Appl1	179	830	23.6	235	5	US-10-516-429-11	Sequence 11, Appl1
107	895	25.4	216	5	US-10-488-074-85	Sequence 85, Appl1	180	827.5	23.5	470	4	US-10-216-484-143	Sequence 143, Appl1
108	894	25.4	218	4	US-10-679-620-80	Sequence 80, Appl1	181	827.5	23.5	470	4	US-10-384-933-143	Sequence 143, Appl1
109	894	25.4	218	6	US-11-132-143-80	Sequence 80, Appl1	182	825.5	23.4	470	4	US-10-216-484-145	Sequence 145, Appl1
110	894	25.4	712	4	US-10-679-620-116	Sequence 116, Appl1	183	825.5	23.4	470	4	US-10-384-933-145	Sequence 145, Appl1
111	894	25.4	712	6	US-11-132-143-116	Sequence 116, Appl1	184	825	23.4	442	5	US-10-822-300-124	Sequence 124, Appl1
112	892.5	25.3	463	5	US-10-860-322-2	Sequence 2, Appl1	185	825	23.4	442	5	US-10-822-300-125	Sequence 125, Appl1
113	891	25.3	218	5	US-10-488-074-82	Sequence 82, Appl1	186	825	23.4	442	5	US-10-822-300-127	Sequence 127, Appl1
114	890.5	25.3	215	4	US-10-679-620-120	Sequence 120, Appl1	187	824.5	23.4	470	4	US-10-216-484-117	Sequence 117, Appl1
115	890.5	25.3	215	6	US-11-132-143-120	Sequence 120, Appl1	188	824.5	23.4	470	4	US-10-216-484-147	Sequence 147, Appl1
116	890.5	25.3	483	4	US-10-679-620-122	Sequence 122, Appl1	189	824.5	23.4	470	4	US-10-384-933-117	Sequence 117, Appl1
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118	890	25.3	214	5	US-10-488-074-72	Sequence 72, Appl1	191	824	23.4	442	5	US-10-822-300-128	Sequence 128, Appl1
119	889	25.2	467	5	US-10-500-696-2	Sequence 2, Appl1	192	822	23.3	442	5	US-10-822-300-126	Sequence 126, Appl1
120	888	25.2	214	5	US-10-488-074-70	Sequence 70, Appl1	193	821.5	23.3	222	5	US-10-937-048-13	Sequence 13, Appl1
121	885	25.1	363	4	US-10-291-265-335	Sequence 335, Appl1	194	821	23.3	367	4	US-10-291-265-899	Sequence 899, Appl1
122	884.5	25.1	451	4	US-10-679-620-78	Sequence 78, Appl1	195	818.5	23.2	468	5	US-10-981-738-13	Sequence 13, Appl1
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125	881	25.0	214	5	US-10-488-074-68	Sequence 68, Appl1	198	817.5	23.2	447	5	US-10-822-300-130	Sequence 130, Appl1
126	880	25.0	234	5	US-10-500-696-4	Sequence 4, Appl1	199	816.5	23.2	470	4	US-10-216-484-89	Sequence 89, Appl1
127	876	24.8	206	5	US-10-488-074-81	Sequence 81, Appl1	200	816.5	23.2	470	4	US-10-384-933-89	Sequence 89, Appl1
128	872	24.8	236	5	US-10-877-467A-8	Sequence 8, Appl1	201	816	23.2	446	5	US-10-822-300-136	Sequence 136, Appl1
129	872	24.8	236	5	US-10-877-467A-10	Sequence 10, Appl1	202	816	23.2	446	5	US-10-822-300-137	Sequence 137, Appl1
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131	872	24.8	453	3	US-09-301-593-18	Sequence 18, Appl1	204	815	23.1	446	5	US-10-822-300-140	Sequence 140, Appl1
132	872	24.8	453	4	US-10-159-006-18	Sequence 18, Appl1	205	814.5	23.1	447	5	US-10-822-300-131	Sequence 131, Appl1
133	870	24.7	234	3	US-09-770-916-4	Sequence 4, Appl1	206	814.5	23.1	447	5	US-10-822-300-133	Sequence 133, Appl1
134	870	24.7	234	3	US-10-496-059-4	Sequence 4, Appl1	207	813.5	23.1	447	5	US-10-822-300-134	Sequence 134, Appl1
135	868.5	24.7	215	4	US-10-683-815-5	Sequence 5, Appl1	208	813.5	23.1	575	4	US-10-737-208A-6	Sequence 6, Appl1
136	866.5	24.6	215	4	US-10-410-907A-34	Sequence 34, Appl1	209	813	23.1	446	5	US-10-822-300-132	Sequence 132, Appl1
137	863.5	24.5	472	3	US-09-301-593-30	Sequence 30, Appl1	210	812.5	23.1	447	5	US-10-822-300-138	Sequence 138, Appl1
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140	855.5	24.3	473	3	US-09-910-059-131	Sequence 131, Appl1	213	809.5	23.0	443	6	US-11-040-071-1	Sequence 1, Appl1
141	854.5	24.3	470	6	US-11-019-180A-4	Sequence 4, Appl1	214	809.5	23.0	449	4	US-10-318-397-22	Sequence 22, Appl1
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153	849	24.1	446	5	US-10-822-300-119	Sequence 119, Appl1	226	800	22.7	452	4	US-10-861-049-16	Sequence 16, Appl1
154	849	24.1	448	4	US-10-378-567-2	Sequence 2, Appl1	227	800	22.7	452	6	US-11-021-874-16	Sequence 16, Appl1
155	846	24.0	446	5	US-10-822-300-120	Sequence 120, Appl1	228	800	22.7	452	6	US-11-005-677-4	Sequence 4, Appl1
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158	845.5	24.0	470	6	US-11-004-639-40	Sequence 40, Appl1	231	800	22.7	471	5	US-10-922-651-4	Sequence 4, Appl1
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161	845.5	24.0	641	5	US-10-723-003-46	Sequence 46, Appl1	234	799.5	22.7	453	4	US-10-813-483-6	Sequence 6, Appl1
162	845.5	24.0	641	6	US-11-004-639-46	Sequence 46, Appl1	235	799.5	22.7	453	6	US-11-013-966-6	Sequence 6, Appl1
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267	793	22.5	467	4	US-10-428-894-30	Sequence 30, Appl
268	793	22.5	467	4	US-10-699-874-30	Sequence 30, Appl
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270	792	22.5	448	4	US-10-171-452A-60	Sequence 60, Appl
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273	792	22.5	448	4	US-10-731-984-16	Sequence 16, Appl
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275	792	22.5	461	3	US-09-249-011A-24	Sequence 24, Appl
276	792	22.5	467	4	US-10-171-452A-41	Sequence 41, Appl
277	792	22.5	467	4	US-10-171-452A-47	Sequence 47, Appl
278	792	22.5	467	4	US-10-171-452A-59	Sequence 59, Appl
279	792	22.5	467	4	US-10-353-708-41	Sequence 41, Appl
280	792	22.5	467	4	US-10-353-708-47	Sequence 47, Appl
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291	790	22.4	260	4	US-10-454-660-8	Sequence 8, Appl
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298	790	22.4	450	5	US-10-503-504-11	Sequence 11, Appl
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ALIGNMENTS

RESULT 1
US-09-900-766-1
; Sequence 1, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 672
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(672)
; OTHER INFORMATION: Conjugate protein
US-09-900-766-1

Query Match 100.0%; Score 3522; DB 3; Length 672;
Best Local Similarity 100.0%; Pred. No. 4.6e-152;
Matches 672; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 661 SPIVKSFNRNES 672
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RESULT 2
US-10-679-620-72
; Sequence 72, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reinl, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING

; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679,620
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 72
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pLSBC1740 , see Example 12
US-10-679-620-72

Query Match 52.0%; Score 1832.5; DB 4; Length 478;
Best Local Similarity 56.5%; Pred. No. 1.3e-75;
Matches 379; Conservative 32; Mismatches 65; Indels 195; Gaps 5;

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RESULT 3

US-11-132-143-72
; Sequence 72, Application US/1132143
; Publication No. US2005020797A1
; GENERAL INFORMATION:

; APPLICANT: Large Scale Biology
; APPLICANT: Reinal, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/11/132,143
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: US/10/679,620
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 72
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pLSBC1740 , see Example 12
US-11-132-143-72

Query Match 52.0%; Score 1832.5; DB 6; Length 478;
Best Local Similarity 56.5%; Pred. No. 1.3e-75;
Matches 379; Conservative 32; Mismatches 65; Indels 195; Gaps 5;

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Db 2 QVLOQSGDELKPGASLKLCTASGFNKTDTYIHWKQRPQGLEWIGRIYPTNGYTRY 61
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 NOKFKDKATLTVDKSTTAYMELSLTSDSAVYICARSTMTITNYVMDYWGQGTSTVSS 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 62 DPKFQDKATITADTSNTAYLQVSRLTSEDVAVYICSRWGGDGFYAMDYWGQASVTSS 121
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 AKTTPSPVYPLAPGSAQAQNSMVTLCGLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSD 180
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 122 AKTTPSVYPLAPGSAQAQNSMVTLCGLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSD 181
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 181 LYTSSSVTPSPSTWSPSETVTCNVAHPASSTKVDDKIIVPRDGGPSEKSENEKDLRKK 240
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 182 LYTSSSVTPSPSTWSPSETVTCNVAHPASSTKVDDKIIVPRDCGG-----GK 227
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 241 SELOQTALGNLQKIYYYNKAITTSSEKSDAQFLTNTLLFKGFFTGHPPWYNLDLLVGSTA 300
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 228 RIQDSA-----TDT-----VDLGAEL 244
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTBEKKVPINLWDGKQ 360
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 245 HRDDPPPTASDI-----GKRGKGGD----- 256
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 361 TTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDFGKQVQGLIVFHSSEGSTVS 420
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 257 -----GKRGKGGD----- 265
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 421 YDLFDAQGOYPTLLRIYRDNNTTISSTLSISLYLTTSIVMTQTPTSLVSAGDRVTIT 480
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 266 -----IVMTQSHKPMSTSVGDRVSIT 286
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 481 CKASQSVNDVAWYQOKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDTFTLTSSVQAE 540
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 287 CKASQDVNTAVAWYQOKPGHSPKLLIYSASFRYTGVPDRFTGNRSCTDFTFTLTSSVQAE 346
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 541 AAVYFCQDYNSPPTFGGQTKLEIKRADAAPTYSIFPPSSEQLTSGGASVVCFLNNFYPK 600
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 347 LAVYYCQHYHTTPTFGGQTKLEIKRADAAPTYSIFPPSSEQLTSGGASVVCFLNNFYPK 406
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 601 DINVKWKIDGSRQNGVLNSWTDQDSKSTYSMSSTLTITKDEYERHNSYTCETHKTST 660
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 407 DINVKWKIDGSRQNGVLNSWTDQDSKSTYSMSSTLTITKDEYERHNSYTCETHKTST 466
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 661 SPIVKSFRNE 671
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 467 SPIVKSFRNE 477
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

RESULT 4
US-10-679-620-90
; Sequence 90, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reinl, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679,620
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pLSBC1766, see Example 12
US-10-679-620-90

Query Match 52.0%; Score 1832.5; DB 4; Length 509;
Best Local Similarity 56.5%; Pred. No. 1.4e-75;
Matches 379; Conservative 32; Mismatches 65; Indels 195; Gaps 5;

QY	1	EVQLQSGDPLVKPGASVKISCKASGYSTFGYTHHWKSPGKGLWIGRIINPNNGVTL	60
DB	33	QVQLQSGPELVKPGASLKLSCTASGFNIDKTYIHVKQRPQGLEWIGRIYPTNGYTRY	92
QY	61	NQKFKDKATLTVDKSTTAYMELRSLTSDSAVYICARSTMITNYMDYWGQGTSTVTS	120
DB	93	DPKFQDKAITADTSNTAYLQVRLTSEDYAVYCSRWGGDGFYAMDYWGQASVTSS	152
QY	121	AKTTPPSVYPLAPGSAQAQNSMTVLGCLVKGYPEPVTVTWNSGSLSSGVHTTFAVLQSD	180
DB	153	AKTTPPSVYPLAPGSAQAQNSMTVLGCLVKGYPEPVTVTWNSGSLSSGVHTTFAVLQSD	212
QY	181	LYTLSSSVTPSPSTWSETVTCNVAHPASSTKVDKIVPRDSDGPGSEKSEINEKDLRKK	240
DB	213	LYTLSSSVTPSPSTWSETVTCNVAHPASSTKVDKIVPRDCGG-----GK	258
QY	241	SELQGTALGNLKIYYNNSKAITSEKSAQDQLTNTLLFKGFTGHPWYNDLLVDLGSTA	300
DB	259	RTIQDSA-----TDT-----VDLGAE	275
QY	301	ATSEYEGSSVDLYGAYGYQCAGTGNKTAQMGVTLHDNNRLTEKKVPIINLWIDGKQ	360
DB	276	HRDDPPPTASDI-----GKRGKRGD-----	287
QY	361	TTVPIDKVKTSKEVTQVQELDLQARHLYHCKFGLYNSDSPGKQVQRLIVPHSSEGSTVS	420
DB	288	-----GKRGKRGD-----	296
QY	421	YDLFDAQGVYPTDILLRIYRDNTTISSTLSLSLYLTTSIVMTQPTPTSLLSVAGDRVTIT	480
DB	297	-----IVMTQSHKFMSTSGVDRVSIT	317
QY	481	CKASQSVNDVAVYQKPGSPKLLISYTSRYAGVPDRFSGSGYGTDFTLTISVQAE	540
DB	318	CKASQDVNTAVAVYQKPGSPKLLISYTSRYAGVPDRFSGSGYGTDFTLTISVQAE	377
QY	541	AAVYFCQDYNSPPTFGGKLEIKRADAAPTVSIIPPSSEQLTSGGASVVCFLNFPYK	600
DB	378	LAVYICQHYTTPPTFGGKLEIKRADAAPTVSIIPPSSEQLTSGGASVVCFLNFPYK	437
QY	601	DINVKWKIDGSRQGVNSWTQDSDKSYSSSLTLTKDEYRHNSYTCEATHKTS	660
DB	438	DINVKWKIDGSRQGVNSWTQDSDKSYSSSLTLTKDEYRHNSYTCEATHKTS	497

QY 661 SPIVKSFRNE 671
|||||
DB 498 SPIVKSFRNE 508
|||||

RESULT 5
US-11-132-143-90
; Sequence 90, Application US/11132143
; Publication No. US2005020797A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reinl, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/11/132,143
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: US/10/679,620
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pLSBC1766, see Example 12
US-11-132-143-90

Query Match 52.0%; Score 1832.5; DB 6; Length 509;
Best Local Similarity 56.5%; Pred. No. 1.4e-75;
Matches 379; Conservative 32; Mismatches 65; Indels 195; Gaps 5;

QY	1	EVQLQSGDPLVKPGASVKISCKASGYSTFGYTHHWKSPGKGLWIGRIINPNNGVTL	60
DB	33	QVQLQSGPELVKPGASLKLSCTASGFNIDKTYIHVKQRPQGLEWIGRIYPTNGYTRY	92
QY	61	NQKFKDKATLTVDKSTTAYMELRSLTSDSAVYICARSTMITNYMDYWGQGTSTVTS	120
DB	93	DPKFQDKAITADTSNTAYLQVRLTSEDYAVYCSRWGGDGFYAMDYWGQASVTSS	152
QY	121	AKTTPPSVYPLAPGSAQAQNSMTVLGCLVKGYPEPVTVTWNSGSLSSGVHTTFAVLQSD	180
DB	153	AKTTPPSVYPLAPGSAQAQNSMTVLGCLVKGYPEPVTVTWNSGSLSSGVHTTFAVLQSD	212
QY	181	LYTLSSSVTPSPSTWSETVTCNVAHPASSTKVDKIVPRDSDGPGSEKSEINEKDLRKK	240
DB	213	LYTLSSSVTPSPSTWSETVTCNVAHPASSTKVDKIVPRDCGG-----GK	258
QY	241	SELQGTALGNLKIYYNNSKAITSEKSAQDQLTNTLLFKGFTGHPWYNDLLVDLGSTA	300
DB	259	RTIQDSA-----TDT-----VDLGAE	275
QY	301	ATSEYEGSSVDLYGAYGYQCAGTGNKTAQMGVTLHDNNRLTEKKVPIINLWIDGKQ	360
DB	276	HRDDPPPTASDI-----GKRGKRGD-----	287
QY	361	TTVPIDKVKTSKEVTQVQELDLQARHLYHCKFGLYNSDSPGKQVQRLIVPHSSEGSTVS	420
DB	288	-----GKRGKRGD-----	296
QY	421	YDLFDAQGVYPTDILLRIYRDNTTISSTLSLSLYLTTSIVMTQPTPTSLLSVAGDRVTIT	480
DB	297	-----IVMTQSHKFMSTSGVDRVSIT	317
QY	481	CKASQSVNDVAVYQKPGSPKLLISYTSRYAGVPDRFSGSGYGTDFTLTISVQAE	540
DB	318	CKASQDVNTAVAVYQKPGSPKLLISYTSRYAGVPDRFSGSGYGTDFTLTISVQAE	377
QY	541	AAVYFCQDYNSPPTFGGKLEIKRADAAPTVSIIPPSSEQLTSGGASVVCFLNFPYK	600

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Db 378 LAVVYCOQHYTTPPTFGGKLEIKRADAAPTIVSIFPPSEQLTSGASVVCFLNNFYPK 437
QY 601 DINVKWIDGSRQNGVLNSWTDQDSDSTYSMSSTLTITKDEYERHNSYTCEATHKTST 660
Db 438 DINVKWIDGSRQNGVLNSWTDQDSDSTYSMSSTLTITKDEYERHNSYTCEATHKTST 497
QY 661 SPIVKSFNENE 671
Db 498 SPIVKSFNENE 508

RESULT 6
US-10-679-620-86
; Sequence 86, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reinel, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679,620
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 86
; LENGTH: 552
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pLSBCL736, see Example 15
US-10-679-620-86

Query Match 46.9%; Score 1653; DB 4; Length 552;
Best Local Similarity 51.5%; Pred. No. 2.1e-67;
Matches 351; Conservative 40; Mismatches 85; Indels 206; Gaps 7;

QY 1 EVLOQSGDPLVKPGASVKISKASGYSTGYMHVWKSPKGLIEWIGRINPNNGVTLY 60
Db 65 EVDLVESGDLVKPGGSLKLSCAASGTFPSHYGMSWVRQTPDKRLEWVATIGSRGTTHY 124
QY 61 NQKFKDKATLTVDKSTTAYMELRSITSDSAVYYCARSTMITNY-----VMDYWGOG 113
Db 125 PDSVGRFTISRDNKNALYLQNNLSKSEDTAMYCYARRSEFYFNGNTYYGAMDYWGOG 184
QY 114 TSVTVSSAKTTTPSVYPLAPGSAQAQNSMVTGLCLVKGYFPEPVTVTVNSGSLSSGVHTF 173
Db 185 ASVTSSAKTTTPSVYPLAPGSAQAQNSMVTGLCLVKGYFPEPVTVTVNSGSLSSGVHTF 244
QY 174 PAVLQSDLYTLSSSVTPSPSTWPFSETVTCNVAHPASSTKVDKKIIPRDSGGPSEKSEIN 233
Db 245 PAVLQSDLYTLSSSVTPSPSTWPFSETVTCNVAHPASSTKVDKKIIPRDCGG----- 295
QY 234 EKDLRKSELOQTALGNLKQIYYNSKAITSEKSDAQFLTNTLLPKGFTGHPWYNDLL 293
Db 296 -----GKRTIQDSA-----TDT----- 307
QY 294 VDLGSAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGVTLHDNNRLTEKKVPIN 353
Db 308 VDLGAELHRDDPPPTASDI----- 326
QY 354 LMIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKVQGLIVFHS 413
Db 327 -----GKRGKRGD----- 335
QY 414 SEGSTVSYDLFDAQQGYPTLLRIYRDNTTISTSLISLYLTYTSIYMTQPTSLLYSA 473
Db 336 -----IVLTQSPASLAIVSL 349
QY 474 GDRVTITCKASQSVN-----DVAWYQKPKGPKLLISYTSRYAGVDPDRFSGSGYGTDF 529
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |
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Db 350 GQRATISCRASESDVNYGFSFMNWFQKPGQPPKLLIYVAINRSGVGPAPRFGSGSGCTDF 409
QY 530 TLTISVQAEADAAYVFCQDDYNSPPTFGGTTKLEIKRADAAPTIVSIFPPSSSQTLSGGAS 569
Db 410 SLNIHPVEEDDPAMYFCQQTKEVPWTFGGGTTKLEIKRADAAPTIVSIFPPSSSQTLSGGAS 469
QY 590 VVCFLNFPYKDIINVKWIDGSRQNGVLNSWTDQDSDSTYSMSSTLTITKDEYERHNS 649
Db 470 VVCFLNFPYKDIINVKWIDGSRQNGVLNSWTDQDSDSTYSMSSTLTITKDEYERHNS 529
QY 650 YTCEATHKTSTSPIVKSFNENE 671
Db 530 YTCEATHKTSTSPIVKSFNENE 551

RESULT 7
US-11-132-143-86
; Sequence 86, Application US/11132143
; Publication No. US2005020797A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reinel, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/11/132,143
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: US/10/679,620
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 86
; LENGTH: 552
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pLSBCL736, see Example 15
US-11-132-143-86

Query Match 46.9%; Score 1653; DB 6; Length 552;
Best Local Similarity 51.5%; Pred. No. 2.1e-67;
Matches 351; Conservative 40; Mismatches 85; Indels 206; Gaps 7;

QY 1 EVLOQSGDPLVKPGASVKISKASGYSTGYMHVWKSPKGLIEWIGRINPNNGVTLY 60
Db 65 EVDLVESGDLVKPGGSLKLSCAASGTFPSHYGMSWVRQTPDKRLEWVATIGSRGTTHY 124
QY 61 NQKFKDKATLTVDKSTTAYMELRSITSDSAVYYCARSTMITNY-----VMDYWGOG 113
Db 125 PDSVGRFTISRDNKNALYLQNNLSKSEDTAMYCYARRSEFYFNGNTYYGAMDYWGOG 184
QY 114 TSVTVSSAKTTTPSVYPLAPGSAQAQNSMVTGLCLVKGYFPEPVTVTVNSGSLSSGVHTF 173
Db 185 ASVTSSAKTTTPSVYPLAPGSAQAQNSMVTGLCLVKGYFPEPVTVTVNSGSLSSGVHTF 244
QY 174 PAVLQSDLYTLSSSVTPSPSTWPFSETVTCNVAHPASSTKVDKKIIPRDSGGPSEKSEIN 233
Db 245 PAVLQSDLYTLSSSVTPSPSTWPFSETVTCNVAHPASSTKVDKKIIPRDCGG----- 295
QY 234 EKDLRKSELOQTALGNLKQIYYNSKAITSEKSDAQFLTNTLLPKGFTGHPWYNDLL 293
Db 296 -----GKRTIQDSA-----TDT----- 307
QY 294 VDLGSAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGVTLHDNNRLTEKKVPIN 353
Db 308 VDLGAELHRDDPPPTASDI----- 326
QY 354 LMIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKVQGLIVFHS 413
Db 327 -----GKRGKRGD----- 335
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QY 414 SEGSTVSYDLFDAQGGYPTLLRIYRDNTTISSTLSISLYLVTGIVMTQPTTSLLSVA 473
Db 336 -----IVLTQSPASLAVSL 349
QY 474 GORVTITCKASQSVN---DVAWYQKQKQSPKLLISYTSRYAGVPDRFSGSGYGTDF 529
Db 350 GQRATISCRASESDVNYGFSFMWFQKQKQPPKLLIYALISNRGSGVPAKFSGSGGTDF 409
QY 530 TTITSSVQAEADAAYVFCQDDYNSPPTFGGCTKLEIKRADAAPTVSIFPPSSSEQLTSGGAS 589
Db 410 SLNIHVEEDDPAMYFCQKQETVPWFPGGCTKLEIKRADAAPTVSIFPPSSSEQLTSGGAS 469
QY 590 VVCFLLNFPKQINVKWKIDGSRQNGVLSWTDQDQSKDSTYSMSSTLTITKDEYERHNS 649
Db 470 VVCFLLNFPKQINVKWKIDGSRQNGVLSWTDQDQSKDSTYSMSSTLTITKDEYERHNS 529
QY 650 YTCEATHKTSTSPIVKSEFNE 671
Db 530 YTCEATHKTSTSPIVKSEFNRNE 551
RESULT 8
US-11-084-080-16
; Sequence 16, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDORRN, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSCH, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084, 080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 750
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-845
US-11-084-080-16
Query Match 38.3%; Score 1350; DB 6; Length 750;
Best Local Similarity 41.8%; Pred. No. 1.5e-53;
Matches 321; Conservative 101; Mismatches 208; Indels 138; Gaps 19;
QY 1 EVOLQSGDPLVKPGASVKISCKASGYFTGYVHHWVKQSPGKLEWIGRINPNNGVTLY 60
Db 23 EVOLVSGDGLVPGGSRVRSICASGYFTFYGNWVKKVQPGKLEWIGWINTYTGESTY 82
QY 61 NQKFKDKATLTVDKSSTTAYMELRSLTSEDSAVYICARSTMITNYVMDYWGQGTSTVTS 120
Db 83 ADSFKGRFTSLQTSASAAYLQINSRAEDTAVYICARFAT----KGDYWGQGTLLTVSS 138
QY 121 AKTTPPSVPLAPGSAATNSMTLGLVKGYPPEPVTVTWNSGSLSSGVHTTFAVLQSD 180
Db 139 ASTKGFSPVPLAPSSKTSGGTAAALCLVNDKVPPEPVTVSWNSGALTSGVHTTFAVLQSS 198
QY 181 -LYTLSSSVTPRSTWPFSTVTCNVAPASSTKVDKIVPRDGGGPFSEKSEINEKDLRK 239
Db 199 GLYSLSVSVTPSSSLGTQYICNVNPKSPNTKVDKVEPKSC-----TRHQPRG 249

QY 240 KSELOGTALGNKQIYYNYSKAITSEKSAQDQFLNTLLFKPGFTGHPWVND---LLVDL 296
Db 250 WEQLYNTVSNFNLGEAYEP---TFIQLRLNLAGKGTVCQLPVTLTQTADKRFVLVDI 305
QY 297 GSTAATSEVEGSSVDLYGAY-YGYQCAGCTPNK-----TACMYGGVTLHDNNRL 344
Db 306 --TTTSKKTVKVVAIDVTDVVVGQDKWQKORAVFLDKVPTVATSKLPFGVT---NRV 359
QY 345 TBEKKVPINLWIDGK-QTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGK 403
Db 360 T-----LTFDGSYQKLVAAKADRKALELGVNKLFPST-EAIGHK-----TINGQ 403
QY 404 -----VQRGLIVFHSSEGSTVSYDLFDAQGGYPTLLRI 437
Db 404 EAAKFFLIQVIMVSEAAEFKYEIVEDRGL--YGSFKPNFKVLNLENMNGDISDAIHKS 461
QY 438 YRDNTTISSTLSIS-----LYLYTTS----- 459
Db 462 SPQCTTINPALQLISPSNDPFWVNVKVSQISPDGMILKFKSSKMKYLLPTAAAGLLLLAAQ 521
QY 460 -----IVMTQTPTSLIVSAGDRVITITCKASQSV--SNDVA---WYQKPGQSPK 503
Db 522 PAMAHHHHHHDIQMTQSPSSLSASVQDRVTITCRSTKSLHNSNGITYLYWYQKPGKAPK 581
QY 504 LLISYTSRYAGVDPDRFSGSGYGTDFTLTISSVQAEADAAYVFCQDDYNSPPTFGGCTKLE 563
Db 582 LLTYQMSNLASGVPRFSSSGSGTDFTLTISSLPEDFATYCAQNLPTPTFCQGTKE 641
QY 564 IKRADAAPTVSIFPPSSSEQLTSGGASVWCFLLNFPKQINVKWKIDGSRQNGVLSWTD 623
Db 642 LKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRKAVQWKVQNALQSGNSQESVTE 701
QY 624 QDSKDYSTYSMSSTLTITKDEYERHNSYTCETHKTSTSPIVKSPNRNE 671
Db 702 QDSKDYSTYSMSSTLTITKADYKHKYVACEVTHQGLSSPVTKSFNRGE 749
RESULT 9
US-11-084-080-24
; Sequence 24, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDORRN, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSCH, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084, 080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 750
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-845-NVL-de-bouganin
US-11-084-080-24
Query Match 38.0%; Score 1339; DB 6; Length 750;
Best Local Similarity 41.6%; Pred. No. 4.9e-53;
Matches 320; Conservative 101; Mismatches 202; Indels 146; Gaps 20;

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QY 1 EVOLQSGDPLVKPGASVKISKASGYSTGYVMHWKSPGKGLWIGRIINPNNGVTLY 60
Db 29 EVOLVSGGELVQPGSGVRISCAASGTYFTNYGMNWKQAPGKGLWGMWINTYTGESTY 88
QY 61 NQKFKDKATLTVDKSTTAYMELRSLTSEDSAVYYCARSTMTITNYVMDYWGQGTSTVTS 120
Db 89 ADSFKGRFTFSLDTSASAAYLQINSLRAEDTAVYYCARFAI-----KGDIWGQGTLLTVSS 144
QY 121 AKTTPSVVPLAPGSAQAQNSMTVLCGLVKGYPPPEPTVTVWNSGSLSSGVHTTTPAVLQSD 180
Db 145 ASTKGSVPFLAPSSKSTSGTAAALGCLVKDYPPPEPTVTVWNSGALTSVHTTTPAVLQSS 204
QY 181 -LYTLSSVTVPSSTWPESTVTCNVAHPASSTKVDKKIIPRDSGGSEKSEINEKDLAK 239
Db 205 GLYSLSVVTVPSLSLGTQYICNVNHKPSNTKVDKKVEPKSC-----M 248
QY 240 KSLQGTALG-----NLKQIYYNSKAITSEKSEKADQFLTWTLFLKGF 282
Db 249 KYLLPTAAAGLLLAQAQAMAYNTVSPNLGEAYEP-----TFIQDLRNLAKGTPVCQLP 304
QY 283 FTGHPWYND---LLVDLGSTAAATSEYEGSSVDLYGAY-YGYCAGAGTTPNK-----328
Db 305 VTLQTTIADDKRFVLVDI---TTTSKTKVKAIDVTDVVVGQYQDKWDGKORAVFLDKVPTV 362
QY 329 -TACMYGGVTLHDNNRLTEBKKVPINLWIDGK-QTTVPIDKVKTSKKEVTVOELDLQARH 386
Db 363 ATSKLPPGVT---NRVT-----LTFDGSYQKLVAAMAKADRKALEGVNKLFSI-E 409
QY 387 YLHGKFGLYNSDSFGGK-----VQRGLIVFHSSEGSTVS 420
Db 410 AIHGK-----TINGQEAAKFLLIVIQWSEAAARFKYIETEVVDRLG--YGSFKENFKV 460
QY 421 YDLFDAGQVDPDLLRIYRDNNTI-----SSTLSLSLYLYTTS--459
Db 461 LNLNNWGDIDSAIHKSPPQCTTINPALQLISPNBPWVNVKVSQISPDWGIKLFKSKT 520
QY 460 -----LVMTQTPTSLVASAGDRVTITCKASQSV--SNDVA---WYQCKPFGQSP 502
Db 521 RHQPRGWQLDIQMTQSPSSLSASVGDRTVTICRSTKSLHNSGITYLYWYQCKPFGKAP 580
QY 503 KLLIYSYTRYAGVPRDFSGSGYGTDFTLTITSSVQAEADAAYVFCQDYNSPPTFGGQTKL 562
Db 581 KLLIYQMSNLASGVPSRFSSSGSGTDFTLTITSLQPEDFATYYCAQNLEIPRTFGQTKV 640
QY 563 EIKRAADAAPTYSIFPPSSSQLTSGGASVVCFLNFPKQINVKWKIDGSRQNGVNSWT 622
Db 641 ELKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQMWKDVALQSGNSQESVT 700
QY 623 DQSKDSTYSMSSTLTLTDEYERHNSYTCEATHKSTSTSPIVKSFNRNE 671
Db 701 EQSKDSTYSLSSTLTLSKADYEKKHYACEVTHQGLSPVTKSFNRGE 749
```

RESULT 10

```
US-10-900-928-3
; Sequence 3, Application US/10900928
; Publication No. US2005006952A1
; GENERAL INFORMATION:
; APPLICANT: Bleck, Gregory T.
; APPLICANT: Bleck, Donna
; APPLICANT: Collins, Ian
; TITLE OF INVENTION: Fusion Antibodies
; FILE REFERENCE: GALA-09135
; CURRENT APPLICATION NUMBER: US/10/900, 928
; CURRENT FILING DATE: 2004-07-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
```

US-10-900-928-3

```
Query Match 37.5%; Score 1321.5; DB 5; Length 669;
Best Local Similarity 40.8%; Pred. No. 2.7e-52;
Matches 303; Conservative 94; Mismatches 199; Indels 147; Gaps 17;
```

```
QY 1 EVOLQSGDPLVKPGASVKISKASGYSTGYVMHWKSPGKGLWIGRIINPNNGVTLY 60
Db 1 EVOLVSGGCVQPGRLSLRSLSCASGDFTTIYMSWVRQAPGKGLWIGIHEIHDSDSTINY 60
QY 61 NQKFKDKATLTVDKSTTAYMELRSLTSEDSAVYYCARSTMTITNYVMDYWGQGTSTVTS 120
Db 61 AFSLKDRFTISRDNAKNTLFLQWDSLRLPEDTGVYFCA-SLYFGFPMFAYWGQGTPTVTS 119
QY 121 AKTTPSVVPLAPGSAQAQNSMTVLCGLVKGYPPPEPTVTVWNSGSLSSGVHTTTPAVLQSD 180
Db 120 ASTKGSVPFLAPSSKSTSGTAAALGCLVKDYPPPEPTVTVWNSGALTSVHTTTPAVLQSS 179
QY 181 -LYTLSSVTVPSSTWPESTVTCNVAHPASSTKVDKKIIPRDS-----GG 224
Db 180 GLYSLSVVTVPSLSLGTQYICNVNHKPSNTKVDKREVEPKSCDKTHTCPCPAPELGG 239
QY 225 PSEKSEINEKD---LRKSELGQTALGNLKOIYYNSKAITSEKSAQDLNTLLFKG 281
Db 240 PSVFLFPPKPKDTLMISRTPEVTCVVVD-----VSHEDPEVKF-----277
QY 282 FTGHPWYND-LLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGGTPTNKTACMYGGVTLHD 340
Db 278 -----NWYVDGVEVHNNAKTKPREEQNSTYRVVSVL-----TVLHQ 313
QY 341 NNRLTEBKKVPINLWIDGKQ-----TTVPIDK-----VKTSKKEV 375
Db 314 D-----WLNKGEYKCKVSNKALPAPIEKTISKAKQPREPQVYVTLPPSREEM 360
QY 376 TVQELDQARHYLHGKFGLYNSDSPGCKVQRGILIVFHSSEGS-----TVSYDILFDAGQY 430
Db 361 TKNQVSLTCL-----VKGFPYSD-----IAVEWESNGQPPENNYKTPPVLDSDGSF 406
QY 431 -----PDTLLRIYRDNNTITSTLSLSLYLYTT--SIWMTQTPTS 468
Db 407 FLYSKLTVDKSRWQGNVFCVSMHEALNNHYTKLSLSLSPGLFHATQADIQLTOSPS 466
QY 469 LLVSAGDRVTITCKASQSVNDVAMVYQKPGQSPKLLISYTSRYAGVPRDFSGSGYGT 528
Db 467 LNASVGDRTITCKASQSDYGTSVAMVYQKPGKAPKLLIYTSIRHTGVSPRFSGSGSGTD 526
QY 529 FTLTISVQAEADAAYVFCQDYNSPPTFGGQTKLEIKRAADAAPTYSIFPPSSQLTSGGA 588
Db 527 FTFITSLQPEDIATYYCQ-YSLYRSFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTA 585
QY 589 SVVCFLNFPKQDINVKWKIDGSRQNGVLSNWTQDSDKSDSTYSMSSTLTLTDEYERHN 648
Db 586 SVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKKH 645
QY 649 SYTCEATHKSTSTSPIVKSFNRNE 671
Db 646 VIACEVTHQGLSPVTKSFNRGE 668
```

RESULT 11

```
US-11-084-080-26
; Sequence 26, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDORF, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTHWISTLE, Joycelyn
; APPLICANT: BOSCH, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
```

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; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26
; LENGTH: 751
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-845-gelonin
US-11-084-080-26

Query Match      37.4%; Score 1317.5; DB 6; Length 751;
Best Local Similarity 41.6%; Pred. No. 4.6e-52;
Matches 320; Conservative 101; Mismatches 208; Indels 141; Gaps 26;

QY 1 EVLOQSGDPLVKPGASVKISCKASGYSTGYVMHWKQSPGKLEWIGINPNNGVTLY 60
DB 23 EVOLVSGGLVQPGSGSVIRISCAASGYTFNYGMWVKQAPGKLEWGMWINTYTGESTY 82
QY 61 NQKFKDKATLTVDKSSTTAYMELRSLTSDSAVYCARSTMITNYVMYDYGQGSTVTSS 120
DB 83 ADSFKGRFPTSLDTSASAAVLQINSRAEDTAVYYCARFAI----KGDYWGQGTILTVSS 138
QY 121 AKTTPSVVPLAPGSAQAQNSMTYTLGCLVKGYFPEPVTVTWNSGSLSSGVTHTPPAVLQSD 180
DB 139 ASTKGPVPLAPSSKSTSGCTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 198
QY 181 -LYTLSSSVTPSPSTWPESETVCNVAHPASSTKVDKIKVPR-----DSG 223
DB 259 SFSTKATITYYVFNLE--LRVKLKPEG-----NSHGIPLLRKKDD----- 299
QY 277 LFLKGFPTGHPWYNDLLDLGSLTAATSEYEGSSVDLYGAY-YGYQCAG-----GTPN-- 327
DB 300 -----PGKCFVLVALSND--NGQLAEIAIDVTSVYVVGQYVRNRSYFPFKADPAA 347
QY 328 -----KTACMYGG--VTLHDNRLTEKKV---PINLWIDGKOTVPIDKVK---- 369
DB 348 YEGLFKNTIKTRLHFGSGYSPSLEGEKAYRETTDLGIEPLRIGIK-KLDENAIIDNYKPTI 406
QY 370 TSKEVTVQELDLQARH-VLHGKFGLYNSDSFGKQVQ--RGLIVFHSSEGSTVSYDL--F 424
DB 407 ASLLVVIQWVSEAAFTFIENQI-----RNNFOORIRPTNNTISLENKWK-LSFQIRTS 461
QY 425 DAQGVDPDILLRIYRN-----TTISSTLSLSL-----LYLYTS----- 459
DB 462 GANGMFSEA-VELERANGKYYVYTAVDQVKPKIALLKFDVKDKPKMYLLPTAAAGLLLLA 520
QY 460 -----IVMTQPTSLLSAGDRVTTICKASQSV--SNDVA---WYQKPGQS 501
DB 521 AQPAMAHHHHHDIQMTQSPSSLSASVGDRTVITCRSTSLKLSNGITLYLYWYQKPGKA 580
QY 502 PKLLISYTSRYAGVDRSGSGYGTDFLTLLISSVQAEADAAYFCQODYNSPPTFGGGTK 561
DB 581 PKLLIYQMNLAGSVPRSSSGSGDTFTLTISLQPEDPATYCAQNLEIPTFQGTYK 640
QY 562 LEIKRAADAAPTWSIFPPSSEQLTSGGASVVCFLNNFPYKDIKVKIDGSEKQNGVLSW 621
DB 641 VELKRTVAAPSVEIFPPESDQLKSGTASVVCLLNNFYPREAKYQWKVDNALQSGNSQESV 700
QY 622 TDQDSKDSYMSSTLTILKDEYERINSYTCETHTKTSTSPIVKSFNRE 671
DB 701 TEQDSKDSYLSSTLTLSKADYEKKVYACVETHQGLSPVTKSFNRGE 750
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RESULT 12
US-11-084-080-28
; Sequence 28, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDORN, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSCH, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-011
US-11-084-080-28

Query Match      37.2%; Score 1308.5; DB 6; Length 759;
Best Local Similarity 40.3%; Pred. No. 1.2e-51;
Matches 312; Conservative 109; Mismatches 212; Indels 141; Gaps 20;

QY 1 EVLOQSGDPLVKPGASVKISCKASGYSTGYVMHWKQSPGKLEWIGINPNNGVTLY 60
DB 23 QVQLVESGGVQVPGSRSLRSCAASGFFPRSPAMHWVRQALGKLEWVAIVSDGSTKY 82
QY 61 NQKFKDKATLTVDKSSTTAYMELRSLTSDSAVYCARSTMITN-----YVMYWGQGST 115
DB 83 ADSVKGRFTISRDTSKNTVLYKMSLRTEDTAVYYCARDQSLLDYDHYGLDVMWKGTT 142
QY 116 VIVSSAKTTPPSVYPLAPGSAQAQNSMTYTLGCLVKGYFPEPVTVTWNSGSLSSGVTHTFA 175
DB 143 VIVSSASTKGPSPVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 202
QY 176 VLQSD-LYTLSSSVTPSPSTWPESETVCNVAHPASSTKVDKIKVPRDSGGPSEKSEBINE 234
DB 203 VLOSSGLYSLSSVTVVPSSSLGTQTYICNVNHKPSNTKVDKVKPEKSC-----TRH 253
QY 235 KDLRKKELOGTALGNLKOIYYNNSKAITSSSEKSAQOFLTNTLLFKGFTFGHPWYND--- 291
DB 254 RQPRGWEQLYNTVSNFLGEAYEYP---TFIQDLRNLAKGTVPVCQLPVTLTQIADDKRF 309
QY 292 LLVDLGSTTAATSEYEGSSVDLYGAY-YGYQCAGGTPNK-----TACMYGGVTLH 339
DB 310 VLVDI--TTTSKTKTVKVAIDVTDVYVVGQDKWDGKDRAVFLDKVPTVATSKLPPGVT-- 365
QY 340 DNNRLTEKKVPINLWIDGK-OTTPIDIKVTKSKETVQOELDLQARHYLHGKFGLYNSD 398
DB 366 --NRVT-----LTFDGSYQKLNVAAKADRAKALELVNKLFEFSI-EAHGK----- 407
QY 399 SFEGK-----VORGLIVFHSSEGSTVSYDLFDAQGYPD 432
DB 408 TINGQEAAKFFLIVIQWSEAAARFKYIETEVDRGL--YGSFKPKFVNLNLENNWGDID 465
QY 433 TLLRIYRDNVTTISSTLSLS-----LYLYTS----- 459
DB 466 AIHKSPQCTTINPALQLISPSNDPWWNVKVSQISPDMGILKPKSKMKYLLPTAAAGLL 525
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QY 460 -----IVMTQPTSLLSAGDRVTITCKASQSVND-VAVYQOKPGQSP 502
Db 526 LLAAQAPAMAHHHHDIVLTQSPGTLTSLSPGERATLSCRASQSVSSYLAWYQKPGQAP 585
QY 503 KLLISVTSRYAGVPRFGSGSGTGDTTLTISVQAEADAAYFCQDYNSSP-----TFG 557
Db 586 RLLIYGASTRATGMPRFGSGSGTGDTTLTISRLEPEDFAVYVCOQ-YGSSQTPTQITFG 644
QY 558 GGTGLBIKRAADAPTYSIIPPSSEQLTSGASVVCFLNNFYPKDINVWKIDGSRQNGV 617
Db 645 GGTKEIKRTVAAPSVFIIPPSDEQLKSGTASVVCFLNNFYPREAKVQWKVDNALQSGNS 704
QY 618 LNSWTDQSDKSTYSMSSLTTLTKDYERHNSVTCETHSTSPIVKSFNRNE 671
Db 705 QESVTEQSDKSTYSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGE 758

RESULT 13
US-11-084-080-18
; Sequence 18, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: HELLENDORN, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSC, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; PRIOR FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2004-03-19
; PRIOR FILING DATE: 2004-03-19
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB5-845
US-11-084-080-18

Query Match 35.8%; Score 1260; DB 6; Length 488;
Best Local Similarity 40.6%; Pred. No. 1.2e-49;
Matches 275; Conservative 66; Mismatches 118; Indels 218; Gaps 8;

QY 1 EVOLQSGDPLVKPGASVKISCKASGYFTGYMHVVKQSPGKLEWIGRINPNNGVTLY 60
Db 23 EVOLVSGGELVQPGGSRVISAASGYTFTNGMNMVVKQAPGKLEWGMWINTYTGESTY 82
QY 61 NOKFKDKATLTVDKSSTTAYMELRSLTSDSAVYYCARSTMTITNYMDYWGQSTVTVSS 120
Db 83 ADSFKGRFTFSLDTSASAAYLQINSRAEDTAVYYCARFAI-----KGDYWGQGTLLTVSS 138
QY 121 AKTTPSPVPLAPGSAQNSMVTGLCLVKGYDPEVPTVWNSGSLSSGVHPTFPVAVLQSD 180
Db 139 ASTKGSVPFLAPSSKSTSGTAAALGCLVKDYDPEVPTVWNSGALTSGVHTFPVAVLQSS 198
QY 181 -LYTLSSVTVPSSTWPESTVTCNVAHPASSTVDKKIIVPRDGGPGSEKSEINEKDLRK 239
Db 199 GLYSLSSVTVPSSSLGTYIICNVNPKSNTKVDKKVEP----- 238
QY 240 KSELOGTALGNLKIYYNASKAITSSSEKSAQFLTNTLLFKGPFTHGHPWYNLLLDLGS 299
Db 239 -----KSCMKYLLPT----- 248

QY 300 AATSEVEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLTEKKVPINLWIDGK 359
Db 249 -----AAAGLLLLAAQP----- 260
QY 360 QTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGILIVFHSSEGSTV 419
Db 261 -----AMAHHHH----- 268
QY 420 SYDLFDAQOQYPTDLLRIYRDNTTISSTLSLSLYLYTTSIVMTQPTSLLSVAGDRVTI 479
Db 269 -----HDIQMTQSPSSLSASVGRVTI 290
QY 480 TCKASQSV--SNDVA---WYQKPGSPKLLISYTSRVRAGVDPDRFSGSGGYGDTFTLTIS 534
Db 291 TCRSTKSLHNSGITVLYWYQKPGKAPKLLIYQMSNLASGVPSRFSGSGGDTFTLTIS 350
QY 535 SVQAEDAAYVFCQDYNSSPPTFGGGTGLKLEIKRAADAAPTYSIIPPSSEQLTSGGASVVCFL 594
Db 351 SLQPEDFATYCYCAQNLEIPRTFGQTKVELKRTVAAPSVFIIPPSDEQLKSGTASVVCLL 410
QY 595 NNFPYKIDINVWKIDGSRQNGVLNSWTDQSDKSTYSMSSLTTLTKDYERHNSVTCFA 654
Db 411 NNFPYPREAKVQWKVDNALQSGNSQESVTEQSDKSTYSLSSTLTLSKADYERKHVYACEV 470
QY 655 THKTSTSPIVKSFNRNE 671
Db 471 THQGLSSPVTKSFNRGE 487

RESULT 14
US-11-084-080-22
; Sequence 22, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDORN, Koen
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSC, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGANIN PROTEINS, CYTOTOXINS AND METHODS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2004-03-19
; PRIOR FILING DATE: 2004-03-19
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 750
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-845-NVH-de-bouganin
US-11-084-080-22

Query Match 35.8%; Score 1260; DB 6; Length 750;
Best Local Similarity 40.6%; Pred. No. 1.9e-49;
Matches 275; Conservative 66; Mismatches 118; Indels 218; Gaps 8;

QY 1 EVOLQSGDPLVKPGASVKISCKASGYFTGYMHVVKQSPGKLEWIGRINPNNGVTLY 60
Db 285 EVOLVSGGELVQPGGSRVISAASGYTFTNGMNMVVKQAPGKLEWGMWINTYTGESTY 344
QY 61 NOKFKDKATLTVDKSSTTAYMELRSLTSDSAVYYCARSTMTITNYMDYWGQSTVTVSS 120
Db 345 ADSFKGRFTFSLDTSASAAYLQINSRAEDTAVYYCARFAI-----KGDYWGQGTLLTVSS 400


```
121 AKTTPSVYPLAPGSAQTNSMWTGLCLVKGYFPEPVTVTVNSGSLSSGVTHTPAVLQSD 180
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 401 ASTKGSPVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVTVNSGALTSGVHTTFAVLQSS 460
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 181 -LYTLSSVTVPSSTWPESTVTCNVNAPASSTKVDKIKVPRDGGGPPSEKSEINEKDLRK 239
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 461 GLYSLSVTVTPSSSLGTQYICNVNHPKNTKVDKKVEP----- 500
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 240 KSELQGTALGNLQIYYYNKAITSSSEKSAQDLTNTLLFKGFFTGHPWYNLLVDLGS 299
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 501 -----KSCWKLLLP----- 510
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 300 AATSEYEGSSVDLYGAYGYQCAGGTENKTCACMGVGVTLHDNNRLTEBKVPINLWIDGK 359
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 511 -----AAAGLLLLAAQP----- 522
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 360 OTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQVORGLIVFHSSEGSTV 419
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 523 -----AMAHHHH----- 530
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 420 SYDLFDAQGYPTDLLRIYRDNTTISSTLSLSISLYVTTSIVMTQPTSLVSAGDRVTI 479
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 531 -----HDIQMTQSPSSLSASVGRVTI 552
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 480 TCKASQSV--SNDVA---WYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDFLTIS 534
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 553 TCRSTKSLHNSGITLYLYWYQKPGKAPKLLIYQMSNLASGVPSRFSSSGSGTDFLTIS 612
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 535 SVQAEDAAYVFCODYNSPTFGGKTKLEIKRADAAPTVAIPPPSEQLTSGGASVVCFL 594
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 613 SLOPEDFATYCAQNLLEIPRTFGQGTVELKRTVAAPSVFIFPPSDEQLKSGTASVVCLL 672
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 595 NNFPYKIDINVKWKIDGSRQGVNSWTDODSKDSTYSMSSTLTLTDEYERHNSYTCEA 654
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 673 NNFPYKIDINVKWKIDGSRQGVNSWTDODSKDSTYSMSSTLTLTDEYERHNSYTCEA 732
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 655 THKTSSTPIVKSFNNE 671
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 733 THOGLSSPVTKSFNRGE 749
| | | | | : : : | | | | | : | | | | | : | | | | |

RESULT 15
US-09-807-721-2
; Sequence 2, Application US/09807721
; Patent No. US20020174453A1
; GENERAL INFORMATION:
; APPLICANT: AUBURN UNIVERSITY
; APPLICANT: UNIVERSITY OF CENTRAL FLORIDA
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES IN TRANSGENIC PLASTIDS
; FILE REFERENCE: 1463-PCT-US-00
; CURRENT APPLICATION NUMBER: US/09/807,721
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: PCT/US01/06274
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-807-721-2
Query Match 35.7%; Score 1257; DB 3; Length 669;
Best Local Similarity 41.6%; Pred. No. 2.3e-49;
Matches 308; Conservative 87; Mismatches 201; Indels 144; Gaps 23;

Qy 2 VQLQQSGPDLVKFGASVKISKASGYSTGYMHWKQSPKGLWIGRINPNNGVTLYN 61
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 3 VQLQQSGPDLVKFGASVKISKASGYSTGYMHWKQSPKGLWIGRINPNNGVTLYN 62
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 62 QKFKDKATLTVDKSSYAYMELSLTSEDASVYCAT-----YFDYWGQGTTLTVSSA 121
| | | | | : : : | | | | | : | | | | | : | | | | |
```

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Db 63 QKFKDKATLTVDKSSYAYMELSLTSEDASVYCAT-----YFDYWGQGTTLTVSSA 115
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 122 KTTTPSVYPLAPGSAQTNSMWTGLCLVKGYFPEPVTVTVNSGSLSSGVTHTPAV--LQ 178
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 116 SPTSPKVPFLSLDSTPDQGNV--VACLQVGFPEPLSVTWSESGQNVARNPPPSODAS 174
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 179 SDLYTLSSSVTVPSSTWTP--SETVTCNVNAPASSTKVDKIKVPRDGGGPPSEKSEINEKDL 237
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 175 GDLYTSSQLTLPATQCPDGKSVTCHVGHYTNSSQ--DVTVPICRVPPP-----PCC 224
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 238 RKSELOGTALGNLQIYYYNKAITSSSEKSAQDLTNTLLFKGFFTGHPWYNLLVDLGS 297
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 225 HPLSLHRLRALEDL-----LIGSEAN-----LTCTL-----TG-----LRDASG 258
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 298 STAATSEYEGSSV-----DLYGAY-----YG--YQCAGGTNPKTACMYG 334
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 259 AATTWTPSSGKSAVOGPPERDLGCYSVSVLPGCAQPNHGETFTCTAAHPELKTPLTA 318
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 335 GVTLDHNNRLTEBKVP-----INLWIDGKQTTVPIDKV 368
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 319 NITKSGNTFRPEVHLLPPPESEELALNELVLTCLARGFSPKDLVLRWLGSO--ELPREKY 377
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 369 KT--SKKE-----VTQELDLQARHYLHGKFGLYNSDSFGKQVORGLIVFHSSEGST 418
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 378 LTWASROEPSGQTTTAVTISILVAAEDWKKG-----ETP-----SCWVGHEALPLA 424
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 419 VSYDLFDAQGYPTDLLRIYRDNTTISSTLSLSISLYL-----YTTSIVMTQPTSLVV 471
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 425 FTQKTTIDRLAGKP-----THINVSVVMAEADGTCYRMDIVMTQSPAIMSA 469
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 472 SAGRVTITCKASQSVNSDVANVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDFTL 531
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 470 SPGEKVTITCSASSMSVY--MHWFOQKPGTSPKLMWLYSTNSLASGVPARFSGSGSGTSYSL 528
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 532 TISSVQAEDAAYVFCODYNSPTFGGKTKLEIKRADAAPTVAIPPPSEQLTSGGASVV 591
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 529 TISRAEDAAYTYCHQRTSYPTFGGKTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVV 588
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 592 CFLNFPYKIDINVKWKIDGSRQGVNSWTDODSKDSTYSMSSTLTLTDEYERHNSYT 651
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 589 CLLNFPYKIDINVKWKIDGSRQGVNSWTDODSKDSTYSMSSTLTLTDEYERHNSYT 648
| | | | | : : : | | | | | : | | | | | : | | | | |
Qy 652 CEATHKTSSTPIVKSFNNE 671
| | | | | : : : | | | | | : | | | | | : | | | | |
Db 649 CEVTHOGLSSPVTKSFNRGE 668
| | | | | : : : | | | | | : | | | | | : | | | | |

RESULT 16
US-11-084-080-20
; Sequence 20, Application US/11084080
; Publication No. US20050238642A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis J.
; APPLICANT: HELLENDORF, Koehn
; APPLICANT: CIZEAU, Jeannick
; APPLICANT: MACDONALD, Glen Christopher
; APPLICANT: ENTWISTLE, Joycelyn
; APPLICANT: BOSCH, Denis Georges
; APPLICANT: GLOVER, Nicholas Ronald
; TITLE OF INVENTION: MODIFIED BOUGAINVILLEAN PROTEINS, CYTOTOXINS AND METHODS AND USES
; FILE REFERENCE: 10241-44
; CURRENT APPLICATION NUMBER: US/11/084,080
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US 60/554,580
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: US 60/630,571
; PRIOR FILING DATE: 2004-11-26
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
; LENGTH: 750
```

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VB6-845-CL-de-bouganin
US-11-084-080-20

Query Match      35.7%; Score 1257; DB 6; Length 750;
Best Local Similarity 40.9%; Pred. No. 2.5e-49;
Matches 277; Conservative 66; Mismatches 110; Indels 224; Gaps 9;

QY 1 EVQLQSGDPLVKPGASVRIKSGSYFTGYIMHWVKQSPGKGLWIGRIINPNNGVTILY 60
Db 29 EVQLVQSGFGLVPGGSGVRIKSGSYFTFYGMVWVKQAPGKGLWGWINTYTGESY 88
QY 61 NQKPKDKATLVDSKSTTAYMELRSLTSDSDAVYICARSTMTINYVMDYWGQSTVTVSS 120
Db 89 ADSFKGRFTSLDTSAAAYLQINSLRAEDTAVYICARFAI-----KGDYWGQGTLLTVSS 144
QY 121 AKTTPEVYPLAPGSAQAQTNMVTGLCLVKGYFPEPVTVTVNSGSLSSGVTHTFPAVLQSD 180
Db 145 ASTKPSVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSMNGALTSVGHVTFPAVLQSS 204
QY 181 -LYTSSSVTVPSSTWPSSETVTCNVAPASSTKVDKKIIVPRDSGGPSEKSEINEKDLRK 239
Db 205 GLYSLSVTVTPSSSLGTQYICNVNPKPSNTKVDKKVEP----- 244
QY 240 KSELOGTALGNLKQIYYNNSKAITSEKSGADQFLNTLLFKGFTGHPWYNLLVDLGST 299
Db 245 -----KSCMKYLL-----PT 254
QY 300 AATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLLHDNNRLTEKKVPINLWIDGK 359
Db 255 AAA----- 257
QY 360 OTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGKGQVGRGLIVFHSSEGSTV 419
Db 258 -----GLL----- 260
QY 420 SYDLFDAQOQYPTLLRIYRDNNTTISSTLSLSLYLYTTSIVMTQPTSLLYSAGDRVTI 479
Db 261 ---LLAQAPAMAD-----IQMTQSPSLSASVGDRTVI 290
QY 480 TKKASQSV--SNDVA---WYQKPGOSPKLLISYTSRVRGVPDRFSGSGYGTDFLTIS 534
Db 291 TCRSTKSLHNSGITVLYWYQKPGAPKLLIQMNSNLASGVPSRFSGSGGTDFLTIS 350
QY 535 SVQAEDAAYVFCQDYNSPPTFGGKTLEIKRADAAPTVSIIPPSSEQLTSGGASVVCFL 594
Db 351 SLQPEDFATYYCAQNLIEIPRTFGQGTKEVLRKRTVAAPSVFIPPPSDEQLKSGTASVVCLL 410
QY 595 NNFPYKDIWVKIDGSEKQNGVLNWTQDSDKSTYSMSSTLTLTKDEYERHNSYTCFA 654
Db 411 NNFPYKDIWVKIDGSEKQNGVLNWTQDSDKSTYSMSSTLTLTKDEYERHNSYTCFA 654
QY 655 THKTSSTPIVKSFNRE 671
Db 471 THQGLSSPTKSFNRGE 487

RESULT 17
US-09-900-766-2
; Sequence 2, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(233)
; OTHER INFORMATION: Chimeric Protein
US-09-900-766-3

Query Match      32.1%; Score 1130; DB 3; Length 233;
Best Local Similarity 91.4%; Pred. No. 4.8e-44;
Matches 213; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKQIYYNNSKAITSEKSGADQFLNTLLFKGFFTG 285
Db 1 SEKSEINEKDLRKSELOGTALGNLKQIYYNNEKAITENKESDDQFLENLLFKGFFTG 60
QY 286 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLLHDNNRLT 345
Db 61 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLLHDNNRLT 120
QY 346 EEKQVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGKQV 405
Db 121 EEKQVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGKQV 180
QY 406 RGLIVFHSSEGSTVSYDLFDAQOQYPTLLRIYRDNNTTISSTLSLSLYLYTT 458
Db 181 RGLIVFHSSEGSTVSYDLFDAQOQYPTLLRIYRDNNTTISSTLSLSLYLYTT 233

RESULT 18
US-09-900-766-3
; Sequence 3, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(233)
; OTHER INFORMATION: Chimeric Protein
US-09-900-766-3

Query Match      32.1%; Score 1130; DB 3; Length 233;
Best Local Similarity 91.4%; Pred. No. 4.8e-44;
Matches 213; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKQIYYNNSKAITSEKSGADQFLNTLLFKGFFTG 285
Db 1 SEKSEINEKDLRKSELOGTALGNLKQIYYNNEKAITENKESDDQFLENLLFKGFFTG 60
QY 286 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLLHDNNRLT 345
Db 61 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLLHDNNRLT 120
QY 346 EEKQVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGKQV 405
Db 121 EEKQVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGKQV 180
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QY 406 RGLIVFHSSEGSTSVSYDLFDAQOQYPTDLLRIYRDNTTSSLSLSLYLYTT 458
|||||
Db 181 RGLIVFHSSEGSTSVSYDLFDAQOQYPTDLLRIYRDNTTSENHIALYLYTT 233

RESULT 19
US-09-900-766-7
; Sequence 7, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0:10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Staphylococcus sp.
US-09-900-766-7

Query Match 31.4%; Score 1107; DB 3; Length 233;
Best Local Similarity 89.7%; Pred. No. 5.3e-43;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLQIYYNKAITSSEKSADQFLTNLLFKGFFTG 285
|||||
Db 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
|||||

QY 286 HPWYNLLVDLGSTATSEYEGSSVDLYGAYYGYQCAGTTPNKTACMYGGVTLLHDNNRLT 345
|||||
Db 61 HPWYNLLVDLGSKDATNKYKGVLDLYGAYYGYQCAGTTPNKTACMYGGVTLLHDNNRLT 120
|||||

QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 405
|||||
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
|||||

QY 406 RGLIVFHSSEGSTSVSYDLFDAQOQYPTDLLRIYRDNTTSSLSLSLYLYTT 458
|||||
Db 181 RGLIVFHSSEGSTSVSYDLFDAQOQYPTDLLRIYRDNTTSENHIALYLYTT 233

RESULT 20
US-10-283-838-8
; Sequence 8, Application US/10283838
; Publication No. US20030092894A1
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
; Johan Hansson, Terje Kalland, Lars
; Abrahamson and Goran Forberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
; AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,838
; FILING DATE: 30-Oct-2002
```

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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,692
; FILING DATE: August 12, 1996
; APPLICATION NUMBER: 9601245-5
; FILING DATE: March 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Krieger, Paul E.
; REGISTRATION NUMBER: 25,886
; REFERENCE/DOCKET NUMBER: 41986/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-283-838-8

Query Match 31.4%; Score 1107; DB 4; Length 233;
Best Local Similarity 89.7%; Pred. No. 5.3e-43;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLQIYYNKAITSSEKSADQFLTNLLFKGFFTG 285
|||||
Db 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
|||||

QY 286 HPWYNLLVDLGSTATSEYEGSSVDLYGAYYGYQCAGTTPNKTACMYGGVTLLHDNNRLT 345
|||||
Db 61 HPWYNLLVDLGSKDATNKYKGVLDLYGAYYGYQCAGTTPNKTACMYGGVTLLHDNNRLT 120
|||||

QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 405
|||||
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
|||||

QY 406 RGLIVFHSSEGSTSVSYDLFDAQOQYPTDLLRIYRDNTTSSLSLSLYLYTT 458
|||||
Db 181 RGLIVFHSSEGSTSVSYDLFDAQOQYPTDLLRIYRDNTTSENHIALYLYTT 233

RESULT 21
US-10-267-682-112
; Sequence 112, Application US/10267682
; Publication No. US20040033235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,682
```

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; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484, 223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-267-682-112

Query Match 31.4%; Score 1107; DB 4; Length 257;
Best Local Similarity 89.7%; Pred. No. 5.8e-43;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SKSEINEKDLRKSELQGTALGNLKQIYYNYSKAITSEKSDAQFLNTLLFKGFFTG 285
Db 25 SKSEINEKDLRKSELQGNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 286 HPWYNLLVDLGSTATSEYEGSSVDLYGAYGYOCAGGTPNKTCMYGGVTLHDNNRLT 345
Db 85 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 405
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 204
QY 406 RGLIVPHSSEGSTSVSYDLFDAQGYPDPTLLRIYRDNTTSSLSLSLYTT 458
Db 205 RGLIVPHSSEGSTSVSYDLFDAQGYPDPTLLRIYRDNTTSSLSLSLYTT 257

RESULT 22
US-10-267-748-112
; Sequence 112, Application US/10267748
; Publication No. US20040052820A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/10/267,748
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484, 223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-267-748-112

Query Match 31.4%; Score 1107; DB 4; Length 257;
Best Local Similarity 89.7%; Pred. No. 5.8e-43;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SKSEINEKDLRKSELQGTALGNLKQIYYNYSKAITSEKSDAQFLNTLLFKGFFTG 285
Db 25 SKSEINEKDLRKSELQGNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 286 HPWYNLLVDLGSTATSEYEGSSVDLYGAYGYOCAGGTPNKTCMYGGVTLHDNNRLT 345
Db 85 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 405
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 204
QY 406 RGLIVPHSSEGSTSVSYDLFDAQGYPDPTLLRIYRDNTTSSLSLSLYTT 458
Db 205 RGLIVPHSSEGSTSVSYDLFDAQGYPDPTLLRIYRDNTTSSLSLSLYTT 257

RESULT 23
US-10-428-817A-188
; Sequence 188, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 188
; LENGTH: 257

```

```
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-188

Query Match      31.4%; Score 1107; DB 4; Length 257;
Best Local Similarity 89.7%; Pred. No. 5.8e-43;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKKSSELOQTALGNLQIYYYSKAITSEKSDAQFLTNTLLFKGFPTG 285
Db 25 SEKSEINEKDLRKKSSELOQTALGNLQIYYYSKAITSEKSDAQFLTNTLLFKGFPTG 84

QY -286 HPWYNLLVLDLGGTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
Db 85 HPWYNLLVLDLGGTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 346 EEKVPINLWDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 145 EEKVPINLWDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204

QY 406 RGLIVHSSSGSTVSVDLFDAGQGYPTDLLRIYRDNTTISSTLSISLYLYTT 458
Db 205 RGLIVHSSSGSTVSVDLFDAGQGYPTDLLRIYRDNTTINSENHLDLYLYTT 257

RESULT 24
US-09-751-708A-16
; Sequence 16, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-16

Query Match      30.4%; Score 1072; DB 3; Length 248;
Best Local Similarity 90.2%; Pred. No. 2.2e-41;
Matches 202; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKKSSELOQTALGNLQIYYYSKAITSEKSDAQFLTNTLLFKGFPTG 285
Db 25 SEKSEINEKDLRKKSSELOQTALGNLQIYYYSKAITSEKSDAQFLTNTLLFKGFPTG 84

QY 286 HPWYNLLVLDLGGTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
Db 85 HPWYNLLVLDLGGTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 346 EEKVPINLWDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 145 EEKVPINLWDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204

QY 406 RGLIVHSSSGSTVSVDLFDAGQGYPTDLLRIYRDNTTISSTLSISLYLYTT 449
Db 205 RGLIVHSSSGSTVSVDLFDAGQGYPTDLLRIYRDNTTINSENHLDLYLYTT 248

RESULT 25
US-09-751-708A-16
; Sequence 16, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
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; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-16

Query Match      30.4%; Score 1072; DB 3; Length 248;
Best Local Similarity 90.2%; Pred. No. 2.2e-41;
Matches 202; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKKSSELOQTALGNLQIYYYSKAITSEKSDAQFLTNTLLFKGFPTG 285
Db 25 SEKSEINEKDLRKKSSELOQTALGNLQIYYYSKAITSEKSDAQFLTNTLLFKGFPTG 84

QY 286 HPWYNLLVLDLGGTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
Db 85 HPWYNLLVLDLGGTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 346 EEKVPINLWDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 145 EEKVPINLWDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204

QY 406 RGLIVHSSSGSTVSVDLFDAGQGYPTDLLRIYRDNTTISSTLSISLYLYTT 449
Db 205 RGLIVHSSSGSTVSVDLFDAGQGYPTDLLRIYRDNTTINSENHLDLYLYTT 248

RESULT 26
US-10-428-817A-12
; Sequence 12, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-12

Query Match      30.4%; Score 1072; DB 4; Length 248;
Best Local Similarity 90.2%; Pred. No. 2.2e-41;
Matches 202; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKKSSELOQTALGNLQIYYYSKAITSEKSDAQFLTNTLLFKGFPTG 285
Db 25 SEKSEINEKDLRKKSSELOQTALGNLQIYYYSKAITSEKSDAQFLTNTLLFKGFPTG 84
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QY 286 HPKYNLLVLDLGGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMVGVTLLHNNRLT 345
Db 85 HPWYNLLVLDLGGKDATNKYKKVDLYGAYGYQCAGGTPNKTCMVGVTLLHNNRLT 144
QY 346 EEKVPINLWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 145 EEKVPINLWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVPHSSEGSTSVYDLFDAQOQYPTLLRIYRDNTTISSTSL 449
Db 205 RGLIVPHSSEGSTSVYDLFDAQOQYPTLLRIYRDNTTINSENL 248

RESULT 27
US-10-937-758A-16
; Sequence 16, Application US/10937758A
; Publication No. US20050112141A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: FILE REFERENCE 650884
; CURRENT APPLICATION NUMBER: US/10/937,758A
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: 09/650,884
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 16
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-937-758A-16

Query Match 30.4%; Score 1072; DB 5; Length 248;
Best Local Similarity 90.2%; Pred. No. 2.2e-41;
Matches 202; Conservative 9; Mismatches 13; Indels 0; Gaps 0;
QY 226 SEKSEBINEKDLRKSELQALGNLKOIYYNSKAITSEKSADQFLNTLLFKGFFTG 285
Db 25 SEKSEBINEKDLRKSELQALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 286 HPWYNLLVLDLGGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMVGVTLLHNNRLT 345
Db 85 HPWYNLLVLDLGGKDATNKYKKVDLYGAYGYQCAGGTPNKTCMVGVTLLHNNRLT 144
QY 346 EEKVPINLWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 145 EEKVPINLWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVPHSSEGSTSVYDLFDAQOQYPTLLRIYRDNTTISSTSL 449
Db 205 RGLIVPHSSEGSTSVYDLFDAQOQYPTLLRIYRDNTTINSENL 248

RESULT 28
US-10-334-235-38
; Sequence 38, Application US/10334235
; Publication No. US20040131591A1
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Ltd.
; APPLICANT: Kingman, Alan
; APPLICANT: Bebbington, Christopher
; APPLICANT: Carroll, Miles
; APPLICANT: Ellard, Fiona
; APPLICANT: Kingman, Susan
; APPLICANT: Myers, Kevin
; APPLICANT: Lamikandra, Abigail
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: 532682000920
; CURRENT APPLICATION NUMBER: US/10/334,235
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 10/060,585

; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 09/445,375
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of 574Sabl
US-10-334-235-38

Query Match 30.4%; Score 1069; DB 4; Length 600;
Best Local Similarity 37.9%; Pred. No. 6.9e-41;
Matches 254; Conservative 20; Mismatches 60; Indels 336; Gaps 9;
QY 1 EVLOQSGPDLVKPGASVKISCKASGYSTGYMHWKQSPGKLEWIGRINPNNGVTLY 60
Db 23 EVLOQSGPDLVKPGASVKISCKASGYSTGYMHWKQSHGKSLWIGRINPNNGVTLY 82
QY 61 NQKFKDKATLTVDKSSTTAYMELSLTSDSAVYCARSTMITNYMDYMGQTSVTSS 120
Db 83 NQKFKDKATLTVDKSSTTAYMELSLTSDSAVYCARSTMITNYMDYMGQTSVTSS 141
QY 121 AKTTPSPVPLAPGSAQAQNSMVTGLCLVKGYFPEPVTVWNSGSLSSGVHTFPAVLQSD 180
Db 142 ----- 141
QY 181 LYTSSSVTPSPSTWSPSETVTCNVAHPASSTKVDKIVPRDGGPSEKSEINEKDLRKK 240
Db 142 -----SGG----- 144
QY 241 SELQGTALGNLKOIYYNSKAITSEKSADQFLNTLLFKGFFTGHPWYNLDDLGLSTA 300
Db 145 ----- 144
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTCMVGVTLLHNNRLTEKKVPINLWIDGKQ 360
Db 145 -----GGSGGGT----- 154
QY 361 TTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQRLIVPHSSEGSTVS 420
Db 155 -----GG----- 156
QY 421 YDLFDAQOQYPTLLRIYRDNTTISSTSLISLYLYTTSIVMTQTPTSLLSAGDRVIT 480
Db 157 -----SSIVMTQTPTFLLVSAGDRVIT 179
QY 481 CKASQSVSNDAVWYQKPGQSPKLLISYTSRYAGVDPDRFSGSGCYGTDFTLTSSVQAED 540
Db 180 CKASQSVSNDAVWYQKPGQSPKLLISYTSRYAGVDPDRFSGSGCYGTDFTLTSSVQAED 239
QY 541 AAVYFCQDDYNSPPTFGGTTKLEIKRADA-APTVSIFPPPSSEQLTSGGASVVCFLANFYP 599
Db 240 LAVYFCQDDYNSPPTFGGTTKLEIKRASKTGSGVFPFLAPSSKTSKGTALGCLVKDYFP 299
QY 600 KDINVKWK-----IDGSEKQNGVLNSWTDQDSKDYTSMSSTLTLTKDEYERHNSYTCBAT 655
Db 300 EPTVTSWNSGALTSVHTFPAVLQS-----SGLYSLSSVVTVPSSSLGT-QTYICNVN 351
QY 656 HKTSTSPIVK 665
Db 352 HKPSNTKVDK 361

RESULT 29
US-10-742-405-12
; Sequence 12, Application US/10742405
; Publication No. US20040213761A1
; GENERAL INFORMATION:

; APPLICANT: Bowman, Edward P.
; APPLICANT: Chan, Jason R.
; APPLICANT: Moore, Kevin
; APPLICANT: Nguyen, Nhung
; APPLICANT: Churakova, Tatyana
; APPLICANT: Chen, Shi-Juan
; APPLICANT: Cua, Daniel J.
; TITLE OF INVENTION: Uses of mammalian cytokine; related reagents
; FILE REFERENCE: DX01578K
; CURRENT APPLICATION NUMBER: US/10/742,405
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-742-405-12

Query Match 29.6%; Score 1042; DB 4; Length 467;
Best Local Similarity 37.4%; Pred. No. 9.1e-40;
Matches 249; Conservative 57; Mismatches 110; Indels 250; Gaps 14;

QY 1 EVLOQSGDPLVKPGASVKISCKASGYSTGYVMHWKSPGKGLWIGRIINNGVTLY 60
DB 20 QVLOQSGAELVPRGAGKLSCKASGYFTSYWNNWVKQRPQGGLWIGMIDPLDSETHY 79
QY 61 NQFKDKATLTVDKSTTAYMELRSLTSEDYAVYCARSTMTITNYVMDYMGQGSTVTSS 120
DB 80 NQFKDKATLTVDKSSSTAYMQLSSLTSEDYAVYCARGD--NYAYMDYMGQGSTVTSS 137
QY 121 AKTTPSVYPLAPGSAQAQNSMTVLGCLVKGYPEPVTVTWNSGSLSSGVHTTFAVLQSD 180
DB 138 AKTTPSVYPLAPGSAQAQNSMTVLGCLVKGYPEPVTVTWNSGSLSSGVHTTFAVLQSD 197
QY 181 LYTLSSVTPSPSTWSPSETVTCNVAHPASSTKVDKIVPRDSCG--PKDVLITIL 240
DB 198 LYTLSSVTPSPSTWSPSETVTCNVAHPASSTKVDKIVPRDSCG-----240
QY 241 SELQGTALGNLKOIYYNYSKAITSSSEKSAQDQFLNTLLPKGFTGHPWYNDLLVDLGSTA 300
DB 241 CKPCICTVPEVSSVFIPPK-----PKDVLITIL-----269
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTGPNKTAQMYGGVTLHDNNRLTBEKKVPIINLWIDGKQ 360
DB 270 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD---294
QY 361 TTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-PGL-YNSDSPGKVGQRLIVF 411
DB 295 -DVEVHTAQTPREEQFNSTFRSVSELPIMHQDLNGKEPKCRVNSAAFPAPIEK-----348
QY 412 HSSEGSTSVSYDLFDAQQYPTDLLRIYRDNNTTISSTLSISLYLYTTSIVMTQTPTSLLV 471
DB 349 -----TISK-----353
QY 472 SAGDRVITITCKASQSVSNVAMVYQKPGQSPKLLISYTSRYAGVDPFRFSGSGYGTDFTL 531
DB 354 -----353
QY 532 TISSVQAEADAAYFCQDYNSTPFGGTGKLEIKRADAAPTIVSIFPPSSSQLTSGGASVV 591
DB 354 -----KGRPKAPQVYTIPTPKKEQMAKDKVSLT 380
QY 592 CFLNNFYPKDVNWKIDGSEONGVNSWTDODSKDSTYSMSSTLTLTDEYERHNSYT 651
DB 381 CMITDFPEDITVEWQWNGQPAEN--YKNTQIPIMDS--DGSYFYVSKLVNQVSKNWEAGNTFT 438
QY 652 CEATHK 657
DB 439 CSVLHE 444

RESULT 30

US-09-903-327A-11
; Sequence 11, Application US/09903327A
; Patent No. US2002016433A1
; GENERAL INFORMATION:
; APPLICANT: Nemerow, Glen R.
; APPLICANT: Li, Erquang
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGETING
; FILE REFERENCE: 22908-1228
; CURRENT APPLICATION NUMBER: US/09/903,327A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/613,017
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 597
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain
; OTHER INFORMATION: and TNF alpha mature peptide
US-09-903-327A-11

Query Match 29.2%; Score 1028; DB 3; Length 597;
Best Local Similarity 37.2%; Pred. No. 4.9e-39;
Matches 253; Conservative 53; Mismatches 115; Indels 260; Gaps 15;

QY 1 EVLOQSGDPLVKPGASVKISCKASGYSTGYVMHWKSPGKGLWIGRIINNGVTLY 60
DB 20 EVLOQSGPELVPRGAGKLSCKASGYFTDYNNHWVKSHGKSLWELWIGVIYPKGGTGY 79
QY 61 NQFKDKATLTVDKSTTAYMELRSLTSEDYAVYCARSTMTITNYVMDYMGQGSTVTSS 120
DB 80 NQFKDKATLTVDSSNTAYMELRSLTSDASAVYCARG-----LAYMGQGLTIVTSA 132
QY 121 AKTTPSVYPLAPGSAQAQNSMTVLGCLVKGYPEPVTVTWNSGSLSSGVHTTFAVLQSD 180
DB 133 AKTTPSVYPLAPGSAQAQNSMTVLGCLVKGYPEPVTVTWNSGSLSSGVHTTFAVLQSD 192
QY 181 LYTLSSVTPSPSTWSPSETVTCNVAHPASSTKVDKIVPRDSCGSEINEKDLRKK 240
DB 193 LYTLSSVTPSPSTWSPSETVTCNVAHPASSTKVDKIVPRDSCG-----235
QY 241 SELQGTALGNLKOIYYNYSKAITSSSEKSAQDQFLNTLLPKGFTGHPWYNDLLVDLGSTA 300
DB 236 CKPCICTVPEVSSVFIPPK-----PKDVLITIL-----264
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTGPNKTAQMYGGVTLHDNNRLTBEKKVPIINLWIDGKQ 360
DB 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD---289
QY 361 TTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-PGL-YNSDSPGKVGQRLIVF 411
DB 290 -DVEVHTAQTPREEQFNSTFRSVSELPIMHQDLNGKEPKCRVNSAAFPAPIEK-----343
QY 412 HSSEGSTSVSYDLFDAQQYPTDLLRIYRDNNTTISSTLSISLYLYTTSIVMTQTPTSLLV 471
DB 344 -----TISK-----348
QY 472 SAGDRVITITCKASQSVSNVAMVYQKPGQSPKLLISYTSRYAGVDPFRFSGSGYGTDFTL 531
DB 349 -----348
QY 532 TISSVQAEADAAYFCQDYNSTPFGGTGKLEIKRADAAPTIVSIFPPSSSQLTSGGASVV 591
DB 349 -----KGRPKAPQVYTIPTPKKEQMAKDKVSLT 375
QY 592 CFLNNFYPKDVNWKIDGSEONGVNSWTDODSKDSTYSMSSTLTLTDEYERHNSYT 651
DB 376 CMITDFPEDITVEWQWNGQPAEN--YKNTQIPIMDT--DGSYFYVSKLVNQVSKNWEAGNTFT 433

```
QY 652 CEATHKTSPIVKSENRNES 672
Db 434 CSVLHE-----FVRSSRTPS 449

RESULT 31
US-10-216-484-9
; Sequence 9, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976A1ufusa
; APPLICANT: Haryuyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 9
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-216-484-9

Query Match 29.1%; Score 1025.5; DB 4; Length 464;
Best Local Similarity 36.2%; Pred. No. 5e-39;
Matches 243; Conservative 64; Mismatches 106; Indels 259; Gaps 14;

QY 1 EVQLQSGDPLVKPGASVKISKASGYSTGYMHVVKQSPKGLIEWIGRINPNNGVTLY 60
Db 20 QVQLQPGAEVLKPGASVKLSCKASGYTFTSYMQVQKORPGQGLEWIGIDPDSYTN 79

QY 61 NQKFKDKATLVDKSSTAYMELRSLSSEDSAVYYCARS-TWITNYVMYWGQTSVTVS 119
Db 80 NQKFKGKATLVDTSSSTAYMQLSSLTSEDSAVYYCARNRDYSNNWYFDVWGTTVTVS 139

QY 120 SAKTTPPSVYPLAPGSAQTNSMVTLGCLVKGYFPEPPTVTWNSGSLSGVHTFPVAVLS 179
Db 140 SAKTTPPSVYPLAPGSAQTNSMVTLGCLVKGYFPEPPTVTWNSGSLSGVHTFPVAVLS 199

QY 180 DLYTLSSSVTVPSSTWPSQVTCNVAHPASSTKVDKKIVPRDSGGPSEKSEINEKDLRK 239
Db 200 DLYTLSSSVTVPSSTWPSQVTCNVAHPASSTKVDKKIVPRDCG----- 243

QY 240 KSELQGTALGNLKQIYYYNASKAITSSEKSAQDPLTNTLLFKGFTGHPWYNLDDLGLST 299
Db 273 -----TP-KVTCVVVDIS-----PKDVLITL----- 297

QY 360 QTTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVGQRLIV 410
Db 298 --DVEVHTAQTPREEQFNSTFRSVSELPIMHQNLNGKEFKCRVNSAAPPAPIEK---- 351

QY 411 FHSSEGSVSYDLFDAQGGVPTDLLRIYRDNTTISSTLSISLYLYTTSIVMTQTPTSL 470
Db 352 -----TISKT----- 356

QY 471 VSAGDRVTTICKASQSVSNDVAMVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTFT 530
Db 357 ----- 356

QY 531 LTISVQAEDAAYFYCCQDYNPSPTFGGKTKLEIKRADAAPTIVSIFPPSSEQITSGGASV 590
Db 357 -----KGRPKAPQVYTIPTPPKEQWAKDKVSL 382

QY 591 VCFLANFYPKDINVKWKIDGSRQN-----GVLSNWTDDQSKDSTYSMSSTLTLTKEYE 645
Db 383 TCMITDFFPEDITVEMQWNGQPAENYKNTQPIMNT-----NGSYFVYSKLVNQSKEWE 435

QY 646 RHNSYTCEATHK 657
Db 436 AGNTFTCSVLHE 447

RESULT 32
US-10-384-933-9
; Sequence 9, Application US/10384933
; Publication No. US20030170817A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030170817A1ufusa
; APPLICANT: Haryuyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/384,933
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 9
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-384-933-9

Query Match 29.1%; Score 1025.5; DB 4; Length 464;
Best Local Similarity 36.2%; Pred. No. 5e-39;
Matches 243; Conservative 64; Mismatches 106; Indels 259; Gaps 14;

QY 1 EVQLQSGDPLVKPGASVKISKASGYSTGYMHVVKQSPKGLIEWIGRINPNNGVTLY 60
Db 20 QVQLQPGAEVLKPGASVKLSCKASGYTFTSYMQVQKORPGQGLEWIGIDPDSYTN 79

QY 61 NQKFKDKATLVDKSSTAYMELRSLSSEDSAVYYCARS-TWITNYVMYWGQTSVTVS 119
Db 80 NQKFKGKATLVDTSSSTAYMQLSSLTSEDSAVYYCARNRDYSNNWYFDVWGTTVTVS 139

QY 120 SAKTTPPSVYPLAPGSAQTNSMVTLGCLVKGYFPEPPTVTWNSGSLSGVHTFPVAVLS 179
Db 140 SAKTTPPSVYPLAPGSAQTNSMVTLGCLVKGYFPEPPTVTWNSGSLSGVHTFPVAVLS 199

QY 180 DLYTLSSSVTVPSSTWPSQVTCNVAHPASSTKVDKKIVPRDSGGPSEKSEINEKDLRK 239
Db 200 DLYTLSSSVTVPSSTWPSQVTCNVAHPASSTKVDKKIVPRDCG----- 243

QY 240 KSELQGTALGNLKQIYYYNASKAITSSEKSAQDPLTNTLLFKGFTGHPWYNLDDLGLST 299
Db 244 -CKPCICTVPESSVVFIPPK-----PKDVLITL----- 272

QY 300 AATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGK 359
Db 273 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD-- 297

QY 360 QTTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVGQRLIV 410
Db 298 --DVEVHTAQTPREEQFNSTFRSVSELPIMHQNLNGKEFKCRVNSAAPPAPIEK---- 351

QY 411 FHSSEGSVSYDLFDAQGGVPTDLLRIYRDNTTISSTLSISLYLYTTSIVMTQTPTSL 470
Db 352 -----TISKT----- 356

QY 471 VSAGDRVTTICKASQSVSNDVAMVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTFT 530
Db 530 ----- 356
```


Db 357 ----- 356
QY 531 LTISSVQAEAAVYFCQDYNSSPTFGGKLEIKRADAAPTYSIFPPSSSEQLTSGASV 590
Db 357 -----KGRPKAPQVYTIIPPKEQMAKDVSL 382
QY 591 VCLNNFYPKIDINVWKIDGSRQN-----GVLSNWTQDSKDSYMSSTLTLTDEYE 645
Db 383 TCMTIDFFPDITVEMQWQPAENYKNTQPIWNT-----NGSYFVYSKLVNQSWE 435
QY 646 RHNSYTCETHK 657
Db 436 AGNTFTCSVLHE 447
RESULT 33
US-09-903-327A-14
; Sequence 14, Application US/09903327A
; Patent No. US20020164333A1
; GENERAL INFORMATION:
; APPLICANT: Nemerow, Glen R.
; APPLICANT: Li, Erguang
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
; TITLE OF INVENTION: GENE
; FILE REFERENCE: 22908-1228
; CURRENT APPLICATION NUMBER: US/09/903,327A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/613,017
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 613
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain
; OTHER INFORMATION: and SCF mature peptide
US-09-903-327A-14
Query Match 29.1%; Score 1024.5; DB 3; Length 613;
Best Local Similarity 37.3%; Pred. No. 7.3e-39;
Matches 250; Conservative 51; Mismatches 115; Indels 255; Gaps 14;
QY 1 EVLOQSGDPLVKPGASVKISKASGYFTGYMHWKQSPGKLEWIGRINPNNGVTLY 60
Db 20 EVLOQSGDPLVKPGASVKISKASGYFTGYMHWKQSPGKLEWIGRINPNNGVTLY 60
QY 61 NQKFKDKATLTVDKSSSTAYMELSLTSDASAVYYCARSTMTITNYMDYWGQTSVTSS 120
Db 80 NQKFKSKATLTVDSSNTAYMELSLTSDASAVYYCARG-----IAYWQGQTLVTVA 132
QY 121 AKTTPSVVPLAPGSAQAQNSMTVLGCLVKGYFPEPVTVTWNSGSLSSGVHTTFAVLQSD 180
Db 133 AKTTPSVVPLAPGSAQAQNSMTVLGCLVKGYFPEPVTVTWNSGSLSSGVHTTFAVLQSD 192
QY 181 LYTLSSTVTPSSVTPSETVTCNVAHPASSTKVDKIKVPRDSGSPSEKSEINEKDLRKK 240
Db 193 LYTLSSTVTPSSVTPSETVTCNVAHPASSTKVDKIKVPRDCG----- 235
QY 241 SELQGTALGNKQIYYNSKAITSEKSDAQFLTNTLLFKGFTGHPWYNLDLVLGSTA 300
Db 236 CKFCICTVPEVSSVFIPPK-----PKDVLITIL----- 264
QY 301 ATSEYEGSSVDLYGAYGYOCAGGTGNKTCMVGTVLHNNRLTEBKKVPINLWIDGKQ 360
Db 265 -----TP-KVTCVVVDIS-----KODPEVQFSWFVD-- 289
QY 361 TTVPIDKVTSSKEV-----TVQELDLQARHVLHGK-FGL-YNSSDFGKVGQGLIVF 411
Db 290 -DVEVHTAQTPREEQFNSTRFSSELPIMHQDLNGLKEFKCRVNSAAPPAPIEK----- 343

QY 412 HSSEGSTVSYDLFDAQQGYPDTLRLRIYRDNNTTISSTLSLSLYLYTTSIVMTQPTSLLV 471
Db 344 -----TISK----- 348
QY 472 SAGDRVITITKASQSVSNDAVYQKPGQPKLLISYTSRYAGVDPDRFSGSGYGTDFTL 531
Db 349 ----- 348
QY 532 TISSVQAEAAVYFCQDYNSSPTFGGKLEIKRADAAPTYSIFPPSSSEQLTSGASVV 591
Db 349 -----KGRPKAPQVYTIIPPKEQMAKDVSLT 375
QY 592 CFLNNFYPKIDINVWKIDGSRONGVLSNWTQDSKDSYMSSTLTLTDEYERHNSYT 651
Db 376 CMITDFFPDITVEMQWQPAEN-YKNTQPIWNT-DGSYFVYSKLVNQSWEAGNTFI 433
QY 652 CEATHKTSSTSP 662
Db 434 CSVLHEFCRYP 444
RESULT 34
US-09-903-327A-2
; Sequence 2, Application US/09903327A
; Patent No. US20020164333A1
; GENERAL INFORMATION:
; APPLICANT: Nemerow, Glen R.
; APPLICANT: Li, Erguang
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
; TITLE OF INVENTION: GENE
; FILE REFERENCE: 22908-1228
; CURRENT APPLICATION NUMBER: US/09/903,327A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/613,017
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (0)...(0)
; OTHER INFORMATION: DAV-1 heavy chain, penton base monoclonal antibody
US-09-903-327A-2
Query Match 29.1%; Score 1023.5; DB 3; Length 456;
Best Local Similarity 37.4%; Pred. No. 6.1e-39;
Matches 249; Conservative 51; Mismatches 111; Indels 255; Gaps 14;
QY 1 EVLOQSGDPLVKPGASVKISKASGYFTGYMHWKQSPGKLEWIGRINPNNGVTLY 60
Db 20 EVLOQSGDPLVKPGASVKISKASGYFTGYMHWKQSPGKLEWIGRINPNNGVTLY 60
QY 61 NQKFKDKATLTVDKSSSTAYMELSLTSDASAVYYCARSTMTITNYMDYWGQTSVTSS 120
Db 80 NQKFKSKATLTVDSSNTAYMELSLTSDASAVYYCARG-----IAYWQGQTLVTVA 132
QY 121 AKTTPSVVPLAPGSAQAQNSMTVLGCLVKGYFPEPVTVTWNSGSLSSGVHTTFAVLQSD 180
Db 133 AKTTPSVVPLAPGSAQAQNSMTVLGCLVKGYFPEPVTVTWNSGSLSSGVHTTFAVLQSD 192
QY 181 LYTLSSTVTPSSVTPSETVTCNVAHPASSTKVDKIKVPRDSGSPSEKSEINEKDLRKK 240
Db 193 LYTLSSTVTPSSVTPSETVTCNVAHPASSTKVDKIKVPRDCG----- 235
QY 241 SELQGTALGNKQIYYNSKAITSEKSDAQFLTNTLLFKGFTGHPWYNLDLVLGSTA 300
Db 236 CKFCICTVPEVSSVFIPPK-----PKDVLITIL----- 264
QY 301 ATSEYEGSSVDLYGAYGYOCAGGTGNKTCMVGTVLHNNRLTEBKKVPINLWIDGKQ 360

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Db 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD--- 289
Qy 361 TTVPIDKVKTSKEV-----TVQELDLQARHLYHGK-FGL-YNSDSFGGKVQVGLIYF 411
Db 290 -DVEVHTAQTPREQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAPPAPIEK----- 343
Qy 412 HSEGSTVSVDLPDAQGQYPTDLLRIYRDNNTTISSTLSLSISLYLYTTSIVMTQTPTSLLV 471
Db 344 -----TISK----- 348
Qy 472 SAGDRVITICKASQSVNDVAMVYQKPGQPKLLISYTSRYAGVDPDRFSGSGYGTDFTL 531
Db 349 ----- 348
Qy 532 TISSVQAEDAAYFCQDYNSPPTFGGKLEIKRADAAPTYSIFPPSSEQLTSGGASVV 591
Db 349 -----KGRPKAPQVYTIPTPPKEQMAKDKVSLT 375
Qy 592 CFLNPFYPKDINVWKIDGSRQNGVLNSWTQDQSDKSTYSMSSTLTLTCKDEYERHNSYT 651
Db 434 CSVLHE 439
Qy 376 CMITDFPEDITVEWQNGQPAEN-YKNTQPIMDT-DGSYFYVYSKLVNOKSNWEAGNTFI 433
Qy 652 CEATHK 657
Db 434 CSVLHE 439

RESULT 35
US-09-903-327A-13
; Sequence 13, Application US/09903327A
; Patent No. US20020164333A1
; GENERAL INFORMATION:
; APPLICANT: Nemerow, Glen R.
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
; TITLE OF INVENTION: GENE
; TITLE OF INVENTION: DELIVERY
; FILE REFERENCE: 22908-1228
; CURRENT APPLICATION NUMBER: US/09/903,327A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/613,017
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain
; OTHER INFORMATION: and EGF mature peptide
US-09-903-327A-13

Query Match 29.1%; Score 1023.5; DB 3; Length 493;
Best Local Similarity 37.4%; Pred. No. 6.6e-39;
Matches 249; Conservative 51; Mismatches 111; Indels 255; Gaps 14;

Qy 1 EVQLQSGDPLVKPGASVKISKASGYSTGYIMHWVKQSPGKLEWIGRIINPNNGVTLY 60
Db 20 EVQLQSGPELVKPGASVKISKASGYTFTDYNMHWVKQSHGKSLIEWIGYIYPKGGTGY 79
Qy 61 NQKFKDKATLTVDKSTTAYMELRSLTSDSAVYYCARSTMTITNYMDYWGQGTSTVVS 120
Db 80 NQKFKSKATLTDTSSNTAYMELRSLTSDSAVYYCARG-----IAYWQQTLLTVSA 132
Qy 121 AKTTPPSVYPLAPGSAQTNSMTVTLGCLVKGYPEPEPTVTWNVSGSLSSGGVHTFPVQLQSD 180
Db 133 AKTTPSVYPLACGSAQTNSMTVTLGCLVKGYPEPEPTVTWNVSGSLSSGGVHTFPVQLQSD 192
Qy 181 LYTLSSTVTPSPSTWPSSETVTCNVAHPASSTKVDKIVPRDSGGPSEKSEETNEKDLRKK 240
Db 193 LYTLSSTVTPSPSTWPSSETVTCNVAHPASSTKVDKIVPRDCG----- 235
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Qy 241 SEIQGTALGNLKOIYYNSKAITSSSEKSAQDLTLLFKGFFTGHPWYNDLLVDLGSTA 300
Db 236 CKPCICTPEVSSSVFIFPPK-----PKDVLTTITL----- 264
Qy 301 ATSEYEGSSVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLTBEKKVPINLWIDGKQ 360
Db 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD--- 289
Qy 361 TTVPIDKVKTSKEV-----TVQELDLQARHLYHGK-FGL-YNSDSFGGKVQVGLIYF 411
Db 290 -DVEVHTAQTPREQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAPPAPIEK----- 343
Qy 412 HSEGSTVSVDLPDAQGQYPTDLLRIYRDNNTTISSTLSLSISLYLYTTSIVMTQTPTSLLV 471
Db 344 -----TISK----- 348
Qy 472 SAGDRVITICKASQSVNDVAMVYQKPGQPKLLISYTSRYAGVDPDRFSGSGYGTDFTL 531
Db 349 ----- 348
Qy 532 TISSVQAEDAAYFCQDYNSPPTFGGKLEIKRADAAPTYSIFPPSSEQLTSGGASVV 591
Db 349 -----KGRPKAPQVYTIPTPPKEQMAKDKVSLT 375
Qy 592 CFLNPFYPKDINVWKIDGSRQNGVLNSWTQDQSDKSTYSMSSTLTLTCKDEYERHNSYT 651
Db 376 CMITDFPEDITVEWQNGQPAEN-YKNTQPIMDT-DGSYFYVYSKLVNOKSNWEAGNTFI 433
Qy 652 CEATHK 657
Db 434 CSVLHE 439

RESULT 36
US-09-903-327A-12
; Sequence 12, Application US/09903327A
; Patent No. US20020164333A1
; GENERAL INFORMATION:
; APPLICANT: Nemerow, Glen R.
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
; TITLE OF INVENTION: GENE
; TITLE OF INVENTION: DELIVERY
; FILE REFERENCE: 22908-1228
; CURRENT APPLICATION NUMBER: US/09/903,327A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/613,017
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain
; OTHER INFORMATION: and IGF-1 mature peptide
US-09-903-327A-12

Query Match 29.1%; Score 1023.5; DB 3; Length 510;
Best Local Similarity 37.4%; Pred. No. 6.8e-39;
Matches 249; Conservative 51; Mismatches 111; Indels 255; Gaps 14;

Qy 1 EVQLQSGDPLVKPGASVKISKASGYSTGYIMHWVKQSPGKLEWIGRIINPNNGVTLY 60
Db 20 EVQLQSGPELVKPGASVKISKASGYTFTDYNMHWVKQSHGKSLIEWIGYIYPKGGTGY 79
Qy 61 NQKFKDKATLTVDKSTTAYMELRSLTSDSAVYYCARSTMTITNYMDYWGQGTSTVVS 120
Db 80 NQKFKSKATLTDTSSNTAYMELRSLTSDSAVYYCARG-----IAYWQQTLLTVSA 132
Qy 121 AKTTPPSVYPLAPGSAQTNSMTVTLGCLVKGYPEPEPTVTWNVSGSLSSGGVHTFPVQLQSD 180
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Db	133	AKTTPSVPLAPGSAATNSMTLGLVKGYFPEPVTWNSGSLSSGVHTPAVLQSD	192
Qy	181	LYTLSSSVTPSSTWSEVTVCNVAHPASSTKVDDKKIVPRDGGPSEKSEINEKDLRKK	240
Db	193	LYTLSSSVTPSSTWSEVTVCNVAHPASSTKVDDKKIVPRDCG	235
Qy	241	SELQGTALGNLKOIYYNSKAITSSSEKADQFTLTLFKGFTGHPWYNLLVLDLSTA	300
Db	236	CKPCICTVPEVSSVFIFPPK	264
Qy	301	ATSEYEGSSVDLYGAYGYOCAGGTENKTCMYGGVTLHNNRLTBKPKVPINLWIDGKQ	360
Db	265	TP-KVTCVVVDIS	289
Qy	361	TTVPIDKVTSSKEV	411
Db	290	DVEHTAQTPREEQFNSTFRSVSELPIMHQDLNGKEFKCRVNSAAPAPIEK	343
Qy	412	HSSEGSTVSYDLFDAQGYPDTLRLIYRDNTTSSLSISLYLYTTSIVMTQPTSLLV	471
Db	344	TISK	348
Qy	472	SAGDRVITTCASQSVNSDVAMVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDFTL	531
Db	349		348
Qy	532	TISSVQAEADAAYFCQDYNPSPTFGGKLEIKRADAAPTYSIFPPSSBOLTSGGASVV	591
Db	349	KGRPAPQVYTI	375
Qy	592	CFLNFPKIDINVKKIDSERQNGVNSWTDODSKDSTYSMSLTTLTKDEYERHNSYT	651
Db	376	CMITDFPEDITVEWQNGQPAEN-YKNTQPIMDT-DGSYFVYSLNVQKSNWEAGNTFI	433
Qy	652	CEATHK 657	
Db	434	CSVLHE 439	
RESULT 37			
US-09-903-327A-6			
; Sequence 6, Application US/09903327A			
; Patent No. US2002016433A1			
; GENERAL INFORMATION:			
; APPLICANT: Nemerow, Glen R.			
; APPLICANT: Li, Erluang			
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET			
; TITLE OF INVENTION: GENE			
; TITLE OF INVENTION: DELIVERY			
; FILE REFERENCE: 22908-1228			
; CURRENT APPLICATION NUMBER: US/09/903,327A			
; CURRENT FILING DATE: 2001-07-10			
; PRIOR APPLICATION NUMBER: 09/613,017			
; PRIOR FILING DATE: 2000-07-10			
; NUMBER OF SEQ ID NOS: 33			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 6			
; LENGTH: 438			
; TYPE: PRT			
; ORGANISM: Mouse			
; FEATURE:			
; NAME/KEY: PEPTIDE			
; LOCATION: (0)...(0)			
; OTHER INFORMATION: Portion of DAV-1 heavy chain used for fusion protein			
; OTHER INFORMATION: bifunctional antibody			
US-09-903-327A-6			
Query Match			
Best Local Similarity 29.0%; Score 1022.5; DB 3; Length 438;			
Matches 249; Conservative 37.4%; Pred No. 6.5e-39;			
Indels 255; Gaps 14;			
Qy	1	EVQLQSGDPLVPGASVKISKASGYFTGYIMHWVKQSPGKLEWIGRINPNNGVTLY	60

Db	20	EVQLQSGDPLVPGASVKISKASGYFTGYIMHWVKQSPGKLEWIGRINPNNGVTLY	79
Qy	61	NQKFKDKATLTVDKSTTAYMELRSLTSDSAVYCARSTMTNYVMDYMGQGTSTVTSS	120
Db	80	NQKFKSKATLTVDKSTTAYMELRSLTSDSAVYCARSTMTNYVMDYMGQGTSTVTSS	132
Qy	121	AKTTPSVPLAPGSAATNSMTLGLVKGYFPEPVTWNSGSLSSGVHTPAVLQSD	180
Db	133	AKTTPSVPLAPGSAATNSMTLGLVKGYFPEPVTWNSGSLSSGVHTPAVLQSD	192
Qy	181	LYTLSSSVTPSSTWSEVTVCNVAHPASSTKVDDKKIVPRDGGPSEKSEINEKDLRKK	240
Db	193	LYTLSSSVTPSSTWSEVTVCNVAHPASSTKVDDKKIVPRDCG	235
Qy	241	SELQGTALGNLKOIYYNSKAITSSSEKADQFTLTLFKGFTGHPWYNLLVLDLSTA	300
Db	236	CKPCICTVPEVSSVFIFPPK	264
Qy	301	ATSEYEGSSVDLYGAYGYOCAGGTENKTCMYGGVTLHNNRLTBKPKVPINLWIDGKQ	360
Db	265	TP-KVTCVVVDIS	289
Qy	361	TTVPIDKVTSSKEV	411
Db	290	DVEHTAQTPREEQFNSTFRSVSELPIMHQDLNGKEFKCRVNSAAPAPIEK	343
Qy	412	HSSEGSTVSYDLFDAQGYPDTLRLIYRDNTTSSLSISLYLYTTSIVMTQPTSLLV	471
Db	344	TISK	348
Qy	472	SAGDRVITTCASQSVNSDVAMVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDFTL	531
Db	349		348
Qy	532	TISSVQAEADAAYFCQDYNPSPTFGGKLEIKRADAAPTYSIFPPSSBOLTSGGASVV	591
Db	349	KGRPAPQVYTI	375
Qy	592	CFLNFPKIDINVKKIDSERQNGVNSWTDODSKDSTYSMSLTTLTKDEYERHNSYT	651
Db	376	CMITDFPEDITVEWQNGQPAEN-YKNTQPIMDT-DGSYFVYSLNVQKSNWEAGNTFI	433
Qy	652	CEATH 656	
Db	434	CSVLH 438	
RESULT 38			
US-10-679-620-94			
; Sequence 94, Application US/10679620			
; Publication No. US20040110930A1			
; GENERAL INFORMATION:			
; APPLICANT: Large Scale Biology			
; APPLICANT: Reini, Stephen J.			
; APPLICANT: Edwards, Patricia C.			
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING			
; FILE REFERENCE: 34150-004A			
; CURRENT APPLICATION NUMBER: US/10/679,620			
; CURRENT FILING DATE: 2003-10-03			
; PRIOR APPLICATION NUMBER: 60/415,940			
; PRIOR FILING DATE: 2002-10-03			
; NUMBER OF SEQ ID NOS: 122			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 94			
; LENGTH: 700			
; TYPE: PRT			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: pLSBC1773, see Example 14			
US-10-679-620-94			
Query Match			
28.4%; Score 1000; DB 4; Length 700;			

Best Local Similarity 36.8%; Pred. No. 1.1e-37; Matches 242; Conservative 54; Mismatches 131; Indels 230; Gaps 11;	
Qy	1 EVQLQQGGPDLVKPGASVKISKASGYSFTGYMHVWKQSPGKGLEWIGRINPNNGVTLY 60
Db	257 QVQLQQSGPELVKPGASLKSLCTASGNFKDITYIHVWKQREQGLEWIGRIYPNGVTRY 316
Qy	61 NQPKDKATLTVDKSSSTAYMELRSLTSEDSAVYICARSTMITNYMDYWGQGSTVTVSS 120
Db	317 DPKFDKATITADTSSNTAVYLVQSRLTSEDVAVYICRWGGDGFVMDYWGQGSATVTSS 376
Qy	121 AKITPPSVYPLAPGSAQAQTNMWTGLCLVKGYFPEPVTVTVNSGSLSGVHTTFAVLQSD 180
Db	377 AKITPPSVYPLAPGSAQAQTNMWTGLCLVKGYFPEPVTVTVNSGSLSGVHTTFAVLQSD 436
Qy	181 LYTLSSTVTPSSWTPSETVTCNVAHPASSTKVDKIVPRDSGGPSEKSEBINEKDLRKK 240
Db	437 LYTLSSTVTPSSWTPSETVTCNVAHPASSTKVDKIVPRDCG----- 479
Qy	241 SELGTALGNLKQIYYYNKSAITSEKSDAOFLTNTLLFKGFFTHGHPWYNDLLVDLGSTA 300
Db	480 -----CKPC 483
Qy	301 ATSEYEGSSVDLYGAYGYCAGGTPNKTA CMYGGVTLHDNNRLTEBKVKPINLWIDGKQ 360
Db	484 ICTVPEVSSVFIF-----PPK-----PKDVLITLTLPKV 512
Qy	361 TTVPIDKVKTSKKEVTYQELDLQARHVLHGKFLYNSDSFGKVQVQGLIVPHSSEGSTVS 420
Db	513 TCVVVD---ISKDDPEVQ-----FS 529
Qy	421 YDLFDAQQGYPDTLRLIYRDNTTISSTLSISLYLTTSIVMTQTPTSLVSAAGDRVIT 480
Db	530 WFVDDVVEHTAQTQPREEQFNSTPRSVS-----ELPIHQD----- 565
Qy	481 CKASQSVSNDAVWYQKPGQSPKLLISYTSRYAGVDPDRSGSGYGTDTFTLTISVQAED 540
Db	566 -----WLNDRFEKC-----RVNSAAPPAPIEKTIS----- 590
Qy	541 AAVYFCQDYNSSPTFGGGTKLEIKRADAAPTSGIFPPSSBQLTSGGASVVCFLNFPVK 600
Db	591 -----KTKGRPKAPQVVTIPPKPEQMAKDVKVSLTCMTIDTFPE 628
Qy	601 DINVKWIDGSEQRQGVNLNWDQDSKDYSSMSSTLTLTLDKDEYERHNSVYCEATHK 657
Db	629 DITVEMWNGQAPSN-VKNTQPIWDT-DGSFYVYKLVNOKNSWEAGNTFTCSVLHE 683

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RESULT 39
US-11-132-143-94
; Sequence 94, Application US/11132143
; Publication No. US20050207977A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reinn, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/11/132,143
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: US/10/679,620
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 94
; LENGTH: 700
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pLSBC1773, see Example 14
US-11-132-143-94

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RESULT 40
US-10-071-485-90
; Sequence 90, Application US/10071485
; Publication No. US20030099648A1
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Auge
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; TITLE OF INVENTION: SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0

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```
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
; US-10-071-485-90

Query Match      27.8%; Score 980.5; DB 4; Length 711;
Best Local Similarity 35.3%; Pred. No. 8.3e-37;
Matches 254; Conservative 103; Mismatches 180; Indels 183; Gaps 23;

Qy 1 EVLOQSGDPLVKPGASVKISCKASGYSTGYMHVWVKSPGKGLGWIGRINPNNGVTLY 60
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 21 QVQLVQSGSELKPGASVKISCKASGYTFTDYGMNVWVKQAPGQGLKWMGWINTYTGESTY 80
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 NQFKDKATLTVDKSSITTAAMELSLTSDSAVYICARSTMTITNYVDYWGQGTSTVTVSS 120
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 81 VDDFKGRFVFSLDTSSAAYLQISSLKAEADTATYFCARRGF---YANDYWGQGTSTVTVSS 137
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 121 AKTTPSVVPLAPGSAQTNSMVTGLCLVKGYPEPTVTWNSGSLSSGSHVHTPPAVLQSD 180
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 138 ASTKGSVPFLAPSSKSTSGTAAALGCLVKDYPEPTVWNSGALTSGVHTFPAVLQSS 197
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 181 -LYTSSSVTPSSWSPSETVTCNVAHPASSTKVDKKIIPRDS-----GG 224
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 198 GLYSLSVTVTPSSSLGTQTYICNVNHPKSNTKVDKRVPEKSCDKTKHTCCPCPAPELLGG 257
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 225 PS-----EKSEI-----NEKDLRKSELOGTALGNLK---QIYYN 258
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 258 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPRBEQYN 317
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 259 S-----KAITSS-EK-----SADQ 271
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 318 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPASIIEKTISKAKGQPREPOVYTLPPSREE 377
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 272 FLTN-----TLLPKGFTGHPWYNDLLVDLGSTA-ATSEYEGSS--VDLYGAYGYQCAGG 324
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 378 MTKNQVSLTCLVKGFYP-----SDIAVEWESNGOPENNYKTTTPVLDSDGSPFLYSKL-- 430
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 325 TPNKTAACMYGGV-----TLHD--NNRLTEEK-----KVINLWIDGKQTTPIDKV 368
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 431 TVDKSRWQGNVPSFCVSMHEALHNHYTQKSLSLSPGKLGSGSQVQLVQSGSELKPGASV 490
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 369 KTSKKEVTQELDQARHLYLHGKFGLYNSDSFGKVGQRLIVFHSSEGSVSYDLPDAQ 428
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 491 KLSCK-----ASGYTFTDYGMNVWVKQAPGQGLKWMGWINTYTGESTYVD--DFKG 538
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 429 QYPDTLRIYRDNTTISSTLSIS-----LYLYT----- 457
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 539 RF-----VPSLDTSSAAYLQISSLKAEADTATYFCARRGFYANDYWGQGTSTVTVSSGGG 592
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 458 -----TSIVMTQPTSLLSVAGDRVTTICKASQSVNDVAVYQKPGQSPKLLI 506
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 593 GSGGGSGGGGSDIVLTQSPATMSAASGERVITTCASSSISY-MFWYHQPQGSPLLI 651
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 507 SYTSSRYAGVDPDRFSGSGYGTDFLTATISSVQAEADAAVYFCQDYNPPTFGGQTKLEIKR 566
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 652 YDTSNLSAGVPAFPFGSGSGTSLTISRMEPEDFATYFCHQSSSYPTFTFGQGTLEIKR 711
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 41
US-10-985-581-90
; Sequence 90, Application US/10985581
; Publication No. US20050129693A1
; GENERAL INFORMATION:
; APPLICANT: Buysee, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: 11362.0015.DVUS02
; CURRENT APPLICATION NUMBER: US/10/985,581
; CURRENT FILING DATE: 2004-11-10
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; PRIOR APPLICATION NUMBER: US 10/071,485
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: US 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-10-985-581-90

Query Match      27.8%; Score 980.5; DB 5; Length 711;
Best Local Similarity 35.3%; Pred. No. 8.3e-37;
Matches 254; Conservative 103; Mismatches 180; Indels 183; Gaps 23;

Qy 1 EVLOQSGDPLVKPGASVKISCKASGYSTGYMHVWVKSPGKGLGWIGRINPNNGVTLY 60
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 21 QVQLVQSGSELKPGASVKISCKASGYTFTDYGMNVWVKQAPGQGLKWMGWINTYTGESTY 80
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 NQFKDKATLTVDKSSITTAAMELSLTSDSAVYICARSTMTITNYVDYWGQGTSTVTVSS 120
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 81 VDDFKGRFVFSLDTSSAAYLQISSLKAEADTATYFCARRGF---YANDYWGQGTSTVTVSS 137
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 121 AKTTPSVVPLAPGSAQTNSMVTGLCLVKGYPEPTVTWNSGSLSSGSHVHTPPAVLQSD 180
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 138 ASTKGSVPFLAPSSKSTSGTAAALGCLVKDYPEPTVWNSGALTSGVHTFPAVLQSS 197
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 181 -LYTSSSVTPSSWSPSETVTCNVAHPASSTKVDKKIIPRDS-----GG 224
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 198 GLYSLSVTVTPSSSLGTQTYICNVNHPKSNTKVDKRVPEKSCDKTKHTCCPCPAPELLGG 257
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 225 PS-----EKSEI-----NEKDLRKSELOGTALGNLK---QIYYN 258
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 258 PSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPRBEQYN 317
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 259 S-----KAITSS-EK-----SADQ 271
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 318 STYRVSVSLTVLHQDWLNGKEYKCKVSNKALPASIIEKTISKAKGQPREPOVYTLPPSREE 377
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 272 FLTN-----TLLPKGFTGHPWYNDLLVDLGSTA-ATSEYEGSS--VDLYGAYGYQCAGG 324
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 378 MTKNQVSLTCLVKGFYP-----SDIAVEWESNGOPENNYKTTTPVLDSDGSPFLYSKL-- 430
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 325 TPNKTAACMYGGV-----TLHD--NNRLTEEK-----KVINLWIDGKQTTPIDKV 368
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 431 TVDKSRWQGNVPSFCVSMHEALHNHYTQKSLSLSPGKLGSGSQVQLVQSGSELKPGASV 490
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 369 KTSKKEVTQELDQARHLYLHGKFGLYNSDSFGKVGQRLIVFHSSEGSVSYDLPDAQ 428
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 491 KLSCK-----ASGYTFTDYGMNVWVKQAPGQGLKWMGWINTYTGESTYVD--DFKG 538
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 429 QYPDTLRIYRDNTTISSTLSIS-----LYLYT----- 457
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 539 RF-----VPSLDTSSAAYLQISSLKAEADTATYFCARRGFYANDYWGQGTSTVTVSSGGG 592
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 458 -----TSIVMTQPTSLLSVAGDRVTTICKASQSVNDVAVYQKPGQSPKLLI 506
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 593 GSGGGSGGGGSDIVLTQSPATMSAASGERVITTCASSSISY-MFWYHQPQGSPLLI 651
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 507 SYTSSRYAGVDPDRFSGSGYGTDFLTATISSVQAEADAAVYFCQDYNPPTFGGQTKLEIKR 566
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 652 YDTSNLSAGVPAFPFGSGSGTSLTISRMEPEDFATYFCHQSSSYPTFTFGQGTLEIKR 711
Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

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RESULT 42
US-10-410-907A-36
; Sequence 36, Application US/10410907A
; Publication No. US20030215880A1
; GENERAL INFORMATION:
; APPLICANT: Dennis R. Burton
; APPLICANT: R. Anthony Williamson
; APPLICANT: Gianluca Moroncini
; TITLE OF INVENTION: MOTIF-GRAFTED HYBRID POLYPEPTIDES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 22908-1229
; CURRENT APPLICATION NUMBER: US/10/410,907A
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/371,610
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D18 Heavy Chain
US-10-410-907A-36

Query Match      27.8%; Score 979.5; DB 4; Length 223;
Best Local Similarity 87.4%; Pred. No. 3.1e-37;
Matches 194; Conservative 7; Mismatches 16; Indels 5; Gaps 2;

QY 1 EVQLQSGPDLVKPGASVKISKASGYSFTGYMHVWVKSPGKGLIEWIGRIINPNNGVTL 59
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 EVQLLEQSGPELVKPGSSVKISKASRYTFTDNDMDVKQSHGKRLIEWIYIPNTGVIG 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 60 YNQKFKDKATLTVDKSSSTAYMELRLTSDSDSAVYYCARSTMITNYVMYWGQTSVTVS 119
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 YNQRFKGKATLTVDKSSSTAYMELRLTSDSDSAVYYCAG----FYGMGYWGQTSVTVS 118
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 120 SAKTTPPSVYVPLAPGSAQTNSMVTGLCLVKGYFPEPVTVTWNSGSLSSGVHTEFPAVLQS 179
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 119 SAKTTPPSVYVPLAPGSAQTNSMVTGLCLVKGYFPEPVTVTWNSGSLSSGVHTEFPAVLQY 178
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 180 DLYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKVDKKIIVPRD 221
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 179 DLYTMSSSVTVPSSTWPSSETVTCNVAHPASSTKVDKKIIVPRD 220
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 43
US-10-334-235-37
; Sequence 37, Application US/103334235
; Publication No. US20040131591A1
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Ltd.
; APPLICANT: Kingsman, Alan
; APPLICANT: Bebbington, Christopher
; APPLICANT: Carroll, Miles
; APPLICANT: Ellard, Fiona
; APPLICANT: Kingsman, Susan
; APPLICANT: Myers, Kevin
; APPLICANT: Lamikandra, Abigail
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: 532682000920
; CURRENT APPLICATION NUMBER: US/10/334,235
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 10/060,585
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 09/445,375
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 243

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mature secreted protein of 574 scFv, designated
; US-10-334-235-37

Query Match      27.6%; Score 972.5; DB 4; Length 243;
Best Local Similarity 40.1%; Pred. No. 6.9e-37;
Matches 227; Conservative 3; Mismatches 13; Indels 323; Gaps 5;

QY 1 EVQLQSGPDLVKPGASVKISKASGYSFTGYMHVWVKSPGKGLIEWIGRIINPNNGVTLY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EVQLQSGPDLVKPGASVKISKASGYSFTGYMHVWVKSPGKGLIEWIGRIINPNNGVTLY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 NQKFKDKATLTVDKSSSTAYMELRLTSDSDSAVYYCARSTMITNYVMYWGQTSVTVS 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 NQKFKDKATLTVDKSSSTAYMELRLTSDSDSAVYYCARSTMITNYVMYWGQTSVTVS - 119
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 AKTTPPSVYVPLAPGSAQTNSMVTGLCLVKGYFPEPVTVTWNSGSLSSGVHTEFPAVLQSD 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 ----- 119
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 LYTLSSTVTPSSSTWPSSETVTCNVAHPASSTKVDKKIIVPRDSGGPSEKSEINEKDLRKK 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 ----- 122
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 SELQGTALGNLKKIYYNYSKAITSEKSDAQDLTNTLLFKGFTGHPWYNDLLVDLGSTA 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 123 ----- 122
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 301 ATSEYEGSSVDLYGAYGYQCAGTGNKTACVMYGGVTLHDNNRLTTEKKVPINLWIDGKQ 360
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 123 ----- 132
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 361 TTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVGRLIVFHSSEGSTVS 420
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 133 ----- 134
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 421 YDLFDAQQYPTLLRIYRDNTTISSTLSISLYLTTSIVMTQTPTFTLLVSGADRVTTIT 480
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 135 ----- 157
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 481 CKASQSVNDVAWYQKPGQSPKLLISYTSRSYAGVDPDRFSGSGYGTDFLTLTISVQAE 540
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 158 CKASQSVNDVAWYQKPGQSPKLLISYTSRSYAGVDPDRFSGSGYGTDFLTLTISLQAE 217
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 541 AAVYFCQQDYNSPPTFGGQTKLEIKR 566
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 218 LAVYFCQQDYNSPPTFGGQTKLEIKR 243
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 44
US-10-334-235-39
; Sequence 39, Application US/103334235
; Publication No. US20040131591A1
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Ltd.
; APPLICANT: Kingsman, Alan
; APPLICANT: Bebbington, Christopher
; APPLICANT: Carroll, Miles
; APPLICANT: Ellard, Fiona
; APPLICANT: Kingsman, Susan
; APPLICANT: Myers, Kevin
; APPLICANT: Lamikandra, Abigail
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: 532682000920
; CURRENT APPLICATION NUMBER: US/10/334,235
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 10/060,585
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
```

; PRIOR APPLICATION NUMBER: US 09/445,375
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of B7-1.5T4.1
US-10-334-235-39

Query Match 27.5%; Score 967.5; DB 4; Length 488;
Best Local Similarity 40.0%; Pred. No. 2.3e-36;
Matches 226; Conservative 3; Mismatches 13; Indels 323; Gaps 5;
QY 1 EVOLQSGPDLVPGASVKISCKASGYFTGYMHVWKQSPGKLEWIGRINPNNGVTL 60
Db |||||
QY 247 EVOLQSGPDLVPGASVKISCKASGYFTGYMHVWKQSPGKLEWIGRINPNNGVTL 306
Db |||||
QY 61 NQKFKDKATLTVDKSTTAYMELRSLTSDSAVYICARSTMTITNYVMDYWGQTSVTSS 120
Db |||||
QY 307 NQKFKDKATLTVDKSTTAYMELRSLTSDSAVYICARSTMTITNYVMDYWGQTSVTSS- 365
QY 121 AKTTPPSVYPLAPGSAQAQNSMTLGLVKGYFPEPVTVTWNSGSLSSGVHTTTPAVLQSD 180
Db -----
QY 366 ----- 365
QY 181 LYTLSSSVTPSPSTWPSSETVTCNVAHPASSTKVDKIVPRDSGGPSEKSEINEKDLRKK 240
Db |||||
QY 366 -----SGG----- 368
QY 241 SELQGTALGNLKOIYYNSKAITSEKSAQDLTNTLLFKGFTGHPWYNDLLVDLGSTA 300
Db -----
QY 369 ----- 368
QY 301 ATSEYEGSSVDLYGAYGYQCAGTPNKTAQMWGGVTLHDNNRLTEKKVPINLWIDGKQ 360
Db |||||
QY 369 -----GGSGGGT----- 378
QY 361 TTVPIDKVTSSKEVTVQELDLQARHLYHGKFLYNSDSFGKQVQRGLIVFHSSEGSTVS 420
Db |||||
QY 379 -----GG----- 380
QY 421 YDLFDAQQGYPTDLLRIYRDNTTISSTLSLSLYLTTSIVMTQTPTSLVLSAGDRVIT 480
Db :|||
QY 381 -----SSIVMTQTPTFLVLSAGDRVIT 403
QY 481 CKASQSVNDVAMVYQKPGQSPKLLISYTSRYAGVDPDRFSGGYGTDFTLTISVQAE 540
Db |||||
QY 404 CKASQSVNDVAMVYQKPGQSPKLLISYTSRYAGVDPDRFSGGYGTDFTLTISVQAE 463
QY 541 AAVYFCQDYNPSPTFGGKLEIK 565
Db |||||
QY 464 LAVYFCQDYNPSPTFGGKLEIK 488

RESULT 45
US-10-473-127-1954
; Sequence 1954, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 1954
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1954
Query Match 27.5%; Score 967.5; DB 5; Length 488;
Best Local Similarity 40.0%; Pred. No. 2.3e-36;
Matches 226; Conservative 3; Mismatches 13; Indels 323; Gaps 5;
QY 1 EVOLQSGPDLVPGASVKISCKASGYFTGYMHVWKQSPGKLEWIGRINPNNGVTL 60
Db |||||
QY 247 EVOLQSGPDLVPGASVKISCKASGYFTGYMHVWKQSPGKLEWIGRINPNNGVTL 306
Db |||||
QY 61 NQKFKDKATLTVDKSTTAYMELRSLTSDSAVYICARSTMTITNYVMDYWGQTSVTSS 120
Db |||||
QY 307 NQKFKDKATLTVDKSTTAYMELRSLTSDSAVYICARSTMTITNYVMDYWGQTSVTSS- 365
QY 121 AKTTPPSVYPLAPGSAQAQNSMTLGLVKGYFPEPVTVTWNSGSLSSGVHTTTPAVLQSD 180
Db -----
QY 366 ----- 365
QY 181 LYTLSSSVTPSPSTWPSSETVTCNVAHPASSTKVDKIVPRDSGGPSEKSEINEKDLRKK 240
Db |||||
QY 366 -----SGG----- 368
QY 241 SELQGTALGNLKOIYYNSKAITSEKSAQDLTNTLLFKGFTGHPWYNDLLVDLGSTA 300
Db -----
QY 369 ----- 368
QY 301 ATSEYEGSSVDLYGAYGYQCAGTPNKTAQMWGGVTLHDNNRLTEKKVPINLWIDGKQ 360
Db |||||
QY 369 -----GGSGGGT----- 378
QY 361 TTVPIDKVTSSKEVTVQELDLQARHLYHGKFLYNSDSFGKQVQRGLIVFHSSEGSTVS 420
Db |||||
QY 379 -----GG----- 380
QY 421 YDLFDAQQGYPTDLLRIYRDNTTISSTLSLSLYLTTSIVMTQTPTSLVLSAGDRVIT 480
Db :|||
QY 381 -----SSIVMTQTPTFLVLSAGDRVIT 403
QY 481 CKASQSVNDVAMVYQKPGQSPKLLISYTSRYAGVDPDRFSGGYGTDFTLTISVQAE 540
Db |||||
QY 404 CKASQSVNDVAMVYQKPGQSPKLLISYTSRYAGVDPDRFSGGYGTDFTLTISVQAE 463
QY 541 AAVYFCQDYNPSPTFGGKLEIK 565
Db |||||
QY 464 LAVYFCQDYNPSPTFGGKLEIK 488

RESULT 46
US-10-473-127-1963
; Sequence 1963, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21

```
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1963
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-1963

Query Match      27.5%; Score 967.5; DB 5; Length 488;
Best Local Similarity 40.0%; Pred. No. 2.3e-36;
Matches 226; Conservative 3; Mismatches 13; Indels 323; Gaps 5;

QY 1 EVLOQSGDPLVKPGASVKISCKASGYSTGYMHVWKSPGKLEWIGRINPNNGVTLY 60
Db 247 EVLOQSGDPLVKPGASVKISCKASGYSTGYMHVWKSPGKLEWIGRINPNNGVTLY 306
QY 61 NQKFKDKATLTVDKSTTAYMELRLSLTSDSAVYYCARSTMTITNYMDYWGQTSVTSS 120
Db 307 NQKFKDKATLTVDKSTTAYMELRLSLTSDSAVYYCARSTMTITNYMDYWGQTSVTSS 365
QY 121 AKTTTPSVVPLAPGSAQAQNSMVTLCGLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSD 180
Db 366 -----
QY 181 LYTSSSVTPSPSTWPESETVTCNVAHPASSTKVDKIIIPRDGGPSEKSEINEKDLRKK 240
Db 366 -----
QY 241 SELQGTALGNLKIYYNYSKAITSEKSAQDLTNTLLFKGFTGHPWYNLLVDLGSTA 300
Db 369 -----
QY 301 ATSEYEGSDVLYGAYGYQCAAGTGNKTCMVGVTLLHNNRLTBEKKVPINLMIDGKQ 360
Db 369 -----
QY 361 TTVPIDKVTSKKEVTVQELDLQARHYLHGKPGCLYNSDFGKVGQRLIVFHSSEGSTVS 420
Db 379 -----
QY 421 YDLFDAQGYPDTLRIYRDNTTISSTLSLSLYLTTISVMTQTPTSLLSAGDRVTIT 480
Db 381 -----
QY 481 CKASQSVNDVAVYQKPGQSKLLISYTSRYAGVDPDRFSGSGYGTDTFTLTSSVQABD 540
Db 404 CKASQSVNDVAVYQKPGQSKLLISYTSRYAGVDPDRFSGSGYGTDTFTLTSSVQABD 463
QY 541 AAVYFCQDYNSPPTFGGKTLEIK 565
Db 464 LAVYFCQDYNSPPTFGGKTLEIK 488

RESULT 47
US-10-488-074-83
; Sequence 83, Application US/10488074
; Publication No. US20050118638A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Bernard Rees
; APPLICANT: Furmaniak, Jadwiga
; APPLICANT: Sanders, Jane Pina
; TITLE OF INVENTION: Epitope Regions of a Thyrotrophin (TSH) Receptor, Uses Thereof and
; FILE REFERENCE: 7500.412USMO
; CURRENT APPLICATION NUMBER: US/10/488,074
```

```
; CURRENT FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: PCT/GB02/03831
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: GB 0120649.9
; PRIOR FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: GB 0215212.2
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 209
; TYPE: PRT
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Figures 45 & 46
US-10-488-074-83

Query Match      27.4%; Score 966.5; DB 5; Length 209;
Best Local Similarity 87.4%; Pred. No. 1.1e-36;
Matches 187; Conservative 9; Mismatches 13; Indels 5; Gaps 1;

QY 1 EVLOQSGDPLVKPGASVKISCKASGYSTGYMHVWKSPGKLEWIGRINPNNGVTLY 60
Db 1 DVQLKHSGPDLVKPGASVKISCKASGYSTGYTMNVWKSHGKNLDWIGLINPYNGGTSY 60
QY 61 NQKFKDKATLTVDKSTTAYMELRLSLTSDSAVYYCARSTMTITNYMDYWGQTSVTSS 120
Db 61 DQKFKGKATLTVDKSSSTAYMELLSLTSDSAVYYCARDGL-----MDYWGQTSVTSS 115
QY 121 AKTTTPSVVPLAPGSAQAQNSMVTLCGLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSD 180
Db 116 AKTTTPSVVPLAPGSAQAQNSMVTLCGLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSD 175
QY 181 LYTSSSVTPSPSTWPESETVTCNVAHPASSTKVD 214
Db 176 LYTSSSVTPSPSTWPESETVTCNVAHPASSTKVD 209

RESULT 48
US-10-682-845-38
; Sequence 38, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: LanzaVecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 468
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: OKT3 heavy chain with signal peptide
US-10-682-845-38

Query Match      27.4%; Score 966; DB 4; Length 468;
Best Local Similarity 34.9%; Pred. No. 2.5e-36;
Matches 241; Conservative 56; Mismatches 126; Indels 268; Gaps 14;

QY 1 EVLOQSGDPLVKPGASVKISCKASGYSTGYMHVWKSPGKLEWIGRINPNNGVTLY 60
Db 20 QVLOQSGALARPAGSAVKMSCKASGYFTRTMHWKQRPQGLEWIGYINPSRYTNY 79
QY 61 NQKFKDKATLTVDKSTTAYMELRLSLTSDSAVYYCARSTMTITNYMDYWGQTSVTSS 120
```



```
; APPLICANT: Large Scale Biology
; APPLICANT: Reinl, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/11/132,143
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: US/10/679,620
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 74
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pLSBC1741 , see Example 13
US-11-132-143-74

Query Match      27.4%; Score 965.5; DB 6; Length 510;
Best Local Similarity 77.7%; Pred. No. 2.9e-36;
Matches 188; Conservative 13; Mismatches 30; Indels 11; Gaps 1;

QY 441 NNTTISTSLISISLYL-----TTSIVMTQPTPTSLLSAGDRVTITCKASQSVSN 489
DB 5 NTMVNKHFLSLSLVLLGLSSNLTAGMLDVTMTQSHKFMSTSVGDRVSIITCKASQDVNT 64
QY 490 DVANVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDFTLTISVQAEADAIVFCQD 549
DB 65 AVANVYQKPGHSPKLLIYASFRYTGVPDRFTGNRSGTDTFTTISVQAEADLAIVYCCQH 124
QY 550 YNSPPTFGGCTKLEIKRADAAPTIVSIFPPSSQLTSGGASVVCFLNNFYPKDINVVKWID 609
DB 125 YTPPTFGGCTKLEIKRADAAPTIVSIFPPSSQLTSGGASVVCFLNNFYPKDINVVKWID 184
QY 610 GSERQNGVLNSWTDQDSKDYSTMSSTLTLTCKDEYERHNSYTCETHKTSPTPIVKSFNR 669
DB 185 GSERQNGVLNSWTDQDSKDYSTMSSTLTLTCKDEYERHNSYTCETHKTSPTPIVKSFNR 244
QY 670 NE 671
DB 245 NE 246

RESULT 52
US-11-132-143-92
; Sequence 92, Application US/11132143
; Publication No. US2005020797A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reinl, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/11/132,143
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: US/10/679,620
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 92
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pLSBC1767, see Example 13
US-11-132-143-92

Query Match      27.4%; Score 965.5; DB 6; Length 510;
```

```
Best Local Similarity 77.7%; Pred. No. 2.9e-36;
Matches 188; Conservative 13; Mismatches 30; Indels 11; Gaps 1;

QY 441 NNTTISTSLISISLYL-----TTSIVMTQPTPTSLLSAGDRVTITCKASQSVSN 489
DB 5 NTMVNKHFLSLSLVLLGLSSNLTAGMLDVTMTQSHKFMSTSVGDRVSIITCKASQDVNT 64
QY 490 DVANVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDFTLTISVQAEADAIVFCQD 549
DB 65 AVANVYQKPGHSPKLLIYASFRYTGVPDRFTGNRSGTDTFTTISVQAEADLAIVYCCQH 124
QY 550 YNSPPTFGGCTKLEIKRADAAPTIVSIFPPSSQLTSGGASVVCFLNNFYPKDINVVKWID 609
DB 125 YTPPTFGGCTKLEIKRADAAPTIVSIFPPSSQLTSGGASVVCFLNNFYPKDINVVKWID 184
QY 610 GSERQNGVLNSWTDQDSKDYSTMSSTLTLTCKDEYERHNSYTCETHKTSPTPIVKSFNR 669
DB 185 GSERQNGVLNSWTDQDSKDYSTMSSTLTLTCKDEYERHNSYTCETHKTSPTPIVKSFNR 244
QY 670 NE 671
DB 245 NE 246

RESULT 53
US-10-679-620-84
; Sequence 84, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reinl, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679,620
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 84
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p4D5Lt-TOPO, see Example 11
US-10-679-620-84

Query Match      27.2%; Score 958; DB 4; Length 214;
Best Local Similarity 86.3%; Pred. No. 2.8e-36;
Matches 183; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 460 IVMTQPTPTSLLSAGDRVTITCKASQSVNDVAVYQKPGQSPKLLIYSTSRVAGVDPDR 519
DB 2 IVMTQSHKFMSTSVGDRVSIITCKASQDVNTAVAVYQKPGHSPKLLIYASFRYTGVPDR 61
QY 520 FSGSGYGTDFTLTISVQAEADAIVFCQDYNPPTFGGCTKLEIKRADAAPTIVSIFPPS 579
DB 62 FTGNRSGTDTFTTISVQAEADLAIVYCCQHTTPTTPTFGGCTKLEIKRADAAPTIVSIFPPS 121
QY 580 SEQLTSGGASVVCFLNNFYPKDINVVKWIDGSRQNGVLNSWTDQDSKDYSTMSSTLTTL 639
DB 122 SEQLTSGGASVVCFLNNFYPKDINVVKWIDGSRQNGVLNSWTDQDSKDYSTMSSTLTTL 181
QY 640 TKDEYERHNSYTCETHKTSPTPIVKSFNRNE 671
DB 182 TKDEYERHNSYTCETHKTSPTPIVKSFNRNE 213

RESULT 54
US-11-132-143-84
; Sequence 84, Application US/11132143
; Publication No. US2005020797A1
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```
Db 20 QVLOQSGAELARPGASVKMSCKASGYTFTRYTHHWKQRPQGLEWIGVINPSRGYTNV 79
Qy 61 NQFKDKATLTVDKSSTAYMELRSLTSEDSAVYYCARSTMITYVMDYWGQGTSTVTVSS 120
Db 80 NQFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCAR-YDDHCLDYWGQGTTLTVSS 138
Qy 121 AKTTPSVYPLAGSAAQTNSMTLGLVKGYPEPVPVTVWNSGSLSSGVHTTTPAVLQSD 180
Db 139 AKTTAPSVYPLARVCGDTTGSSVTGLCLVKGTPEPVPVTLTWNSGSLSSGVHTTTPAVLQSD 198
Qy 181 LYTSSSVTVPSWTSEITVCNVAHPASTKVDKIVPRDSGPGSEKSEINEKDLRKK 240
Db 199 LYTSSSVTVTSWTSPQSITCNVAHPASTKVDKIEPR---GPTIKPCP----- 246
Qy 241 SELQGTALGNLKOIYYNKAITSSEKSADQFLNTLLFKGFTGHPWYNDLLVLDLGSTA 300
Db 247 ----- 246
Qy 301 ATSEYEGSSVDLYGAYGYOCAGGTGNKTCMYGGVTLHDNNRLTEKKVPINLWIDGKQ 360
Db 247 -----PCKCPAPN-----LLGGPSVF----- 262
Qy 361 TTVPIDKVKTSKEVTVQELDLQARHVLHGKFGLYNSDSFGGKVORGLIVFHSSEGSTVS 420
Db 263 -----IPPKIKOVLM-----AAPTIVSIFPPSSSEQLT 584
Qy 421 YDLFDAQGVPTDLLRIYRDNNTTSSLSISLYLTTSIVMTQTPTSLLSVAGDRVIT 480
Db 282 CVVDVSEDDPD-----VQISFVNVEVHTAQTQT----- 312
Qy 481 CKASQSVNDVAWYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDFLTITSSVQAE 540
Db 313 -----HREDYNSTLRV----- 324
Qy 541 AAVYFCQDYNPSPTFGGTKLEIKRAD-----AAPTIVSIFPPSSSEQLT 584
Db 325 SALPIQHODWMSGKEF-----KCKVNNKDLPAPIERTISKPGSVRAPQVTVLPPPEE 380
Qy 585 SGASVVCFLNFPYKDIWVKWIDGSERON-----GVLSWTDQDSKDSYMSSTLT 639
Db 381 KKQVTLTCMWTDFWPEDIYVEWTNNGKTELNYKNTPEVLDS-----DGSYFMYSKLRV 433
Qy 640 TKDEYERHNSYTCETHK-TSTSPVKSFN 669
Db 434 EKKNWVERNSYSCSVVHGLNHHHTTKFSR 464

RESULT 58
US-10-703-963-7
; Sequence 7, Application US/10703963
; Publication No. US20040202662A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; Athwal, Diljeet S.
; Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10703,963
; FILING DATE: 07-Jan-2003
; CLASSIFICATION: 424
```

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,658
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-703-963-7

Query Match 27.2%; Score 957; DB 4; Length 468;
Best Local Similarity 34.7%; Pred. No. 6.5e-36;
Matches 240; Conservative 56; Mismatches 127; Indels 268; Gaps 14;

Qy 1 EVLOQSGDPLVKPGASVKISCKASGYFTGYTHHWKQSPGKLEWIGRINPNNGVTLY 60
Db 20 QVLOQSGAELARPGASVKMSCKASGYTFTRYTHHWKQRPQGLEWIGVINPSRGYTNV 79
Qy 61 NQFKDKATLTVDKSSTAYMELRSLTSEDSAVYYCARSTMITYVMDYWGQGTSTVTVSS 120
Db 80 NQFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCAR-YDDHCLDYWGQGTTLTVSS 138
Qy 121 AKTTPSVYPLAGSAAQTNSMTLGLVKGYPEPVPVTVWNSGSLSSGVHTTTPAVLQSD 180
Db 139 AKTTAPSVYPLARVCGDTTGSSVTGLCLVKGTPEPVPVTLTWNSGSLSSGVHTTTPAVLQSD 198
Qy 181 LYTSSSVTVPSWTSEITVCNVAHPASTKVDKIVPRDSGPGSEKSEINEKDLRKK 240
Db 199 LYTSSSVTVTSWTSPQSITCNVAHPASTKVDKIEPR---GPTIKPCP----- 246
Qy 241 SELQGTALGNLKOIYYNKAITSSEKSADQFLNTLLFKGFTGHPWYNDLLVLDLGSTA 300
Db 247 ----- 246
Qy 301 ATSEYEGSSVDLYGAYGYOCAGGTGNKTCMYGGVTLHDNNRLTEKKVPINLWIDGKQ 360
Db 247 -----PCKCPAPN-----LLGGPSVF----- 262
Qy 361 TTVPIDKVKTSKEVTVQELDLQARHVLHGKFGLYNSDSFGGKVORGLIVFHSSEGSTVS 420
Db 263 -----IPPKIKOVLM-----AAPTIVSIFPPSSSEQLT 584
Qy 421 YDLFDAQGVPTDLLRIYRDNNTTSSLSISLYLTTSIVMTQTPTSLLSVAGDRVIT 480
Db 282 CVVDVSEDDPD-----VQISFVNVEVHTAQTQT----- 312
Qy 481 CKASQSVNDVAWYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDFLTITSSVQAE 540
Db 313 -----HREDYNSTLRV----- 324
Qy 541 AAVYFCQDYNPSPTFGGTKLEIKRAD-----AAPTIVSIFPPSSSEQLT 584
Db 325 SALPIQHODWMSGKEF-----KCKVNNKDLPAPIERTISKPGSVRAPQVTVLPPPEE 380
Qy 585 SGASVVCFLNFPYKDIWVKWIDGSERON-----GVLSWTDQDSKDSYMSSTLT 639
Db 381 KKQVTLTCMWTDFWPEDIYVEWTNNGKTELNYKNTPEVLDS-----DGSYFMYSKLRV 433
Qy 640 TKDEYERHNSYTCETHK-TSTSPVKSFN 669
Db 434 EKKNWVERNSYSCSVVHGLNHHHTTKFSR 464

RESULT 59
```

```
US-10-937-971-7
; Sequence 7, Application US/10937971
; Publication No. US20050123534A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; Athwal, Diljeet S.
; Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/10/937,971
; FILING DATE: 10-Sep-2004
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yatko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-937-971-7
Query Match 27.2%; Score 957; DB 5; Length 468;
Best Local Similarity 34.7%; Pred. No. 6.5e-36;
Matches 240; Conservative 56; Mismatches 127; Indels 268; Gaps 14;
QY 1 EVQLQSGDPLVKPGASVKISCKASGYSTGYIMHWVKQSPGKLEWIGRIINPNNGVTLY 60
Db :||||| : :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 QVQLQSGAELARPGASVMSCKASGYTFTRYTHHWKQRPQGQLEWIGVINPSRGYTN 79
QY 61 NQKFKDKATLVTDKSTTAYMELRSLTSDSAVYYCARSTMITNYMDYWGQTSVTVSS 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
80 NQKFKDKATLVTDKSTTAYMQLSSTSDSAVYYCAR-YYDDHCLDYWGQGTTLTVSS 138
QY 121 AKTTPSVVPLAPGSAQAQNSMTVLGCLVKGYPEPVTVTWNSGSLSSGVHFPFPAVLQSD 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
139 AKTARSVVPLAPVCGDTCSSVTLCGLVKGYPEPVTLTWNSGSLSSGVHFPFPAVLQSD 198
QY 181 LYTSLSSVTVPSTWPSVETTCNVNHPASTKVKDKIVPRDGGPSEKSEENKDLRKK 240
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
199 LYTSLSSVTVPSTWPSQSITCNVHPASTKVKDKIEPR--GPTIKPCP----- 246
QY 241 SELOGTALGNLKOIYYNNSKATTSSEKSADQFLTNLLFGPFTGHPWYNDLLVDLGSTA 300
Db -----
247 ----- 246
QY 301 ATSEYEGSSVDLYGAYYGYQCAGGTPTNKTAKMYGGVTLHDNNRLTBEKKVPINLWIDGKQ 360
Db -----PCKCPAN-----LLGGSVP----- 262
QY 361 TTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKQKGLIVFHSSEGSTVS 420
Db -----IPPKIKDVLMI---SLSPIVT 281
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Db 20 QVLOQSGAELARPGASVMSCKASGYTFTRYTMHWKQRPQGLEWIGYNPSRGYTN 79
Qy 61 NOKFKDKATLTVDKSSSTAYMELSLTSDSAVYCYCARSTMTITNYVMDYWGQSTVTVSS 120
Db 80 NOKFKDKATLTVDKSSSTAYMELSLTSDSAVYCYCARSTMTITNYVMDYWGQSTVTVSS 138
Qy 121 AKTTTPSVPLAPGSAQAQNSMTVLGCLVKGYPEPVTVTWNSGSLSSGVHTTTPAVLQSD 180
Db 139 AKTTASVPLAPVCGDITGSSVTLGCLVKGTPEPVTLTWNSGSLSSGVHTTTPAVLQSD 198
Qy 181 LYTSSSVTVPSSTWPSSTVTCNVNHPASSTKVDKIVPRDSCGPGKEEINEKDLRKK 240
Db 199 LYTSSSVTVPSSTWPSSTVTCNVNHPASSTKVDKIVPRDSCGPGKEEINEKDLRKK 246
Qy 241 SELQGTALGNLKIYYNKAITSSEKSAQDQFLTNLLFKGFTGHPWYNLVLVLDGSTA 300
Db 247 ----- 246
Qy 301 ATSEYEGSSVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLTBEKKVPIINLWIDGKQ 360
Db 247 ----- 246
Qy 361 TTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVGRLIVFHSSEGSTVS 420
Db 263 ----- 262
Qy 421 YDLFDAQGGYPTDLLRIYRDNTTISSTLSISLYLTTSIVMTQTPTSLVLSAGDRVIT 480
Db 282 CVVDVSEDDPD-----VOISFWANNVEVHTAQOT----- 312
Qy 481 CRASQSVNDVAWYQKPGQSKLLISYTSRYAGVDRFSGSGYGTDFTLTISVQAE 540
Db 313 ----- 324
Qy 541 AAVYFCQDYNPSPTFGGKTLKIKRAD-----AAPTVISIPPPSEQLT 584
Db 325 SALPIQHQDWMGKEF-----KCKVNNKDLPAPIERTISKPGSVRAPQVYVLPPEEEMT 380
Qy 585 SGGASVVCFLNFPYKDIIVKWKIDGSERON-----GVLNSWTDQDSKOSTYSMSSTLTL 639
Db 381 KKQVTLTCMVTDPMFEDIYVEWTNNKTELNYKNTPEVLDS-----DGSYFMYSKLRV 433
Qy 640 TKDEYERHNSYTCETHK-TSTSPIVKSFRN 669
Db 434 EKKQWVERNSYSCSVVHEGLNHHHTTKSF 464

RESULT 61
US-10-703-344-7
; Sequence 7, Application US/10703344
; Publication No. US20050202529A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; Athwal, Diljeet S.
; Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10703,344
; FILING DATE: 07-Nov-2003

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/846, 658
FILING DATE: 01-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yacko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-703-344-7

Query Match 27.2%; Score 957; DB 5; Length 468;
Best Local Similarity 34.7%; Pred. No. 6.5e-36;
Matches 240; Conservative 56; Mismatches 127; Indels 268; Gaps 14;
Qy 1 EVLOQSGDPLVKPGASVKISKASGYSTGYTMHWKQSPKGLEWIGYNPNNGVTV 60
Db 20 QVLOQSGAELARPGASVMSCKASGYTFTRYTMHWKQRPQGLEWIGYNPSRGYTN 79
Qy 61 NOKFKDKATLTVDKSSSTAYMELSLTSDSAVYCYCARSTMTITNYVMDYWGQSTVTVSS 120
Db 80 NOKFKDKATLTVDKSSSTAYMELSLTSDSAVYCYCARSTMTITNYVMDYWGQSTVTVSS 138
Qy 121 AKTTTPSVPLAPGSAQAQNSMTVLGCLVKGYPEPVTVTWNSGSLSSGVHTTTPAVLQSD 180
Db 139 AKTTASVPLAPVCGDITGSSVTLGCLVKGTPEPVTLTWNSGSLSSGVHTTTPAVLQSD 198
Qy 181 LYTSSSVTVPSSTWPSSTVTCNVNHPASSTKVDKIVPRDSCGPGKEEINEKDLRKK 240
Db 199 LYTSSSVTVPSSTWPSSTVTCNVNHPASSTKVDKIVPRDSCGPGKEEINEKDLRKK 246
Qy 241 SELQGTALGNLKIYYNKAITSSEKSAQDQFLTNLLFKGFTGHPWYNLVLVLDGSTA 300
Db 247 ----- 246
Qy 301 ATSEYEGSSVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLTBEKKVPIINLWIDGKQ 360
Db 247 ----- 246
Qy 361 TTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVGRLIVFHSSEGSTVS 420
Db 263 ----- 262
Qy 421 YDLFDAQGGYPTDLLRIYRDNTTISSTLSISLYLTTSIVMTQTPTSLVLSAGDRVIT 480
Db 282 CVVDVSEDDPD-----VOISFWANNVEVHTAQOT----- 312
Qy 481 CRASQSVNDVAWYQKPGQSKLLISYTSRYAGVDRFSGSGYGTDFTLTISVQAE 540
Db 313 ----- 324
Qy 541 AAVYFCQDYNPSPTFGGKTLKIKRAD-----AAPTVISIPPPSEQLT 584
Db 325 SALPIQHQDWMGKEF-----KCKVNNKDLPAPIERTISKPGSVRAPQVYVLPPEEEMT 380
Qy 585 SGGASVVCFLNFPYKDIIVKWKIDGSERON-----GVLNSWTDQDSKOSTYSMSSTLTL 639
Db 381 KKQVTLTCMVTDPMFEDIYVEWTNNKTELNYKNTPEVLDS-----DGSYFMYSKLRV 433
Qy 640 TKDEYERHNSYTCETHK-TSTSPIVKSFRN 669
Db 434 EKKQWVERNSYSCSVVHEGLNHHHTTKSF 464

```
RESULT 62
US-10-516-429-10
; Sequence 10, Application US/10516429
; Publication No. US20050191617A1
; GENERAL INFORMATION:
; APPLICANT: INOUE, Makoto
; APPLICANT: HIRONAKA, Mamoru
; APPLICANT: HASEGAWA, Takashi
; TITLE OF INVENTION: Paramyxoviral Vectors Encoding
; TITLE OF INVENTION: Antibodies and Uses Thereof
; FILE REFERENCE: 50026/049001
; CURRENT APPLICATION NUMBER: US/10/516,429
; CURRENT FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: PCT/JP03/07005
; PRIOR FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 2002-161964
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: an immunoglobulin IN-1 heavy chain
US-10-516-429-10

Query Match      27.1%; Score 955.5; DB 5; Length 244;
Best Local Similarity 82.9%; Pred. No. 4.1e-36;
Matches 184; Conservative 13; Mismatches 24; Indels 1; Gaps 1;

QY 1 EVQLQSGDPLVKPGASVKISKASGYSTGYMHVVKQSPGKLEWIGRIHPNNGVTLY 60
DB 22 EVKLHSGPLVRPGTSVKISKASGYSTGYMHVVKQSPGKLEWIGRIHPNNGVTLY 81
QY 61 NQKFKDKATLTVDKSTTAYMELRLSTSDSAVYICARSTMTIN-YVMDYWGQGTSTVVS 119
DB 82 NEKFKGKATLTADTSSTAYMQLSLTSDSAVYFCARFYGSSYWFYFDVWGQGTITVVS 141
QY 120 SAKTTTPSVYVPLAPGSAQTNSMVTGLCLVKGYFPEPVTVTWNSGSLSGVHTFPVAVLOS 179
DB 142 SAKTTTPSVYVPLAPGSAQTNSMVTGLCLVKGYFPEPVTVTWNSGSLSGVHTFPVAVLOS 201
QY 180 DLYTLSSSVTPVPSSTWPSSETVTCNVAHPASSTKVDKKIVPRD 221
DB 202 DLYTLSSSVTPVPSSTWPSSETVTCNVAHPASSTKVDKKIVPRD 243

RESULT 63
US-10-860-322-4
; Sequence 4, Application US/10860322
; Publication No. US20050138692A1
; GENERAL INFORMATION:
; APPLICANT: Hilary Koprowski
; APPLICANT: Kieung Ko
; APPLICANT: Pauline Rudd
; TITLE OF INVENTION: Production of Cancer Specific
; TITLE OF INVENTION: Antibodies in Plants
; FILE REFERENCE: 08321-0146 US1
; CURRENT APPLICATION NUMBER: US/10/860,322
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: 60/475,311
; PRIOR FILING DATE: 2003-06-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-860-322-4

Query Match      27.1%; Score 954; DB 5; Length 239;
Best Local Similarity 82.7%; Pred. No. 4.7e-36;

Matches 186; Conservative 14; Mismatches 23; Indels 2; Gaps 1;

QY 449 LSIISLYLYTT--SIYMTQTPTSLLYSAGDRVTITCKASQSVNDVAVYQOKPQSPKLLI 506
DB 13 ISILLWLYGADGNIVMTQSPKSMSSVGERVTLTCKASENVVTVYSWYQOKPQSPKLLI 72
QY 507 SYTSRYAGVDPDRFSGSGYGTDTLTITSSVQAEDAAVYFCQDDYNSPPTFGGQTKLEIKR 566
DB 73 YGASNRYTGVPDRFTGSGSATDFTLTITSSVQAEDADYHCGQGYSPYTFGGQTKLEIKR 132
QY 567 ADAAPTVISIFFPSSSQLTSGGASVVCFLNNFYPKQINVKWKIDGSRQNGVLNSWTDQDS 636
DB 133 ADAAPTVISIFFPSSSQLTSGGASVVCFLNNFYPKQINVKWKIDGSRQNGVLNSWTDQDS 192
QY 627 KOSTYSMSSTLTLTVDYERHNSYTCETHTKTSTSPIVKSFNRE 671
DB 193 KOSTYSMSSTLTLTVDYERHNSYTCETHTKTSTSPIVKSFNRE 237

RESULT 64
US-10-679-620-82
; Sequence 82, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reini, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679,620
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p4D5Hy-TOPO, see Examl 11
US-10-679-620-82

Query Match      27.0%; Score 952; DB 4; Length 222;
Best Local Similarity 81.4%; Pred. No. 5.4e-36;
Matches 180; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

QY 1 EVQLQSGDPLVKPGASVKISKASGYSTGYMHVVKQSPGKLEWIGRIHPNNGVTLY 60
DB 1 QVQLQSGPELVKPGASLKSCTASGFNIKDTYIHWVKQRPEQGLEWIGRIYPTNGVTRY 60
QY 61 NQKFKDKATLTVDKSTTAYMELRLSTSDSAVYICARSTMTIN-YVMDYWGQGTSTVVS 120
DB 61 DPKFQDKATITADTSNTAYLQVSRLTSDTAVYICARSTMTIN-YVMDYWGQGTSTVVS 120
QY 121 AKTTTPSVYVPLAPGSAQTNSMVTGLCLVKGYFPEPVTVTWNSGSLSGVHTFPVAVLOS 180
DB 121 AKTTTPSVYVPLAPGSAQTNSMVTGLCLVKGYFPEPVTVTWNSGSLSGVHTFPVAVLOS 180
QY 181 LYTLSSSVTPVPSSTWPSSETVTCNVAHPASSTKVDKKIVPRD 221
DB 181 LYTLSSSVTPVPSSTWPSSETVTCNVAHPASSTKVDKKIVPRD 221

RESULT 65
US-11-132-143-82
; Sequence 82, Application US/11132143
; Publication No. US20050207977A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reini, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
```



```

; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/11/132,143
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: US/10/679,620
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p4DSHy-TOPO, see Examl 11
US-11-132-143-82

Query Match      27.0%; Score 952; DB 6; Length 222;
Best Local Similarity 81.4%; Pred. No. 5.4e-36;
Matches 180; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

QY      1  EVLOQSGDPLVKPGASVKISKASGYSFTGYMHVWKSPGKLEWIGRINPNNGVTLY 60
Db      1  QVLOQSGDELVKPGASLKLSCASSFNKDTYIHVWKRPQGLEWIGRIYPTNGTRY 60

QY      61  NQKFKDKATLTVDKSSSTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQGTSTVTS 120
Db      61  DPRFQDKATITADTSSNTAYLVQSRLTSEDTAVYYCSRWGGDGFYAMDYWGQASVTVSS 120

QY      121  AKTTPSVVPLAPGSAQAQNSMTGLCLVKGYFPEPVPTVNSGSLSSGVHPTPAVLQSD 180
Db      121  AKTTPSVVPLAPGSAQAQNSMTVTLCLVKGYFPEPVPTVNSGSLSSGVHPTPAVLQSD 180

QY      181  LYTLSSTVTPSSTWPSSETVTCNVAHPASSTKVDKVIKVRD 221
Db      181  LYTLSSTVTPSSTWPSSETVTCNVAHPASSTKVDKVIKVRD 221

RESULT 66
US-09-900-766-4
; Sequence 4, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Staphylococcus sp.
US-09-900-766-4

Query Match      26.9%; Score 948; DB 3; Length 233;
Best Local Similarity 76.4%; Pred. No. 8.6e-36;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY      226  SEKSEINEKDLRKSELOQTALGNLKOIYYNYSKAITSEKSADQFLNTTLFKGFFTG 285
Db      1  SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESHDFLOHTILFKGFFTD 60

QY      286  HPWYNLLVDLGLSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 345
Db      61  HSWYNLLVDVDFSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120

QY      346  EEKVPINLWIDGKQTPIDVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVK 405
Db      61  HSWYNLLVDVDFSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120

QY      406  EEKVPINLWIDGKQTPIDVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVK 405
Db      121  EEKVPINLWIDGKQTPIDVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVK 180

QY      406  RGLIVHSGSEGSTVSYDLFDAQGYPTDILLRIYRDNNTTSSLSLSLYTT 458
Db      121  EEKVPINLWIDGKQNTVPLETVTKNKNVTVQELDLQARRYLOEKYNLNSVDFGKVQ 180

; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/11/132,143
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: US/10/679,620
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p4DSHy-TOPO, see Examl 11
US-11-132-143-82

Query Match      27.0%; Score 952; DB 6; Length 222;
Best Local Similarity 81.4%; Pred. No. 5.4e-36;
Matches 180; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

QY      1  EVLOQSGDPLVKPGASVKISKASGYSFTGYMHVWKSPGKLEWIGRINPNNGVTLY 60
Db      1  QVLOQSGDELVKPGASLKLSCASSFNKDTYIHVWKRPQGLEWIGRIYPTNGTRY 60

QY      61  NQKFKDKATLTVDKSSSTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQGTSTVTS 120
Db      61  DPRFQDKATITADTSSNTAYLVQSRLTSEDTAVYYCSRWGGDGFYAMDYWGQASVTVSS 120

QY      121  AKTTPSVVPLAPGSAQAQNSMTGLCLVKGYFPEPVPTVNSGSLSSGVHPTPAVLQSD 180
Db      121  AKTTPSVVPLAPGSAQAQNSMTVTLCLVKGYFPEPVPTVNSGSLSSGVHPTPAVLQSD 180

QY      181  LYTLSSTVTPSSTWPSSETVTCNVAHPASSTKVDKVIKVRD 221
Db      181  LYTLSSTVTPSSTWPSSETVTCNVAHPASSTKVDKVIKVRD 221

RESULT 67
US-10-283-838-7
; Sequence 7, Application US/10283838
; Publication No. US20030092894A1
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
;              Johan Hansson, Terje Kalland, Lars
;              Abrahamson and Goran Forsberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
;              AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,838
; FILING DATE: 30-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,692
; FILING DATE: August 12, 1996
; APPLICATION NUMBER: 9601245-5
; FILING DATE: March 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Krieger, Paul E.
; REGISTRATION NUMBER: 25,886
; REFERENCE/DOCKET NUMBER: 41986/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-283-838-7

Query Match      26.9%; Score 948; DB 4; Length 233;
Best Local Similarity 76.4%; Pred. No. 8.6e-36;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY      226  SEKSEINEKDLRKSELOQTALGNLKOIYYNYSKAITSEKSADQFLNTTLFKGFFTG 285
Db      1  SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESHDFLOHTILFKGFFTD 60

QY      286  HPWYNLLVDLGLSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 345
Db      61  HSWYNLLVDVDFSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120

QY      346  EEKVPINLWIDGKQTPIDVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVK 405
Db      61  HSWYNLLVDVDFSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120

QY      406  EEKVPINLWIDGKQTPIDVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVK 405
Db      121  EEKVPINLWIDGKQNTVPLETVTKNKNVTVQELDLQARRYLOEKYNLNSVDFGKVQ 180

QY      406  RGLIVHSGSEGSTVSYDLFDAQGYPTDILLRIYRDNNTTSSLSLSLYTT 458
Db      121  EEKVPINLWIDGKQNTVPLETVTKNKNVTVQELDLQARRYLOEKYNLNSVDFGKVQ 180
```



```

; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-354-948-4

Query Match      26.8%; Score 944; DB 4; Length 233;
Best Local Similarity 76.3%; Pred. No. 1.3e-35;
Matches 177; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 227 EKSEEEINEKDLRKSELOQTALGNLQIYYYNSEKAITSSSEKADQFLTNTLLFKGFFTGH 286
Db 2 EKSEEEINEKDLRKSELOQTALGNLQIYYYNSEKAITSSSEKADQFLTNTLLFKGFFTGH 61

QY 287 PWYNDLLVDLGGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLLHNNRLTE 346
Db 62 SWYNDLLVDFDSKDIVDKYKGVVLYGAYGYQCAGGTPNKTCMYGGVTLLHNNRLTE 121

QY 347 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGCKVQR 406
Db 122 EKKVPINLWIDGKQNTVPLETVTNKKNVTVQELDLQARRYLQEKYLYNSDVFDGKQVR 181

QY 407 GLIVFHSSEGSTVSYDLFDAQGOYPTLLRIYRDNTTISSTLSISLYLYTT 458
Db 182 GLIVFHTSTEPSVNYDLFGAQQYNTLLRIYRDNTINSENNHIDIYLYTS 233
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Search completed: February 15, 2006, 20:38:30
Job time : 186.042 secs

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OM protein - protein search, using sw model

Run on: February 15, 2006, 20:34:56 ; Search time 16.3359 Seconds
(without alignments)
584.618 Million cell updates/sec

Title: US-09-900-766-1

Perfect score: 3522

Sequence: 1 EVLOQSGDLVKPGASVKI.....EATHKTSPIVKSFRNRES 672

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 107799 seqs, 14211699 residues

Total number of hits satisfying chosen parameters: 107799

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications AA.New.*

1: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep.*

2: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*

3: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep.*

4: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep.*

5: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep.*

6: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep.*

7: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep.*

8: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1069	30.4	592	6	US-10-016-686-4
2	972.5	27.6	243	6	US-10-016-686-1
3	967.5	27.5	488	6	US-10-016-686-3
4	944	26.8	233	7	US-11-022-562-226
5	885	25.1	363	7	US-11-000-463-335
6	855.5	24.3	666	6	US-10-981-356A-29
7	855.5	24.3	667	7	US-11-096-046-29
8	852.5	24.2	462	7	US-11-177-648-9
9	850.5	24.1	451	7	US-11-124-620-7
10	849	24.1	446	7	US-11-102-621-119
11	846	24.0	446	7	US-11-102-621-120
12	846	24.0	446	7	US-11-102-621-122
13	845.5	24.0	451	7	US-11-124-620-5
14	845	24.0	446	7	US-11-102-621-123
15	844.5	24.0	462	7	US-11-177-648-33
16	844	24.0	446	7	US-11-102-621-121
17	841.5	23.9	384	7	US-11-000-463-804
18	841.5	23.9	384	7	US-11-000-463-805
19	841.5	23.9	384	7	US-11-000-463-806
20	841.5	23.9	384	7	US-11-000-463-807
21	838.5	23.8	462	7	US-11-177-648-30
22	838.5	23.8	462	7	US-11-177-648-32
23	833.5	23.7	462	7	US-11-177-648-31
24	829.5	23.6	462	7	US-11-177-648-28
25	827.5	23.5	462	7	US-11-177-648-97
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					Sequence 3, Appl
					Sequence 226, App
					Sequence 335, App
					Sequence 29, Appl
					Sequence 9, Appl
					Sequence 7, Appl
					Sequence 119, App
					Sequence 120, App
					Sequence 122, App
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					Sequence 123, App
					Sequence 33, Appl
					Sequence 121, App
					Sequence 804, App
					Sequence 805, App
					Sequence 806, App
					Sequence 807, App
					Sequence 30, Appl
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					Sequence 31, Appl
					Sequence 28, Appl
					Sequence 97, Appl

Sequence 96, Appl
Sequence 124, App
Sequence 125, App
Sequence 127, App
Sequence 29, Appl
Sequence 128, App
Sequence 126, App
Sequence 899, App
Sequence 95, Appl
Sequence 130, App
Sequence 93, Appl
Sequence 136, App
Sequence 137, App
Sequence 139, App
Sequence 94, Appl
Sequence 140, App
Sequence 131, App
Sequence 133, App
Sequence 27, Appl
Sequence 134, App
Sequence 138, App
Sequence 132, App
Sequence 92, Appl
Sequence 98, Appl
Sequence 78, Appl
Sequence 22, Appl
Sequence 14, Appl
Sequence 32, Appl
Sequence 26, Appl
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Sequence 30, Appl

99	779.5	22.1	667	7	US-11-096-046-28	Sequence 28, Appl	172	702.5	19.9	213	7	US-11-102-621-135	Sequence 135, Appl
100	779.5	22.1	667	7	US-11-096-046-30	Sequence 30, Appl	173	702.5	19.9	451	6	US-10-923-327-7	Sequence 7, Appl
101	776.5	22.0	232	7	US-11-173-564-2	Sequence 2, Appl	174	702.5	19.9	451	6	US-10-923-327-9	Sequence 9, Appl
102	775.5	22.0	253	7	US-11-106-820-20	Sequence 20, Appl	175	702.5	19.9	464	7	US-11-128-900-2	Sequence 2, Appl
103	775.5	22.0	253	7	US-11-190-364-18	Sequence 18, Appl	176	702.5	19.9	464	7	US-11-128-900-66	Sequence 66, Appl
104	774.5	22.0	666	6	US-10-981-356A-25	Sequence 25, Appl	177	702	19.9	473	7	US-11-144-248-50	Sequence 50, Appl
105	774.5	22.0	667	7	US-11-096-046-25	Sequence 25, Appl	178	702	19.9	473	7	US-11-144-223-50	Sequence 50, Appl
106	779	21.6	449	7	US-11-154-337-15	Sequence 15, Appl	179	702	19.9	473	7	US-11-182-343-50	Sequence 50, Appl
107	759	21.6	449	7	US-11-182-908-14	Sequence 14, Appl	180	702	19.9	524	7	US-11-041-095-58	Sequence 58, Appl
108	757	21.5	489	7	US-11-072-512-3329	Sequence 3329, Ap	181	701.5	19.9	449	7	US-11-080-587-6	Sequence 6, Appl
109	756.5	21.5	447	7	US-11-004-590-230	Sequence 230, App	182	701	19.9	214	7	US-11-173-564-1	Sequence 1, Appl
110	756	21.5	450	7	US-11-025-712-12	Sequence 12, Appl	183	701	19.9	214	7	US-11-049-536-700	Sequence 700, App
111	749.5	21.3	447	7	US-11-004-590-231	Sequence 231, App	184	701	19.9	236	7	US-11-144-248-48	Sequence 48, Appl
112	749	21.3	444	7	US-11-004-590-232	Sequence 232, App	185	701	19.9	236	7	US-11-144-222-48	Sequence 48, Appl
113	747	21.2	444	7	US-11-004-590-233	Sequence 233, App	186	701	19.9	236	7	US-11-182-343-48	Sequence 49, Appl
114	738.5	21.0	474	7	US-11-000-463-284	Sequence 284, App	187	698.5	19.8	470	7	US-11-144-248-49	Sequence 49, Appl
115	737	20.9	238	7	US-11-158-505-1	Sequence 1, Appl	188	698.5	19.8	470	7	US-11-144-222-49	Sequence 49, Appl
116	737	20.9	238	7	US-11-158-505-3	Sequence 3, Appl	189	698.5	19.8	470	7	US-11-182-343-49	Sequence 49, Appl
117	737	20.9	238	7	US-11-158-505-25	Sequence 25, Appl	190	697.5	19.8	213	7	US-11-158-505-34	Sequence 34, Appl
118	737	20.9	238	7	US-11-158-505-27	Sequence 27, Appl	191	697	19.8	236	7	US-11-144-248-52	Sequence 52, Appl
119	734	20.8	218	7	US-11-158-505-4	Sequence 4, Appl	192	697	19.8	236	7	US-11-144-222-52	Sequence 52, Appl
120	734	20.8	218	7	US-11-158-505-28	Sequence 28, Appl	193	697	19.8	236	7	US-11-182-343-52	Sequence 52, Appl
121	734	20.8	579	7	US-11-174-186-41	Sequence 41, Appl	194	696.5	19.8	235	7	US-11-128-900-14	Sequence 14, Appl
122	731	20.8	233	7	US-11-182-908-17	Sequence 17, Appl	195	696.5	19.8	235	7	US-11-128-900-65	Sequence 65, Appl
123	730	20.7	450	7	US-11-049-536-701	Sequence 701, App	196	696.5	19.8	307	7	US-11-000-463-332	Sequence 332, App
124	727	20.6	217	7	US-11-182-908-23	Sequence 23, Appl	197	695	19.7	218	7	US-11-084-554-11	Sequence 11, Appl
125	727	20.6	238	7	US-11-158-505-9	Sequence 9, Appl	198	695	19.7	218	7	US-11-136-250-11	Sequence 11, Appl
126	727	20.6	238	7	US-11-158-505-11	Sequence 11, Appl	199	695	19.7	234	7	US-11-128-900-17	Sequence 17, Appl
127	727	20.6	238	7	US-11-158-505-17	Sequence 17, Appl	200	695	19.7	234	7	US-11-128-900-69	Sequence 69, Appl
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129	727	20.6	238	7	US-11-158-505-74	Sequence 74, Appl	202	694	19.7	463	7	US-11-128-900-68	Sequence 68, Appl
130	726	20.6	214	7	US-11-025-712-11	Sequence 11, Appl	203	693.5	19.7	291	7	US-11-041-095-60	Sequence 60, Appl
131	726	20.6	214	7	US-11-094-625-9	Sequence 9, Appl	204	693.5	19.7	468	7	US-11-086-289-22	Sequence 22, Appl
132	726	20.6	214	7	US-11-154-337-14	Sequence 14, Appl	205	693.5	19.7	472	7	US-11-086-289-2	Sequence 2, Appl
133	726	20.6	214	7	US-11-154-337-16	Sequence 16, Appl	206	693	19.7	236	7	US-11-086-289-4	Sequence 4, Appl
134	726	20.6	214	7	US-11-182-908-13	Sequence 13, Appl	207	692.5	19.7	232	7	US-11-106-820-23	Sequence 23, Appl
135	726	20.6	214	7	US-11-182-908-15	Sequence 15, Appl	208	692.5	19.7	232	7	US-11-190-364-21	Sequence 21, Appl
136	724	20.6	218	7	US-11-158-505-12	Sequence 12, Appl	209	692.5	19.7	451	7	US-11-128-900-70	Sequence 70, Appl
137	724	20.6	218	7	US-11-158-505-20	Sequence 20, Appl	210	691.5	19.6	239	7	US-11-139-499-6	Sequence 6, Appl
138	722	20.5	477	7	US-11-158-505-20	Sequence 395, App	211	690.5	19.6	235	7	US-11-166-994-2	Sequence 2, Appl
139	719	20.4	444	7	US-11-173-969-6	Sequence 6, Appl	212	690	19.6	236	7	US-11-144-248-47	Sequence 47, Appl
140	719	20.4	444	7	US-11-173-969-6	Sequence 6, Appl	213	690	19.6	236	7	US-11-144-248-47	Sequence 47, Appl
141	718.5	20.4	232	7	US-11-025-712-10	Sequence 10, Appl	214	690	19.6	236	7	US-11-144-222-47	Sequence 47, Appl
142	718.5	20.4	470	7	US-11-144-248-45	Sequence 45, Appl	215	690	19.6	236	7	US-11-182-343-47	Sequence 47, Appl
143	718.5	20.4	470	7	US-11-144-222-45	Sequence 45, Appl	216	690	19.6	475	7	US-11-041-095-16	Sequence 16, Appl
144	718.5	20.4	470	7	US-11-182-343-45	Sequence 45, Appl	217	690	19.6	526	7	US-11-041-095-10	Sequence 10, Appl
145	717	20.4	214	7	US-11-102-621-129	Sequence 129, App	218	689.5	19.6	220	7	US-11-094-623-10	Sequence 10, Appl
146	717	20.4	236	7	US-11-086-289-8	Sequence 8, Appl	219	689.5	19.6	451	7	US-11-158-505-33	Sequence 33, Appl
147	717	20.4	236	7	US-11-221-900-2	Sequence 2, Appl	220	689	19.6	312	7	US-11-000-463-334	Sequence 334, App
148	715	20.3	234	7	US-11-041-095-25	Sequence 25, Appl	221	688.5	19.5	235	7	US-11-086-289-16	Sequence 16, Appl
149	715	20.3	236	7	US-11-086-289-20	Sequence 20, Appl	222	688.5	19.5	235	7	US-11-120-338-13	Sequence 13, Appl
150	714	20.3	214	7	US-11-128-900-71	Sequence 71, Appl	223	687.5	19.5	213	7	US-11-120-338-16	Sequence 16, Appl
151	713	20.2	290	7	US-11-041-095-13	Sequence 13, Appl	224	687.5	19.5	213	7	US-11-107-028-31	Sequence 31, Appl
152	711	20.2	214	7	US-11-183-205-55	Sequence 55, Appl	225	687.5	19.5	213	7	US-11-107-028-44	Sequence 44, Appl
153	709	20.1	239	7	US-11-041-095-19	Sequence 19, Appl	226	687.5	19.5	213	7	US-11-106-820-24	Sequence 24, Appl
154	706.5	20.1	451	7	US-11-102-621-142	Sequence 142, App	227	687.5	19.5	213	7	US-11-106-820-29	Sequence 29, Appl
155	706.5	20.1	451	7	US-11-102-621-143	Sequence 143, App	228	687.5	19.5	213	7	US-11-106-820-44	Sequence 44, Appl
156	706.5	20.1	451	7	US-11-102-621-145	Sequence 145, App	229	687.5	19.5	213	7	US-11-143-077-13	Sequence 13, Appl
157	706.5	20.1	470	7	US-11-144-248-46	Sequence 46, Appl	230	687.5	19.5	213	7	US-11-143-077-16	Sequence 16, Appl
158	706.5	20.1	470	7	US-11-144-222-46	Sequence 46, Appl	231	687.5	19.5	233	7	US-11-128-900-15	Sequence 15, Appl
159	706.5	20.1	470	7	US-11-182-343-46	Sequence 46, Appl	232	687.5	19.5	233	7	US-11-128-900-67	Sequence 67, Appl
160	706	20.0	241	7	US-11-106-820-15	Sequence 15, Appl	233	687	19.5	218	6	US-10-923-327-6	Sequence 6, Appl
161	706	20.0	241	7	US-11-190-364-14	Sequence 14, Appl	234	686.5	19.5	468	7	US-11-086-289-14	Sequence 14, Appl
162	706	20.0	248	7	US-11-106-820-16	Sequence 16, Appl	235	686.5	19.5	472	7	US-11-086-289-10	Sequence 10, Appl
163	706	20.0	248	7	US-11-190-364-15	Sequence 15, Appl	236	686	19.5	471	7	US-11-086-289-6	Sequence 6, Appl
164	706	20.0	450	7	US-11-005-726-161	Sequence 161, App	237	684	19.4	218	6	US-10-923-327-8	Sequence 8, Appl
165	705.5	20.0	451	7	US-11-102-621-146	Sequence 146, App	238	684	19.4	218	6	US-10-923-327-10	Sequence 10, Appl
166	705.5	20.0	478	7	US-11-139-499-8	Sequence 8, Appl	239	684	19.4	218	6	US-10-923-327-12	Sequence 12, Appl
167	703.5	20.0	451	6	US-10-923-327-11	Sequence 11, Appl	240	684	19.4	218	6	US-10-923-327-17	Sequence 17, Appl
168	703.5	20.0	451	7	US-11-102-621-144	Sequence 144, App	241	683.5	19.4	215	7	US-11-102-621-141	Sequence 141, App
169	703.5	20.0	451	7	US-11-166-906-1	Sequence 1, Appl	242	683.5	19.4	215	7	US-11-166-906-2	Sequence 2, Appl
170	703	20.0	218	7	US-11-004-590-229	Sequence 229, App	243	681.5	19.3	213	7	US-11-172-320-4	Sequence 4, Appl
171	703	20.0	237	7	US-11-054-669-109	Sequence 109, App	244	681.5	19.3	213	7	US-11-173-969-4	Sequence 4, Appl

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247	679	19.3	463	7	US-11-128-900-64
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249	678	19.3	463	7	US-11-128-900-63
250	677	19.2	236	7	US-11-144-248-51
251	677	19.2	236	7	US-11-144-248-51
252	677	19.2	236	7	US-11-182-343-51
253	675.5	19.2	470	7	US-11-072-512-3730
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259	666.5	18.9	574	6	US-10-493-909-45
260	665.5	18.9	238	7	US-11-177-648-34
261	664.5	18.9	230	7	US-11-032-773-957
262	664.5	18.9	319	7	US-11-032-773-955
263	663	18.8	214	7	US-11-005-726-163
264	661.5	18.8	238	7	US-11-177-648-35
265	661.5	18.8	478	7	US-11-072-512-3812
266	660.5	18.8	213	7	US-11-174-186-42
267	660.5	18.8	236	7	US-11-106-820-19
268	660.5	18.8	236	7	US-11-190-364-17
269	660.5	18.8	476	7	US-11-139-499-4
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272	655.5	18.6	238	7	US-11-177-648-39
273	655.5	18.6	543	6	US-10-495-664-3
274	654.5	18.6	238	7	US-11-177-648-36
275	651.5	18.5	238	7	US-11-177-648-38
276	649.5	18.4	250	7	US-11-054-669-110
277	646.5	18.4	239	7	US-11-086-289-12
278	646.5	18.4	238	7	US-11-177-648-37
279	645.5	18.3	238	7	US-11-177-648-40
280	638.5	18.1	249	7	US-11-054-515-1635
281	638	18.1	248	7	US-11-054-515-1104
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283	636	18.1	233	6	US-10-923-327-19
284	635	18.0	229	6	US-10-923-327-13
285	635	18.0	233	6	US-10-923-327-18
286	632.5	18.0	239	7	US-11-177-648-10
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297	602.5	17.1	248	6	US-10-512-184-36
298	602	17.1	248	7	US-11-054-515-1446
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300	599	17.0	236	7	US-11-000-463-394

ALIGNMENTS

RESULT 1	
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Sequence 4, Application US/10016686	
Publication No. US20060014222A1	
GENERAL INFORMATION:	
APPLICANT: Oxford Biomedica (UK) Limited	
APPLICANT: Kingeman, Alan	
APPLICANT: Kingeman, Susan Mary	
APPLICANT: Bebbington, Christopher Robert	
APPLICANT: Carrol, Miles William	
APPLICANT: Ellard, Fiona Margaret	
APPLICANT: Myers, Kevin Alan	
Query Match 30.4%; Score 1069; DB 6; Length 592;	
Best Local Similarity 37.9%; Pred. No. 9.5e-49;	
Matches 254; Conservative 20; Mismatches 60; Indels 336; Gaps 9;	
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QY 61 NOKFKDKAILTVDKSSTTAYMELRLSITSDSAVYICARSTMTITNYMDYWGQTSVTVSS 120	
DB 80 NOKFKDKAILTVDKSSTTAYMELRLSITSDSAVYICARSTMTITNYMDYWGQTSVTVS- 138	
QY 121 AKTTPPSVPLAPGSAQTNSMVTLCGLVKGYPEPVTVTWNSGSLSSGVHTTTPAVLQSD 180	
DB 139 -----SOG----- 141	
QY 241 SELQGTALGNLKOIYYNNSKAITSEKSAQDFLTNTLLFKGFTGHPWYNDLLVDLGSTA 300	
DB 142 ----- 141	
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTGPKTACMYGGVTLHDNNRLTEBKVPINLWIDGKQ 360	
DB 142 -----GGSGGGT-----GG----- 151	
QY 361 TTVPIDKVTSKKEVTVQBELDQARHYLHGKFLGYNLSDSFGGKVGRLIVFHSSEGSTVS 420	
DB 152 -----GG----- 153	
QY 421 YDLFDAQQQVPTLLRIYRDNTTISSTLSLSLYLTTSIVMTQTPTSLLSVSGADRVIT 480	
DB 154 -----SSIVMTQTPTFLLSVSGADRVIT 176	
QY 481 CKASQSVNDVAMVYQKPGSKLLISYTSRRVAGVPDRFSGSGYGTDFTLTSSVOAED 540	
DB 177 CKASQSVNDVAMVYQKPGSKPTLLISYTSRRVAGVPDRFSGYGTDFTLTSTLOAED 236	
QY 541 AAVYFCQDYNSPPTFGGGTKLEIKRADA-APTVSIFFPSSEQLTSGGASVWCFLNNFYP 599	
DB 237 LAVYFCQDYNSPPTFGGGTKLEIKRATKSPSVFPPLAPSSKSTSGTAAALGCLVKDYFP 296	
QY 600 KDINVKW-----IDGERONGVNLNSWTDQDSKDSYMSSTLTLTLDKDEYRHNSYTCAT 655	
DB 297 EPTVTSWNSGALTSVGVHTTTPAVLQS-----SGLYSLSVVTVPSSSLGT-QTYICNVN 348	
QY 656 HKTSTSPIVK 665	
DB 349 HKPSNTKVDK 358	
RESULT 2	
US-10-016-686-1	
Sequence 1, Application US/10016686	
Publication No. US20060014222A1	

GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Limited
; APPLICANT: Kingeman, Alan
; APPLICANT: Kingeman, Susan Mary
; APPLICANT: Bebbington, Christopher Robert
; APPLICANT: Carroll, Miles William
; APPLICANT: Ellard, Fiona Margaret
; APPLICANT: Myers, Kevin Alan
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 674523-2012
; CURRENT APPLICATION NUMBER: US/10/016,686
; CURRENT FILING DATE: 2002-11-02
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of the mature secreted protein
US-10-016-686-1

Query Match 27.6%; Score 972.5; DB 6; Length 243;
Best Local Similarity 40.1%; Pred. No. 3.9e-44;
Matches 227; Conservative 3; Mismatches 13; Indels 323; Gaps 5;

QY 1 EVLOQSGPDLVKPGASVKISCKASGYSTGYMHVWKSPGKLEWIGRIINPNNGVTLV 60
DB 1 EVLOQSGPDLVKPGASVKISCKASGYSTGYMHVWKSPGKLEWIGRIINPNNGVTLV 60

QY 61 NQKFKDKAILTVDKSSTTAYMELRLSTSDSAVYYCARSTMTINYYMDYWGQTSVTSS 120
DB 61 NQKFKDKAILTVDKSSTTAYMELRLSTSDSAVYYCARSTMTINYYMDYWGQTSVTSS- 119

QY 121 AKTTPPSVYPLAPGSAQTNSMVTLCGLVKGYFPEPVTVTWNSGSLSSGVHTFPFVLQSD 180
DB 120 ----- 119

QY 181 LYTSSSVTPSPSTWPSSETVTCNVAHPASSTKVDDKIIPRDSGGPSEKSEINEKDLRKK 240
DB 120 -----SGG----- 122

QY 241 SELQGTALGNLKOIYYNSKAITSSSEKADQFLTNTLLFKGFTGHPWYNDLLVDLGSTA 300
DB 123 ----- 122

QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEBEKKVPINLWIDGKQ 360
DB 123 -----GGSGGGT----- 132

QY 361 TTVPIDKVKTSKEVTVQELDLOARHYLHGKFLGYNDSFGGKVQKGLIVFHSSEGSTVS 420
DB 133 -----GG----- 134

QY 421 YDLFDAQGOQYPTDLLRIYRDNTTISSTLSISLYLTTSIVMTQTPTSLVNSAGDRVITIT 480
DB 135 -----SSIVMTQTPTFLVNSAGDRVITIT 157

QY 481 CKASQSVNDVAWYQKPGSKLLISYTSRRYAGVDPDRFSGSGYGTDFTLTISVQAE 540
DB 158 CKASQSVNDVAWYQKPGSKPFLLLISYTSRRYAGVDPDRFSGSGYGTDFTLTISTLOAED 217

QY 541 AAVYFCQDYNSPPTFGGKTLEIKR 566
DB 218 LAVYFCQDYNSPPTFGGKTLEIKR 243

RESULT 3
US-10-016-686-3
; Sequence 3, Application US/10016686
; Publication No. US20060014222A1

GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Limited
; APPLICANT: Kingeman, Alan
; APPLICANT: Kingeman, Susan Mary
; APPLICANT: Bebbington, Christopher Robert
; APPLICANT: Carroll, Miles William
; APPLICANT: Ellard, Fiona Margaret
; APPLICANT: Myers, Kevin Alan
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 674523-2012
; CURRENT APPLICATION NUMBER: US/10/016,686
; CURRENT FILING DATE: 2002-11-02
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: deduced amino acid sequence for the B7-1.5T4.1 fusion protein
US-10-016-686-3

Query Match 27.5%; Score 967.5; DB 6; Length 488;
Best Local Similarity 40.0%; Pred. No. 1.4e-43;
Matches 226; Conservative 3; Mismatches 13; Indels 323; Gaps 5;

QY 1 EVLOQSGPDLVKPGASVKISCKASGYSTGYMHVWKSPGKLEWIGRIINPNNGVTLV 60
DB 247 EVLOQSGPDLVKPGASVKISCKASGYSTGYMHVWKSPGKLEWIGRIINPNNGVTLV 306

QY 61 NQKFKDKAILTVDKSSTTAYMELRLSTSDSAVYYCARSTMTINYYMDYWGQTSVTSS 120
DB 307 NQKFKDKAILTVDKSSTTAYMELRLSTSDSAVYYCARSTMTINYYMDYWGQTSVTSS- 365

QY 121 AKTTPPSVYPLAPGSAQTNSMVTLCGLVKGYFPEPVTVTWNSGSLSSGVHTFPFVLQSD 180
DB 366 ----- 365

QY 181 LYTSSSVTPSPSTWPSSETVTCNVAHPASSTKVDDKIIPRDSGGPSEKSEINEKDLRKK 240
DB 366 -----SGG----- 368

QY 241 SELQGTALGNLKOIYYNSKAITSSSEKADQFLTNTLLFKGFTGHPWYNDLLVDLGSTA 300
DB 369 ----- 368

QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEBEKKVPINLWIDGKQ 360
DB 369 -----GGSGGGT----- 378

QY 361 TTVPIDKVKTSKEVTVQELDLOARHYLHGKFLGYNDSFGGKVQKGLIVFHSSEGSTVS 420
DB 379 -----GG----- 380

QY 421 YDLFDAQGOQYPTDLLRIYRDNTTISSTLSISLYLTTSIVMTQTPTSLVNSAGDRVITIT 480
DB 381 -----SSIVMTQTPTFLVNSAGDRVITIT 403

QY 481 CKASQSVNDVAWYQKPGSKLLISYTSRRYAGVDPDRFSGSGYGTDFTLTISVQAE 540
DB 404 CKASQSVNDVAWYQKPGSKPFLLLISYTSRRYAGVDPDRFSGSGYGTDFTLTISTLOAED 463

QY 541 AAVYFCQDYNSPPTFGGKTLEIK 565
DB 464 LAVYFCQDYNSPPTFGGKTLEIK 488

RESULT 4
US-11-022-562-226
; Sequence 226, Application US/11022562
; Publication No. US20050249742A1

```

; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; APPLICANT: Shisong, Jiang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
; FILE REFERENCE: DFN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 226
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-11-022-562-226

Query Match      26.8%; Score 944; DB 7; Length 233;
Best Local Similarity 76.0%; Pred. No. 1.le-42;
Matches 177; Conservative 22; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLKKSELOQTALGNLKQIYYNSKAITSEKSAOQFLTNLLFKGFFTG 285
Db 1 SEKSEINEKDLKKSELOQTALGNLKQIYYNEKAKTENKESHDQFLOHTILFKGFFTD 60

QY 286 HPYNDLLVDLGSTAATSEVEGSSVDLYGAYGOCAGGTPNKTACMYGGVTLHDNNRLT 345
Db 61 HSWYNDLLVDLGSKIDVRYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 120

QY 346 EEKKVPINLWIDGKQTTPIDKVKTSKEVTQVGLDQARHYLHGKFGLYNSDSFGKQV 405
Db 121 EEKKVPINLWIDGKQNTVPLETKNKQNTVQVGLDQARRYLOEKYLNLYNSDVFQKQ 180

QY 406 RGLIVFHSSEGSTSVSDLDFAQOQYPTLLRIYRDNTTISSTLSLSLYTT 458
Db 181 RGLIVFHTPEPSVNYDLFGAQOQYSNTLRIYRDNKSINSENHIDIYLYTS 233

RESULT 5
US-11-000-463-335
; Sequence 335, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03

; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; APPLICANT: Shisong, Jiang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
; FILE REFERENCE: DFN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 226
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-11-022-562-226

Query Match      25.1%; Score 885; DB 7; Length 363;
Best Local Similarity 30.8%; Pred. No. 1.9e-39;
Matches 205; Conservative 56; Mismatches 82; Indels 328; Gaps 5;

QY 1 EVOLQOQPDLVKPGASVKISKASGYSTGYVMHWKQSPGKGLWIGIRPNNGVTLY 60
Db 20 EVQLLESGGGLVQPGGSLRLSCAASGFTPSFSMSVVRQAPGKGLWVSSISGSGTTY 79

QY 61 NQKFKDKATLTVDKSTTAYMELRLSTSDSAVYVYCARSTMTIYNYVNDYWGQTSVTSS 120
Db 80 ADSVKGRFTISRDNKNTLYLQWNSLRAREDVAVYCAKPPP-----YFDYWGQGLTVTSS 135

QY 121 AKTTPSVVPLAPGSAQAQTNMVTGLCLVKGYGPEPVTVTWNSGSLSSGVHTTTPAVLQSD 180
Db 136 G-----

QY 181 LVTLSSTVTPSSTWTPSETVTCNVAHPASSTKVDKIVPRDSGGPSEKSEINEKDLKK 240
Db 137 -----

QY 241 SELQGTALGNLKQIYYNSKAITSEKSAOQFLTNLLFKGFTGHPWYNDLLVDLGSTA 300
Db 137 -----

QY 301 ATSEYEGSSVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQ 360
Db 137 -----DGSS-----GGS-----

QY 361 TTVPIDKVKTSKEVTQVGLDQARHYLHGKFGLYNSDSFGKQVQRLIVFHSSEGSTVS 420
Db 144 -----VTVSSSDIQ-----

QY 421 YDLFDAQOQYPTLLRIYRDNTTISSTLSLSLYTTISVMTQTPTSLVLSAGDRVITIT 480
Db 153 -----MTQSPSTLSASVGDRTIT 171

QY 481 CKASQSVNDVAVYQOKPGQSPKLLISYTTSSRYAGVDRPSGSGYGTDTFTLTSSVQAE 540
Db 172 CRASQSIISWLAWYQOKPGKAPKLLIYKASSUESGVPSPSGSGGTFDTLTSSVQPD 231

QY 541 AAVYFCQDYNPGPTFGGKTKLEIKRADAAAPTYSIFPPSSEQLTSGASVVCFLNNFPYK 600
Db 232 FAYYCOQVYVYPLTFEGGKTKVEIKTVAAPSVFIFFPSDEQLKSGTASVCLNNFPYR 291

QY 601 DINVKWKIDGSEKQNGVLNSWTDQDSKSTYSMSSTLTITKDYERHNSVTCATHKST 660
Db 292 EAKVQWKVDNALQSGNSQESVTEQDSKSTYSLSLTLSKADYKHKLVACEVTHQGLS 351

QY 661 SPIVKSFRNE 671
Db 352 SPVTKSFRNGE 362

RESULT 6
US-10-981-356A-29
; Sequence 29, Application US/10981356A
; Publication No. US20060015952A1
; GENERAL INFORMATION:
; APPLICANT: FILVAROFF, ELLEN H.
; TITLE OF INVENTION: SCREENING ASSAYS AND METHODS OF TUMOR TREATMENT
; FILE REFERENCE: P2068R1
; CURRENT APPLICATION NUMBER: US/10/981,356A
; CURRENT FILING DATE: 2004-11-04
```



```
Db          648 MHE 650
RESULT 8
US-11-177-648-9
; Sequence 9, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMELIN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; PRIOR FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Homo sapien
US-11-177-648-9

Query Match      24.2%; Score 852.5; DB 7; Length 462;
Best Local Similarity 32.4%; Pred. No. 1.1e-37;
Matches 220; Conservative 59; Mismatches 126; Indels 273; Gaps 17;

QY      1 EVLOQSGDPLVKPGASVKISCKASGYSTFGYMHVWVKQSPGKLEWIGRINPNNGVTLY 60
Db      20 QVLOQPGTGLVKPGASVKLSCKASGYTFTSYMHVWVKQSPGKLEWIGRINPNNGVTNY 79
QY      61 NQKFKDKATLVKDSSTTAYMELSLTSEDVAVYCARSTMTITNYVMDYMGQGTSTVTS 120
Db      80 NEAFKSKATLVKDSSTAYMQLSSLTSEDVAVYCELG-----QGYMGQGTSTVTS 132
QY      121 AKTTPSVVPLAPGSAQAQNSMTVLGCLVKGYFPEPVTVTWNSGSLSSGVHTTTPAVLQSD 180
Db      133 ASTKGPSVFPPLAPSGKSTGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQSS 192
QY      181 -LYTLSSVTVPSSTWPSSETVTCNVAHPASSTKVDKKIVPRD-----SGG 224
Db      193 GLYSLSVTVPSSSLGTQTYICNVNHKPSNTKVDKKEPKSCDKTHTCPPCPAPELAGA 252
QY      225 PSEKSEINEKOLRKKSELGQTALGNLKQIYYNSKAITSSSEKSAQDQFLNTLLFKGFFT 284
Db      253 PS-----VFLPPKP-----KDTLM----- 268
QY      285 GHPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYQCAGTTPNKTCMYGGVTLHDNRL 344
Db      269 -----SRTPEVT-CVVVDVS----- 282
QY      345 TEKKVPINLWIDGKQTTPIDKVKTSKKEVTVQELDLQARHLHGKFGLYNSDSFGKV 404
Db      283 HEDPEVKFNWYDVG-----VEVHNAKTPREQ-----YNSTY---RV 317
QY      405 QRGLIVFHSSEGSTVSYDLFDAQQQYDPTLLRIYRDNTTISSTLSLSLYTTSIVMTQ 464
Db      318 VSVLTVLHQDWLNGKEY----- 334
QY      465 TPTSLVAGDRVITITCKASQSVSNVAVYQKPGQSPKLLISYTSRYAGVDPDRPSGSG 524
Db      335 -----KCKVS-----NKALPAP-----IEKTISKAKGP----- 358
QY      525 YGTDFTLTISVQAEADNAVYFCQDYNSPTFFGGTKLEIKRADAAPTVSIFFPSSEQLT 584
Db      359 -----REFQVYTLPPSRDELT----- 374
```

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QY      585 SGCASVVCFLNFPKDIINVKIDGSERON-----GVLSWTDQDSKDSSTYSMSSTLT 639
Db      375 KNQVSLTCLVKGYFSPSDIAVWESNGPENNYTKTPVLDL-----DGSFFLYSKLTV 427
QY      640 TKDEYERHNSYTCETHK 657
Db      428 DKSRWQQGNVFCSCVMHE 445

RESULT 9
US-11-124-620-7
; Sequence 7, Application US/11124620
; Publication No. US20060024298A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Dang, Wei
; APPLICANT: Desjarlais, John R.
; APPLICANT: Karki, Sher Bahadur
; APPLICANT: Vafa, Omid
; APPLICANT: Hayes, Robert
; TITLE OF INVENTION: OPTIMIZED FC VARIANTS
; FILE REFERENCE: A-71386-9
; CURRENT APPLICATION NUMBER: US/11/124,620
; PRIOR FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: US 60/568,440
; PRIOR FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/589,906
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 60/627,026
; PRIOR FILING DATE: 2004-11-09
; PRIOR APPLICATION NUMBER: US 60/626,991
; PRIOR FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US 60/627,774
; PRIOR FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 10/822,231
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 10/672,280
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US 10/379,392
; PRIOR FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 7
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-620-7

Query Match      24.1%; Score 850.5; DB 7; Length 451;
Best Local Similarity 33.6%; Pred. No. 1.4e-37;
Matches 223; Conservative 58; Mismatches 146; Indels 237; Gaps 17;

QY      1 EVLOQSGDPLVKPGASVKISCKASGYSTFGYMHVWVKQSPGKLEWIGRINPNNGVTLY 60
Db      1 QVLOQPGAEVLKPGASVKMSCKASGYTFTSYNMHWVKQTPGRGLEWIGAIYPCNGDTSY 60
QY      61 NQKFKDKATLVKDSSTTAYMELSLTSEDVAVYCARSTMI-TNYVMDYMGQGTSTVTS 119
Db      61 NQKFKGKATLVKDSSTAYMQLSSLTSEDVAVYCARSTYCGDYFNVWAGATTVTVS 120
QY      120 SAKTTPSVVPLAPGSAQAQNSMTVLGCLVKGYFPEPVTVTWNSGSLSSGVHTTTPAVLQS 179
Db      121 AASTKGPSVFPPLAPSGKSTGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQS 180
QY      180 D-LYTLSSVTVPSSTWPSSETVTCNVAHPASSTKVDKKIVPRDSGGPSEKSEINEKDLR 238
Db      181 SGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVDKCAEPKSC----- 224
QY      239 KKSELOGTALGNLKQIYYNSKAITSSSEKSAQDQFLNTLLFKGFFTGHWPYNDLLVLDGS 298
Db      225 -----DKTHTCPPCPAPELGGPSVF--LFPKP--KDTLM----- 256
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QY 299 TAATSEYEGSSVDLYGAYYGQCAGGTGPNKTACMYGGVTLHDNNRLTEBKVPINLWIDG 358
Db 257 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVDG 285
QY 359 KQTTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKQVORGILIVFHSSEGST 418
Db 286 ----VEVHNKTKPREEQ-----YNSTY----RVVSVLTVLHQDWLNG 320
QY 419 VSYDLFDAQOQYPTLLRIYRDNTTISSTLSISLYLYTTSIVMTQPTPTSLLSAGDRV 478
Db 321 KEY----- 323
QY 479 ITCASQSVNDVAMVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDTLTITSSVQA 538
Db 324 -KCKVS-----NKALPAP---IEKTISKAKGQP----- 347
QY 539 EDAAVFYCOQDYNSPPTFGGGTKLEIKRADAAPTIVSIFPPSSSEQLTSGGASVVCFLNFPY 598
Db 348 -----REPQVYTLPPSRDELTKNQVSLTCLVKGFY 377
QY 599 PKDINVWKIDGSERON-----GVLSNWTDDQSKDSTYSMSSTLTLTQDEYERHNSYTCB 653
Db 378 PSDIAVEWESNGQPENNYKTTPPVLDSE-----DGSFFLYSKLTVDKSRWQQGNVFSCS 430
QY 654 ATHK 657
Db 431 VMHE 434

RESULT 10
US-11-102-621-119
; Sequence 119, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tseo, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT FILING DATE: 2005-04-08
; CURRENT APPLICATION NUMBER: US/11/102,621
; PRIOR FILING DATE: 2004-04-09
; PRIOR APPLICATION NUMBER: US 10/822,300
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 119
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-119

Query Match 24.1%; Score 849; DB 7; Length 446;
Best Local Similarity 33.0%; Pred. No. 1.6e-37;
Matches 219; Conservative 62; Mismatches 142; Indels 240; Gaps 17;

QY 1 EVLOQSGDPLVKPGASVKISKASGYSTGYTHMHWKQSPGKGLWIGRIINPNNGVTLY 60
Db 1 QVQLVQSGAEVKKPGSSVKVCKASGYTFTSYRMHWVRQAPGQGLWIGVINPSTGYTEY 60
QY 61 NQKFKDKATLTVDKSTTAYMELRSLTSEDSAVYYCARSTMTITNYVMDYWGQGTSTVVS 120
Db 61 NQKFKDKATITADESTNTAYMELSLRSEDTAVYYCARG-----GGVFDYWGQGTLTVVS 116
QY 121 AKTTPPSVPLAPGSAQTNSMVTGLCLVKGYFPEPVPTVITWNSGSLSSGVHTHPAVLQSD 180
Db 117 ASTKGFSPVPLAPSSKTSQGTALGLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 176
QY 181 -LYLTSSSVTPSPSTWPESTVTCNVAHPASSTKVDKKIIPRDSGGPSEKSEENKDLRK 239
Db 177 GLYSLSVSVTPSSSLGTQYICNVNHPKSTNKKVBPKSC----- 219
```

```
QY 240 KSELQGTALGNLKQIYYNSKAITSEKSADQFLTNLTLLPKGFETGHPWVNDLLVDLGST 299
Db 220 -----DKTHTCPPCPAPPELLGSPVF--LFPPKP-KDDLMI----- 252
QY 300 AATSEYEGSSVDLYGAYYGQCAGGTGPNKTACMYGGVTLHDNNRLTEBKVPINLWIDG 359
Db 253 -----SRTPEVT-CVVVDVS-----HEDPEVKFNWYVDG- 280
QY 360 QTTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKQVORGILIVFHSSEGSTV 419
Db 281 ----VEVHNKTKPREEQ-----YNSTY----RVVSVLTVLHQDWLNGK 316
QY 420 SYDLFDAQOQYPTLLRIYRDNTTISSTLSISLYLYTTSIVMTQPTPTSLLSAGDRV 479
Db 317 EY----- 318
QY 480 TCKASQSVNDVAMVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDTLTITSSVQA 539
Db 319 KCKVS-----NKALPAP---IEKTISKAKGQP----- 342
QY 540 DAAVYFCQDYNSPPTFGGGTKLEIKRADAAPTIVSIFPPSSSEQLTSGGASVVCFLNFPY 599
Db 343 -----REPQVYTLPPSRDELTKNQVSLTCLVKGFY 373
QY 600 KDINVWKIDGSERON-----GVLSNWTDDQSKDSTYSMSSTLTLTQDEYERHNSYTCB 654
Db 374 SDIAVEWESNGQPENNYKTTPPVLDSE-----DGSFFLYSKLTVDKSRWQQGNVFSCSV 426
QY 655 THK 657
Db 427 MHE 429

RESULT 11
US-11-102-621-120
; Sequence 120, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tseo, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT FILING DATE: 2005-04-08
; CURRENT APPLICATION NUMBER: US/11/102,621
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 120
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-120

Query Match 24.0%; Score 846; DB 7; Length 446;
Best Local Similarity 32.0%; Pred. No. 2.3e-37;
Matches 217; Conservative 62; Mismatches 129; Indels 270; Gaps 17;

QY 1 EVLOQSGDPLVKPGASVKISKASGYSTGYTHMHWKQSPGKGLWIGRIINPNNGVTLY 60
Db 1 QVQLVQSGAEVKKPGSSVKVCKASGYTFTSYRMHWVRQAPGQGLWIGVINPSTGYTEY 60
QY 61 NQKFKDKATLTVDKSTTAYMELRSLTSEDSAVYYCARSTMTITNYVMDYWGQGTSTVVS 120
Db 61 NQKFKDKATITADESTNTAYMELSLRSEDTAVYYCARG-----GGVFDYWGQGTLTVVS 116
QY 121 AKTTPPSVPLAPGSAQTNSMVTGLCLVKGYFPEPVPTVITWNSGSLSSGVHTHPAVLQSD 180
Db 121 AKTTPPSVPLAPGSAQTNSMVTGLCLVKGYFPEPVPTVITWNSGSLSSGVHTHPAVLQSD 180
```

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Db 117 ASTKGPVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTFAVLQSS 176
QY 181 -LYTLSSVTVPSSTWSPSETVTCNVAHPASSTKVDKIVPRDS-----GG 224
Db 177 GLYSLSVTVPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKTHTCTPCPAPELLGG 236
QY 225 PSKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSEKSAQOFLNTLLFKGFFT 284
Db 237 PS-----VFLF-----PPKPKDQLMISR----- 254
QY 285 GHPWYNLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGVTLHDNNRL 344
Db 255 -----TPEVT-CVVVDVS----- 266
QY 345 TEEKKVPINLWIDGKOTVPIDKVKTSKKEVTVOELDQARHYLHGKFLGYNDSFGKV 404
Db 267 HEDPEVKFNWYVDG---VEVHNAKTPREEQ-----YNSTY---RV 301
QY 405 QRLIVPHSSEGSTVSVDLFDAGQGYPTDLLRIYRNTTISLSISLYTTSIMVMTQ 464
Db 302 VSVLTVLHQDWLNGKEY-----NKAHPAP---IEKTISKAKGQP----- 318
QY 465 TPTSLLSVAGSDRVTITCKASQSVSNVAVYQKPGOSPKLLISYTSRYAGVDRFSGSG 524
Db 319 -----KCKVS-----NKAHPAP---IEKTISKAKGQP----- 342
QY 525 YGDTFTLTISSVOAEDAAYVFCQDYNSPPTFGGKLEIKRADAAPTIVSIPPPSSEQLT 584
Db 343 -----REPQVYTLPPSRDELT 358
QY 585 SGGASVVCFLNNFPKDVNKKIDGSEKRON-----GVLSNWTDDQSKSTYSMSSTLTL 639
Db 359 KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD-----DGSFFLYSKLTV 411
QY 640 TKDEYERHNSYTCETHK 657
Db 412 DKSRWQOQGNVFCSCVLHE 429

RESULT 13
US-11-102-621-122
; Sequence 122, Application US/11102621
; Publication No. US2005027699A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 122
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-122

Query Match 24.0%; Score 846; DB 7; Length 446;
Best Local Similarity 32.08; Pred. No. 2.3e-37;
Matches 217; Conservative 62; Mismatches 129; Indels 270; Gaps 17;

QY 1 EVOLQSGDPLVLPFGASVKLSCKASGYSTFTGYMHVWVQSPGKGLGWIGRINPNNGVTLY 60
Db 1 QVQLVSGAEVLPFGSSVKVSKASGYSTFTSYRHHVWRQAPGGQGLEWIGVINFSTGYEY 60
QY 61 NQKFKDKATLTVDKSTTAYMELRSITSEDSAVYYCARSTMTITNYVNDYWGQGTSTVTVSS 120
```

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Db 61 NQKFKDKATITADESTNTAYMELSSLRSEDTAVYYCARG-----GGVFDYWGQGTSTVTVSS 116
QY 121 AKTTPPSVTVPLAPSGAQAQNSMTVTLCLVKGYPEPEPVTVTWNSGSLSSGVTTPPAVLQSD 180
Db 117 ASTKGPVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTFAVLQSS 176
QY 181 -LYTLSSVTVPSSTWSPSETVTCNVAHPASSTKVDKIVPRDS-----GG 224
Db 177 GLYSLSVTVPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKTHTCTPCPAPELLGG 236
QY 225 PSKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSEKSAQOFLNTLLFKGFFT 284
Db 237 PS-----VFLF-----PPKPKDQLMISR----- 254
QY 285 GHPWYNLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGVTLHDNNRL 344
Db 255 -----TPEVT-CVVVDVS----- 266
QY 345 TEEKKVPINLWIDGKOTVPIDKVKTSKKEVTVOELDQARHYLHGKFLGYNDSFGKV 404
Db 267 HEDPEVKFNWYVDG---VEVHNAKTPREEQ-----YNSTY---RV 301
QY 405 QRLIVPHSSEGSTVSVDLFDAGQGYPTDLLRIYRNTTISLSISLYTTSIMVMTQ 464
Db 302 VSVLTVLHQDWLNGKEY-----NKAHPAP---IEKTISKAKGQP----- 318
QY 465 TPTSLLSVAGSDRVTITCKASQSVSNVAVYQKPGOSPKLLISYTSRYAGVDRFSGSG 524
Db 319 -----KCKVS-----NKAHPAP---IEKTISKAKGQP----- 342
QY 525 YGDTFTLTISSVOAEDAAYVFCQDYNSPPTFGGKLEIKRADAAPTIVSIPPPSSEQLT 584
Db 343 -----REPQVYTLPPSRDELT 358
QY 585 SGGASVVCFLNNFPKDVNKKIDGSEKRON-----GVLSNWTDDQSKSTYSMSSTLTL 639
Db 359 KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD-----DGSFFLYSKLTV 411
QY 640 TKDEYERHNSYTCETHK 657
Db 412 DKSRWQOQGNVFCSCVLHE 429

RESULT 13
US-11-124-620-5
; Sequence 5, Application US/11124620
; Publication No. US20060024298A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Dang, Wei
; APPLICANT: Desjarlais, John R.
; APPLICANT: Karki, Sher Bahadur
; APPLICANT: Vafa, Omid
; APPLICANT: Hayes, Robert
; TITLE OF INVENTION: OPTIMIZED FC VARIANTS
; FILE REFERENCE: A-71386-9
; CURRENT APPLICATION NUMBER: US/11/124,620
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: US 60/568,440
; PRIOR FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/589,906
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 60/627,026
; PRIOR FILING DATE: 2004-11-09
; PRIOR APPLICATION NUMBER: US 60/626,991
; PRIOR FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US 60/627,774
; PRIOR FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 10/822,231
; PRIOR FILING DATE: 2004-03-26
; PRIOR APPLICATION NUMBER: US 10/672,280
; PRIOR FILING DATE: 2003-09-26
```

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; PRIOR APPLICATION NUMBER: US 10/379,392
; PRIOR FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (243)..(243)
; OTHER INFORMATION: xaa can be Serine, Aspartic Acid, Glutamic Acid, Asparagine,
; OTHER INFORMATION: Glutamine or Threonine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (244)..(244)
; OTHER INFORMATION: xaa can be Valine, Isoleucine or Methionine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (268)..(268)
; OTHER INFORMATION: xaa can be Valine, Isoleucine, Threonine or Tyrosine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (272)..(272)
; OTHER INFORMATION: xaa can be Histidine, Aspartic Acid or Glutamic Acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (276)..(276)
; OTHER INFORMATION: xaa can be Glutamic Acid or Tyrosine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (278)..(278)
; OTHER INFORMATION: xaa can be Lysine or Glutamic Acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (301)..(301)
; OTHER INFORMATION: xaa can be Asparagine or Aspartic Acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (302)..(302)
; OTHER INFORMATION: xaa can be Serine, Alanine or Aspartic Acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (330)..(330)
; OTHER INFORMATION: xaa can be Lysine, Glutamic Acid or Threonine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (334)..(334)
; OTHER INFORMATION: xaa can be Alanine, Tyrosine, Leucine or Isoleucine
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (336)..(336)
; OTHER INFORMATION: xaa can be Isoleucine, Aspartic Acid, Glutamic Acid, Asparagine
; OTHER INFORMATION: or Glutamine
; US-11-124-620-5

```

Query Match	24.0%	Score 845.5;	DB 7;	Length 451;
Best Local Similarity	32.8%;	Pred. No. 2.5e-37;		
Matches 220:	Conservative	58;	Mismatches 142;	Indels 251; Gaps 17

[illegible]

180	Qy	D-LYTLSSVTVPSSTWSEVTVCNAHPASSTKVDKKIVPRDSGGSPSEKSEINEKD	238
181	Db	SGLYSLSSVVTVPPSSSLGTQYI CNVNHKPSNTKVDKKAEPKSC-	224
239	Qy	KKSELQGTALGNLKQIYYYNASKAITSEKSADQFLTNTLFLFKGFFTHGHPWYNLDLVLGS	298
225	Db	-----DKTHCTPCCPAPELLGGPXXF--LFPKP--KDTLM-----	256
299	Qy	TAATSEYEGSSVDLYGAYYGQCAGGTPTNCTACMYGGVTLHDNNRLTEEEKVFINLWIDG	358
257	Db	-----ISRTPEVT-CVVXDV-----XEDPVXVFNMYVDG	285
359	Qy	KQTTVPIDKVTSSKEV-----TVQBLDQARHYLHGKFLGYNLSDSFGKGQVGRGLIV	411
286	Db	-----VEVHNAKTKPREEQXXXYRVVSVLTVLHQDLNGK-----	321
412	Qy	HSSEGSTVSYDLFDAQQGYPTDLLRIYRDNTTISSTSLSLSLYLYTTSIWNQTPTSLV	471
322	Db	-----EY-----	323
472	Qy	SAGDRVITTCASQSVSNDVAWYQKQSGSKLLISVYTSRKYAGVPDRFSGSGYGTFTL	531
324	Db	-----KCKVSXNA-----LPXPXEK-----TISKAKGP-----	347
532	Qy	TISSVQAEADAAYFCQDYNSPPTFGGKTLEIKRAADAPTVISIFPPSSSOLTSGGASVV	591
348	Db	-----REPVYTLPPSRDELTKNQVSLT	370
592	Qy	CFLNNFPKIDINVKKIDGSEQRN-----GVLNSWTDQDSKDSYSMSSTLTITKDEYER	646
371	Db	CLVKGFFSDIAVENESNGQPNYKITPPVLDS-----DGSFFLYSLKLTVDKSRWQ	423
647	Qy	HNSYTCEATHK	657
424	Db	GNVFFCSVMHE	434

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RESULT 14
US-11-102-621-123
; Sequence 123, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FCGR BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 123
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-123

```

Query Match	24.0%	Score 845;	DB 7;	Length 446;
Best Local Similarity	32.0%;	Pred. No. 2.6e-37;		
Matches	217;	Conservative	62;	Mismatches 129;
				Indels 270;
				Gaps 17;

[illegible]

Db 61 NQPKDKATITADSTNTAYMELSLRSEDNAVYICARG-----GGVFDYMGQGGFLVTVSS 116
Qy 121 AKTTPPSVYPLAPGSAQAQTNMTVLGCLVKGYPPEPVTVTWNSGSLSSGVHTFPFVQLQSD 180
Db 117 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALTSGVHTFPFVQLQSS 176
Qy 181 -LYTLSSSVTPSPSTPSETVTCNVAHPASSTKVDKKIVPRDS-----GG 224
Db 177 GLXSLSSVTPSPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCPCPAPELGG 236
Qy 225 PSEKSEBINEKDLRKSELOQTALGNLQIYYVNSKAITSEKSDAQFLNTLLFKGFFT 284
Db 237 PS-----VFLP-----PPKPKDQLMISR----- 254
Qy 285 GHPWYNDLLVDLSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRL 344
Db 255 -----TPEVT-CVVVDVS----- 266
Qy 345 TEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFLYNSDSFGKV 404
Db 267 HEDPEVKFNWYVDG-----VEVHNAKTPREEQ-----YNSTY---RV 301
Qy 405 QRGILVPHSSEGSTVSYDLFDPAQOQYPTLLRIYRDNTTISSTLSLSLYLTTSIWMTQ 464
Db 302 VSVLTVLHQDLNGKEY----- 318
Qy 465 TPTSLVLSAGDRVTITCKASQSVSNVAVYQOQPGQSPKLLISYTSRYAGVPDRFSGSG 524
Db 319 -----KCKVS-----NKALPAP-----IEKTISKAKGQP----- 342
Qy 525 YGTDFTLTISVQAEADAAYFCQDYNSPPTFGGGTKLEIKRADAAPTTSIFPPSSSEOLT 584
Db 343 -----REPQVYTLPPSRDELT 358
Qy 585 SGGASVVCFLNNFYPKDINVKWKIDGSERON-----GVLSWTDQDSKSTYSMSLTLL 639
Db 359 KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSE-----DGSFFLYSKLTV 411
Qy 640 TKDEYERHNSYTCETHK 657
Db 412 DKSRWQOQGNVFCSCVFHE 429

RESULT 15
US-11-177-648-33
; Sequence 33, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMELIN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR FILING DATE: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H18
US-11-177-648-33

Query Match 24.0%; Score 844.5; DB 7; Length 462;

Best Local Similarity 32.3%; Pred. No. 2.9e-37;
Matches 219; Conservative 59; Mismatches 127; Indels 273; Gaps 17;
Qy 1 EVOLQSGGPDLPKASVKISCKASGYSTFTGYNHHVWKQSPGKLEWIGRINPNNGVTLY 60
Db 20 QVQLVQSGAEVAPFGASVKLSCKASGYFTFTSYNHHVWKQSPGQGLEWIGNINPNSGGTNY 79
Qy 61 NQPKDKATITVDKSTTAYMELSLRSEDNAVYICARSTMTIYNVMDYMGQGGTSVTVSS 120
Db 80 NEKPKSKATITVDKSSSTAYMELSLRSEDNAVYICELG-----QGYMGQGGFLVTVSS 132
Qy 121 AKTTPPSVYPLAPGSAQAQTNMTVLGCLVKGYPPEPVTVTWNSGSLSSGVHTFPFVQLQSD 180
Db 133 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALTSGVHTFPFVQLQSS 192
Qy 181 -LYTLSSSVTPSPSTPSETVTCNVAHPASSTKVDKKIVPRD-----SGG 224
Db 193 GLXSLSSVTPSPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCPCPAPELAGA 252
Qy 225 PSEKSEBINEKDLRKSELOQTALGNLQIYYVNSKAITSEKSDAQFLNTLLFKGFFT 284
Db 253 PS-----VFLP-----KDTLMI----- 268
Qy 285 GHPWYNDLLVDLSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRL 344
Db 269 -----SRTPEVT-CVVVDVS----- 282
Qy 345 TEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFLYNSDSFGKV 404
Db 283 HEDPEVKFNWYVDG-----VEVHNAKTPREEQ-----YNSTY---RV 317
Qy 405 QRGILVPHSSEGSTVSYDLFDPAQOQYPTLLRIYRDNTTISSTLSLSLYLTTSIWMTQ 464
Db 318 VSVLTVLHQDLNGKEY----- 334
Qy 465 TPTSLVLSAGDRVTITCKASQSVSNVAVYQOQPGQSPKLLISYTSRYAGVPDRFSGSG 524
Db 335 -----KCKVS-----NKALPAP-----IEKTISKAKGQP----- 358
Qy 525 YGTDFTLTISVQAEADAAYFCQDYNSPPTFGGGTKLEIKRADAAPTTSIFPPSSSEOLT 584
Db 359 -----REPQVYTLPPSRDELT 374
Qy 585 SGGASVVCFLNNFYPKDINVKWKIDGSERON-----GVLSWTDQDSKSTYSMSLTLL 639
Db 375 KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSE-----DGSFFLYSKLTV 427
Qy 640 TKDEYERHNSYTCETHK 657
Db 428 DKSRWQOQGNVFCSCVMHE 445

RESULT 16
US-11-102-621-121
; Sequence 121, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882, 0039, 00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 121
; LENGTH: 446

; TYPE: PRT		; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides	
; ORGANISM: Homo sapiens		; FILE REFERENCE: 785CIP4CN	
US-11-102-621-121		; CURRENT APPLICATION NUMBER: US/11/000,463	
Query Match		; CURRENT FILING DATE: 2004-11-29	
Best Local Similarity		; PRIOR APPLICATION NUMBER: 10/291,265	
Matches 219; Conservative 60; Mismatches 144; Indels 240; Gaps 17;		; PRIOR FILING DATE: 2002-11-08	
		; PRIOR APPLICATION NUMBER: PCT/US01/02623	
		; PRIOR FILING DATE: 2001-01-25	
		; PRIOR APPLICATION NUMBER: 09/922,279	
		; PRIOR FILING DATE: 2001-08-03	
		; PRIOR APPLICATION NUMBER: 09/491,404	
		; PRIOR FILING DATE: 2000-01-25	
		; PRIOR APPLICATION NUMBER: 09/617,746	
		; PRIOR FILING DATE: 2000-07-17	
		; PRIOR APPLICATION NUMBER: 09/631,451	
		; PRIOR FILING DATE: 2000-08-03	
		; PRIOR APPLICATION NUMBER: 09/633,870	
		; PRIOR FILING DATE: 2000-09-15	
		; NUMBER OF SEQ ID NOS: 944	
		; SOFTWARE: FastSeq for Windows Version 3.0	
		; SEQ ID NO 804	
		; LENGTH: 384	
		; TYPE: PRT	
		; ORGANISM: Homo sapiens	
		US-11-000-463-804	
Query Match		23.9%; Score 841.5; DB 7; Length 384;	
Best Local Similarity		30.2%; Pred. No. 3.5e-37;	
Matches 203; Conservative 64; Mismatches 95; Indels 311; Gaps 10;			
QY	1	EVQLQSGDPLVKPGASVKISCKASGYSTGYMHVWQSPGKGLWIGRIINPNNG-VTL	59
DB	20	EVQLVESGGLVQPGSLRLSCAASGFTFSSVAMSVRQAPGKGLWVSGLSGSSSTY	79
QY	60	YNQKFKDKATLVDSSTTAYMELSLTSEDSAVYYCARSTMTITNYMDYWGQGTSTVTS	119
DB	80	YADSVKGRFTISGRDNSKGTLYLQMNSLRADDTARYYCAKG-----GVELA	124
QY	120	SAKTPPSVYPLAPGSAAGTNSMVLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQS	179
DB	125	STK-----	127
QY	180	DLVTLSSSVTVPSSTWSPSETVTCNVAHPASSTKVKKIVPRDSGGPSEKSEINEKDLRK	239
DB	128	-----PSSIW-----	132
QY	240	KSELOGTALGNLQIYYYNKSKAITSEKSAQDQFLNTLLFKGFFTGHWPYNDLLVLGST	299
DB	133	-----RLNPIRY-----WYFDLM-QGGTL	150
QY	300	AATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGK	359
DB	151	VTVSSGDGSS-----GGAS-----	167
QY	360	QITVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVQRGLIVFHSSEGSTV	419
DB	168	-----	167
QY	420	SYDLFDAQOQYPTLLRIYRDNTTISSTLSISLYLYTTSIVMTQPTTSLVSGAGRVTI	479
DB	168	-----TGEIVLTQSPFTLSLSPGERATL	190
QY	480	TKCASQSVND-VAMVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGCYGDTFTLTISVQA	538
DB	191	SCRASQSVSSSYLAWYQQKPGQAPRLLIYGASRATGIPDRFSGSGSGDTFTLTISRLEP	250
QY	539	EDAAYVFCQDYNSPPTFGGKTKLEIKRADAAPTIVSIFPPSSSQLTSGGASVVCFLNNFY	598
DB	251	EDFAVYVCCQYGSSTPTFGGKTKVDIKRTVAAPSVFIFPPSDQLKSGTASVVCFLNNFY	310
QY	599	PKDINVKWKIDGSEKRVNLSWTDQDSKDSYMSSTLTLTKDEYERHNSYTCETHKT	658
DB	311	PREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHQG	370

RESULT 17
US-11-000-463-804
; Sequence 804, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.

Qy	1	EVULOQSGPDLVKPGASVKIKSGASGYGFTGYMHVWKQSPGKLEWIGRINPNNG-VTL	59
Db	20	EVQLVDSGGGLVQPGGSLRLSKAASGFTFSSYMSWVRQAPGKLEWVSGLSGSGSSTY	79
Qy	60	YNQKPKDKATLTKVDSKSTTAYNELSLSEDSAVYTCARSTMTINYYMDYWGQGTSTV	119
Db	80	YADSVKGRFTISGRDSKGTFLYLQMSLRADDTARYCAKG-----GVELA	124
Qy	120	SAKTTTPSVYPLAPGSAATNSMWTLGCLVKGYFPEPVTVTWNSGSLSSGVHITFPFV	179
Db	125	STK-----	127
Qy	180	DLYTLSSVTVPSSTWPSSTVTCNVAHPASSTKVDDKILVPRDSGGPSEKSEENKDLRK	239
Db	128	-----PSSIW-----	132
Qy	240	KSELQGTALGNLKQIYYIYNSKAITSEKSADQFLNTLLPKGFTGHPWYNDLLVDLGST	299
Db	133	-----RLNPIRY-----WTFDLW-QGGTL	150
Qy	300	AATSEYEGSSVDLYGAYGYQCAGGTGNKTAQMGVTLHDNNRLTEKKVPINLMDWG	359
Db	151	VTVSSGDGSS-----GGAS-----	167
Qy	360	QTTVPTDKVTKSKEVTVOELDQARHLYHGKFGLYNSDFSGKVQRGLIVFHSSEGSTV	419
Db	168	-----	167
Qy	420	SYDLFDAQCYPDTLRLRIYRDNNTTISSTLSISLYLVTTSIVMTQTPTSLVSGADRVTI	479
Db	168	-----TGEIVLTQSPGTLSLSPGERATL	190
Qy	480	TKCASQSVND-VAMYYQKPGQSPKLLISYTSRYAGVPRFSGSGYGTDTFTITISVQA	538
Db	191	SCRASQSVSSSYLAWYQQKPGQAPRLIYGASSRATGIPDRFSGSGGTDTFTITISRLP	250
Qy	539	EDAAVYFCQDDYNSPPTFGGTGKLRIKADAAPTVSIFFPSSEQLTSGGASVVCFLNNEY	598
Db	251	EDFANVYCOQYGSPTFGGTGKVDIKRTVAAPSVIFPPSDEQLKSGTASVVCCLNNFY	310
Qy	599	PKDINVKWIKDGSEKRGNGVYNSWTQDQSKDSTYSMSSTLTLTDKDEYRHRNSYTCETHKT	658
Db	311	PREAKQWQKVDNALQSGNSQESVTEQDSKDSSTLSSTLTLSKADYEKKHKVYACEVTHQ	370
Qy	659	STSPIVKSFNRNE	671
Db	371	LSSPVTKSFNRGE	383

```

RESULT 20
US-11-000-463-807
; Sequence 807, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong B.
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCES: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623

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[illegible]

RESULT 21

```
US-11-177-648-30
; Sequence 30, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLEN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H15
US-11-177-648-30

Query Match      23.8%; Score 838.5; DB 7; Length 462;
Best Local Similarity 32.2%; Pred. No. 5.9e-37;
Matches 218; Conservative 59; Mismatches 128; Indels 273; Gaps 17;

QY 1 EVLOQSGDPLVKPGASVKLSCKASGYFTSYGMHWVKQSPGKGLEWIGRINPNNGVTLY 60
DB 20 QVQLVQSGAEVFPGLASVKLSCKASGYFTSYGMHWVKQSPGKGLEWIGRINPNNGVTNY 79

QY 61 NQPKDKATLTVDKSTTAYMELRSLSSEDSAVVYCARSTMTITNYMDYQGQSTVTVSS 120
DB 80 NEKFKSKATLTVDTSSTAYMELSSRLSEDSAVVYCELG-----QGYWGQGLTVTVSS 132

QY 121 AKTTPSPVYPLAPGSAQTNSMTVLGCLVKGYPEPVTVTWNSGSLSSGVHTTTPAVLQSD 180
DB 133 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSS 192

QY 181 -LYLTSSVTVPSSTWPSSTETVCNVAHPASSTKVDKKIVPRD-----SGG 224
DB 193 GLYLSVSVTVPSSSLGTQYICNVNHPKSTKVDKKVEPKSCDKTHCTCPAPELAGA 252

QY 225 PSEKSEINEKDLRKKSSELOQTALGNLKQIYYNNSKAITSEKSAQDQFLNTLLFKGFPT 284
DB 253 PS-----VFLPPPKP-----KDTLMI----- 268

QY 285 GHPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRL 344
DB 269 -----SRTPEVT-CVVVDVS----- 282

QY 345 TEKKVPIINLWIDGKQTTPIDIKVTSKKEVTVOELDLQARHVLHGKFGLYNSDSFGKV 404
DB 283 HEDPEVKFNWVDG-----VEVHNAKTPREBQ-----YNSTY---RV 317

QY 405 QRGLIVPHSSEGSTVSYDLFDAQOQYPTDLLRIYRDNNTTISSTLSLSLYTTSIVMTQ 464
DB 318 VSVLTVLHQLWLNKGEY----- 334

QY 465 TPTSLLSAGDRVITITCKASQSVSNVAVTQQKPGQPKLLISYTSRYAGVDPDRFSGSG 524
DB 335 -----KCKVS-----NKALPAP-----IEKTIKAKGP----- 358

QY 525 YGDTFTLTISVQAEDAAYVFCQDYNSPTFFGGGTGKLEIKRADAAPTIVSIFPPSSBOLT 584
DB 359 -----REPQVYTLPPSRDEL 374

QY 585 SGGASVVCFLNNFPKDIVNKKIDGSRQN-----GVLSNWTDDQDSKDSYMSSTLTL 639
```

```
US-11-177-648-32
; Sequence 32, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLEN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H17
US-11-177-648-32

Query Match      23.8%; Score 838.5; DB 7; Length 462;
Best Local Similarity 32.0%; Pred. No. 5.9e-37;
Matches 217; Conservative 61; Mismatches 127; Indels 273; Gaps 17;

QY 1 EVLOQSGDPLVKPGASVKLSCKASGYFTSYGMHWVKQSPGKGLEWIGRINPNNGVTLY 60
DB 20 QVQLVQSGAEVFPGLASVKLSCKASGYFTSYGMHWVKQSPGKGLEWIGRINPNNGVTNY 79

QY 61 NQPKDKATLTVDKSTTAYMELRSLSSEDSAVVYCARSTMTITNYMDYQGQSTVTVSS 120
DB 80 NEKFKSKATLTVDKSTTAYMELSSRLSEDSAVVYCELG-----QGYWGQGLTVTVSS 132

QY 121 AKTTPSPVYPLAPGSAQTNSMTVLGCLVKGYPEPVTVTWNSGSLSSGVHTTTPAVLQSD 180
DB 133 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSS 192

QY 181 -LYLTSSVTVPSSTWPSSTETVCNVAHPASSTKVDKKIVPRD-----SGG 224
DB 193 GLYLSVSVTVPSSSLGTQYICNVNHPKSTKVDKKVEPKSCDKTHCTCPAPELAGA 252

QY 225 PSEKSEINEKDLRKKSSELOQTALGNLKQIYYNNSKAITSEKSAQDQFLNTLLFKGFPT 284
DB 253 PS-----VFLPPPKP-----KDTLMI----- 268

QY 285 GHPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRL 344
DB 269 -----SRTPEVT-CVVVDVS----- 282

QY 345 TEKKVPIINLWIDGKQTTPIDIKVTSKKEVTVOELDLQARHVLHGKFGLYNSDSFGKV 404
DB 283 HEDPEVKFNWVDG-----VEVHNAKTPREBQ-----YNSTY---RV 317

QY 405 QRGLIVPHSSEGSTVSYDLFDAQOQYPTDLLRIYRDNNTTISSTLSLSLYTTSIVMTQ 464
DB 318 VSVLTVLHQLWLNKGEY----- 334
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QY 465 TPTSLVSAGDRVTITCKASQSVNDVAVYQOKPGOSPKLLISYTSRAGVDPDRFSGS 524
Db 335 -----KCKVS-----NKALPAP-----TEKTSKAKGP----- 358
QY 525 YGDTFTLTSSVQAEDAAYVFCQDYNPPTFGGKLEIKRADAAPTVSIIPPSEQLT 584
Db 359 -----KCKVS-----NKALPAP-----TEKTSKAKGP----- 374
QY 585 SGASVVCFLNFPKIDNVKWKIDGSRQN-----GVLSNWTDDQSKDSTYSMSSTLT 639
Db 375 KQVSLTCLVKGFPDIAVEMESNGQPENNYKTTTPVLDS-----DGSFFLYSKLTV 427
QY 640 TKDEYERHNSYTCEATHK 657
Db 428 DKSRWQQGNVFCSCVMHE 445

RESULT 23
US-11-177-648-31
; Sequence 31, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLEN
; APPLICANT: Alan Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H16
US-11-177-648-31
```

```
Query Match 23.7%; Score 833.5; DB 7; Length 462;
Best Local Similarity 31.9%; Pred. No. 1.1e-36;
Matches 216; Conservative 61; Mismatches 128; Indels 273; Gaps 17;

QY 1 EVOLQOSGPDLVKPGASVKISCKASGYSTGYMHVWVKSPGKLEWIGRINPNNGVTLY 60
Db 20 QVOLVQSGAEVKPGASVKVSKASGYTFTSYMHVWVKRPGQGLEWIGNINPSNGGTNY 79
QY 61 NOKFKDKATLTVDKSTTAYMELRSITSDSAVYICARSTMTINYMDYWGQGTSTVTS 120
Db 80 NEKFKSRATLTVDKSTTAYMELSLRSEDATVYICELG-----QGYWGQGTSTVTS 132
QY 121 AKTTPSVVPLAPGSAQAQNSMVTGLCLVKGYFPEPVPTVWNSGSLSSGGVHTFPVQLSD 180
Db 133 ASTKGFVPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQSS 192
QY 181 -LYTLSSSVTPSGTWPSETVTCNVAHPASSTKVDKKIIVPRD-----SGG 224
Db 193 GLYSLSSVTPVPSISLGTQYICNVNHPKSTKVDKKVPEKSCDKTHTCPPCPAPELAGA 252
QY 225 PSEKSEINEKDKRKSELOGTALGNLKQIYYNYSKALITSSSEKSAQDFLTNLLPKGFFT 284
Db 253 PS-----VFLPPPKP-----KDTLMI----- 268
QY 285 GHPWYNDLLVDLGLSTAATSEYEGSSVDLYGAYYGYOCAGGTPNKTACMGYGVTLHDNRL 344
Db 269 -----SRTPEVT-CVVVDVS----- 282
```

```
QY 345 TBEKVPINLWIDGKQTTPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKV 404
Db 283 HEDPEVKFNWYDGG---VEVHNATKPREQ-----YNSTY---RV 317
QY 405 QRGLIVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDNTTISSTLSISLYLTTTSVMTQ 464
Db 318 VSVLTVLHQDWLNGKEY----- 334
QY 465 TPTSLVSAGDRVTITCKASQSVNDVAVYQOKPGOSPKLLISYTSRAGVDPDRFSGS 524
Db 335 -----KCKVS-----NKALPAP-----TEKTSKAKGP----- 358
QY 525 YGDTFTLTSSVQAEDAAYVFCQDYNPPTFGGKLEIKRADAAPTVSIIPPSEQLT 584
Db 359 -----KCKVS-----NKALPAP-----TEKTSKAKGP----- 374
QY 585 SGASVVCFLNFPKIDNVKWKIDGSRQN-----GVLSNWTDDQSKDSTYSMSSTLT 639
Db 375 KQVSLTCLVKGFPDIAVEMESNGQPENNYKTTTPVLDS-----DGSFFLYSKLTV 427
QY 640 TKDEYERHNSYTCEATHK 657
Db 428 DKSRWQQGNVFCSCVMHE 445

RESULT 24
US-11-177-648-28
; Sequence 28, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLEN
; APPLICANT: Alan Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H700
US-11-177-648-28
```

```
Query Match 23.6%; Score 829.5; DB 7; Length 462;
Best Local Similarity 31.6%; Pred. No. 1.7e-36;
Matches 214; Conservative 64; Mismatches 127; Indels 273; Gaps 17;

QY 1 EVOLQOSGPDLVKPGASVKISCKASGYSTGYMHVWVKSPGKLEWIGRINPNNGVTLY 60
Db 20 QVOLVQSGAEVKPGASVKVSKASGYTFTSYMHVWVKRPGQGLEWIGNINPSNGGTNY 79
QY 61 NOKFKDKATLTVDKSTTAYMELRSITSDSAVYICARSTMTINYMDYWGQGTSTVTS 120
Db 80 NEKFKSRATLTVDKSTTAYMELSLRSEDATVYICELG-----QGYWGQGTSTVTS 132
QY 121 AKTTPSVVPLAPGSAQAQNSMVTGLCLVKGYFPEPVPTVWNSGSLSSGGVHTFPVQLSD 180
Db 133 ASTKGFVPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQSS 192
QY 181 -LYTLSSSVTPSGTWPSETVTCNVAHPASSTKVDKKIIVPRD-----SGG 224
Db 193 GLYSLSSVTPVPSISLGTQYICNVNHPKSTKVDKKVPEKSCDKTHTCPPCPAPELAGA 252
QY 225 PSEKSEINEKDKRKSELOGTALGNLKQIYYNYSKALITSSSEKSAQDFLTNLLPKGFFT 284
Db 253 PS-----VFLPPPKP-----KDTLMI----- 268
QY 285 GHPWYNDLLVDLGLSTAATSEYEGSSVDLYGAYYGYOCAGGTPNKTACMGYGVTLHDNRL 344
Db 269 -----SRTPEVT-CVVVDVS----- 282
```

Db 193 GLYSLSSVTVTPSSSLGTQYVICNVNHNKPSNTKVDKKVPEKSCDKTKHTCCPPCAPELAGA 252
Qy 225 PSEKSEINEKDLRKKSELOGTALGNLKQIYYNKSKAITSSEKSAQDQFLNTLTLFKGFFT 284
Db 253 PS-----VFLFPPKP-----KDTLMI----- 268
Qy 285 GHPWYNLLVDLGLSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRL 344
Db 269 -----SRTPEVT-CVVVDVS----- 282
Qy 345 TEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDQARHYLHGKFLGNSDSFGGKV 404
Db 283 HEDEVKFNWYVDG-----VEVHNAKTPREEQ-----YNSTV---RV 317
Qy 405 QRGILVPHSSEGSTVSVDLFDQAQGYEDTLRLIYRDNNTTISSTLSLSLYLTTISIVMTQ 464
Db 318 VSVLTVLHQDLNGKEY-----REPVYTLPPSRDELT 374
Qy 585 SGGASVVCFLNNFPKIDNVKWKIDGSERON-----GVLSNWTDDSKDSTYSMSSTLT 639
Db 375 KNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD-----DGSFFLYSKLTV 427
Qy 640 TKDEYERHNSYTCETHK 657
Db 428 DKSRWQQGNVFCSCVMHE 445

RESULT 25

US-11-177-648-97
; Sequence 97, Application US/11/177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLEN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H24
US-11-177-648-97

Query Match 23.5%; Score 827.5; DB 7; Length 462;
Best Local Similarity 31.7%; Pred. No. 2.2e-36;
Matches 215; Conservative 61; Mismatches 129; Indels 273; Gaps 17;
Qy 1 EVOLQQSGPDLVKPGASVKISCKASGYSTFGYMHVWKQSPGKGLGIMGRINPNNGVTLY 60
Db 20 QVQLVQSGAEVKPKGASVKISCKASGYTFTSYMHVWKQSPGQGLEWIGININPSNGGTNY 79
Qy 61 NQPKFKATLTVDKSTTAYMELRSLTSEDSAVVYCARSTWITNYVMDYWGQGTSTVTVSS 120

Db 80 NEKFASKATLTVDSTSTAYMELSSLRSEDATVYICELG-----QGYWQQGLTVTVSS 132
Qy 121 AKTTPPSVYPLAPGSAQTNSMTVTLGCLVKGYPPEPVTVTWNSGSLSGGVHTFFPAVLQSD 180
Db 133 ASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPPEPVTVSNWNSGALTSVGVHTFFPAVLQSS 192
Qy 181 -LYTLSSSVTVPSSTWSPSETVTCNVAHPASSTKVDDKKIVPRD-----SGG 224
Db 193 GLYSLSSVTVTPSSSLGTQYVICNVNHNKPSNTKVDKKVPEKSCDKTKHTCCPPCAPELAGA 252
Qy 225 PSEKSEINEKDLRKKSELOGTALGNLKQIYYNKSKAITSSEKSAQDQFLNTLTLFKGFFT 284
Db 253 PS-----VFLFPPKP-----KDTLMI----- 268
Qy 285 GHPWYNLLVDLGLSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRL 344
Db 269 -----SRTPEVT-CVVVDVS----- 282
Qy 345 TEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDQARHYLHGKFLGNSDSFGGKV 404
Db 283 HEDEVKFNWYVDG-----VEVHNAKTPREEQ-----YNSTV---RV 317
Qy 405 QRGILVPHSSEGSTVSVDLFDQAQGYEDTLRLIYRDNNTTISSTLSLSLYLTTISIVMTQ 464
Db 318 VSVLTVLHQDLNGKEY-----REPVYTLPPSRDELT 374
Qy 585 SGGASVVCFLNNFPKIDNVKWKIDGSERON-----GVLSNWTDDSKDSTYSMSSTLT 639
Db 375 KNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD-----DGSFFLYSKLTV 427
Qy 640 TKDEYERHNSYTCETHK 657
Db 428 DKSRWQQGNVFCSCVMHE 445

RESULT 26

US-11-177-648-96
; Sequence 96, Application US/11/177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLEN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H23
US-11-177-648-96


```
QY 589 SVVCFLLNNFYPKDINVKWKIDGSRQN-----GVLSWTDQDSDKSDSTYSMSSTLTITKDE 643
Db 359 SLTCLVKGFYPSDIAVWESNGQPENNYKTTPPMLDS-----DGSFFLYSKLTVDKSR 411
QY 644 YERHNSVTCEATHK 657
Db 412 WQGNVFCVSFHE 425

RESULT 32
US-11-102-621-126
; Sequence 126, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102.621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 126
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-126

Query Match 23.3%; Score 822; DB 7; Length 442;
Best Local Similarity 30.6%; Pred. No. 4e-36;
Matches 206; Conservative 71; Mismatches 131; Indels 266; Gaps 15;

QY 1 EVOLQSGDPLVKPGASVKISCKASGYSTGYTHHWVKQSPGKLEWIGRIINPNNGVTLY 60
Db 1 QVQLVQSGAEVKPGSSVKVCKASGYTFSYRHWVRQAPGQGLEWIGVINSTGYTEY 60
QY 61 NQKPKDKATLVTKGSTTAYMELRLSTSESAVYICARSTMTINYNVDYMGQGTSTVTSS 120
Db 61 NQKPKDKATITADESTNTAYMELSSRLSEDAVYICARG-----GGVFDYMGQGTSTVTSS 116
QY 121 AKTTPSPVYPLAPGSAQAQTSMTVTLGCLVKGYGPEPTVTTNSSLSSGVTHTPAVLQSD 180
Db 117 ASTKGPSVFLPLACRSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 176
QY 181 -LYTLSSSVTPSPSTPSETVTCNVAHPASSTKVDKIVPR-----DSGGPSEK 228
Db 177 GLYSLSVTVTPSNFTQYTCNVDHKPNTKVDKTVKRCVCCPCPAPPAAPS-- 234
QY 229 SEBINEKDLKKSELOQTALGNLKIYYIYNSKAITSEKSAQDQLTNTLFLKGFFTGHPW 288
Db 235 -----VFLFPPKP-----KDTLMI----- 248
QY 289 YNDLLVDLGSATSEYEGSSVDLYGAYYQCAGGTPNKTACMYGGVTLDHNNLTTEK 348
Db 249 -----SRTPVTV-CVVVDVS-----HEDP 266
QY 349 KVPINLWIDGKQTVPIDKVTKSKEVTVQELDLQARHYLHGKFLGYNLSDSPGKVGQRL 408
Db 267 EVQFNWYVDG-----VEVHNKTKPRE----- 288
QY 409 IVFHSSEGSTVSYDLFDAQOQYPTDLLRIYRDNTTISTSLSLSLVLYTTSIVMTQPTS 468
Db 289 -----EQFNSTFRVSVLTVHQD----- 307
QY 469 LLVSGDRVTITCKASQSVNDVAVYQKQSPKLLISYTSRYAGVPRFSGSGYGTD 528
Db 308 -----WLNGKEYKC-----KVSNNKGLPAP 326
```

```
QY 529 FTLTISVQAEADAAYFCQDYNPSPTFGGGTKLEIKRADAAPTVAFTVSIFFPSSQLTSGGA 588
Db 327 IEKTIKTKGQ-----PREQVVTLPSPSREMTKNQV 358
QY 589 SVVCFLLNNFYPKDINVKWKIDGSRQN-----GVLSWTDQDSDKSDSTYSMSSTLTITKDE 643
Db 359 SLTCLVKGFYPSDIAVWESNGQPENNYKTTPPMLDS-----DGSFFLYSKLTVDKSR 411
QY 644 YERHNSVTCEATHK 657
Db 412 WQGNVFCVSFHE 425

RESULT 33
US-11-000-463-899
; Sequence 899, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 899
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-899

Query Match 23.3%; Score 821; DB 7; Length 367;
Best Local Similarity 28.2%; Pred. No. 3.8e-16;
Matches 193; Conservative 56; Mismatches 85; Indels 350; Gaps 4;

QY 1 EVOLQSGDPLVKPGASVKISCKASGYSTGYTHHWVKQSPGKLEWIGRIINPNNGV 57
Db 20 EVQLVESGGGLVQPGGSLRLSCAASGFTSSYAMSVWRQAPGKLEWVSGFTSGSGSGS 79
QY 58 TLYNQPKDKATLVTKGSTTAYMELRLSTSESAVYICARSTMTINYNV-----M 107
Db 80 TYVADSVKGRFTISRDNSKNTLFLQMNSLRDAEDTAVYCAKGLLPPRWAYRVYEDSGIFF 139
QY 108 DWGQGTSTVTSSAKTTPPSVYPLAPGSAQAQTSMTVTLGCLVKGYGPEPTVTVNWSGLS 167
Db 140 DWGQGTSTVTSS----- 153
QY 168 SGVHTFPAVLQSDLYTLSSSVTPSPSTPSETVTCNVAHPASSTKVDKIVPRDSGSPSE 227
```

Db 154 ----- 153
QY 228 KSEINEKDLRKSELOGTALGNLKOIYYNSKAITSEKSDAQFLTNTLLFKGFTGHP 287
Db 154 ----- 153
QY 288 WYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLTEE 347
Db 154 ----- 153
QY 348 KKVPIINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVRQG 407
Db 154 ----- 156
QY 408 LIVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDNTTISSTLSISLYLTTSIWMTQPT 467
Db 157 ----- 162
QY 468 SLLVSAGDRVTITCKASQSVNDVAVYQKPGOSPKLLISYTSRVRAGVDPDRFSGSGYCT 527
Db 163 TLSASGDRVTITCRASQSISLWAVYQKPGKPKLLIYKASSLQSGVPSRPSGSGGT 222
QY 528 DFTLTSSVQAEADAAYVFCQDYNSPPTFGGKTKLEIKRADAAPTYSIIPPSSSEQLTSGG 587
Db 223 DFTLTSSLOPDDFAYYQQQLSTYVWTFGQTKVDIKRTVAAPSVFIIPPDSDEQLKSGT 282
QY 588 ASVVCFLNFPYKIDINVKWIDGSRQNGVLNSWTDQSKDSTYSMSSTLTITKDYERH 647
Db 283 ASVVCFLNFPYKIDINVKWIDGSRQNGVLNSWTDQSKDSTYSMSSTLTITKDYERH 647
QY 648 NSYTCEATHKTSPIVKSFNRE 671
Db 343 KVVACEVTHQGLSSPVTKSFRNGE 366

RESULT 34
US-11-177-648-95
; Sequence 95, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBLEN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; PRIOR FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H22
US-11-177-648-95
Query Match 23.2%; Score 818.5; DB 7; Length 462;
Best Local Similarity 31.4%; Pred. No. 6.3e-36;
Matches 213; Conservative 62; Mismatches 130; Indels 273; Gaps 17;

QY 1 EVOLQSGDPLVKPGASVKISKASGYSFTGYNHHVWKOSPGKGLWIGRINPNNGVTLY 60
Db 20 QVQLVQSGAEVKKPGASVKISKASGYSFTGYNHHVWKORPGQGLEWIGNINPSNGGTNY 79

QY 61 NOKFKDKATLTVDKSTTAYMELSLTSEDSAVVYCARSTMITNTVYMDYWGQTSVTSS 120
Db 80 NEKFKSKATMTREDTSTAYMELSLRSEDYAVYCELG-----QGWGQGLTVTVSS 132
QY 121 AKTTTPSVVPLAPGAAQTNMVTGLGVKGFPEPVTVTWNSGSLSSGVHTFPFPAVLQSD 180
Db 133 ASTKGPSVFPAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPFPAVLQSS 192
QY 181 -LYTSSSVTPSSWTPSETVTCNVAHPASSTKDKIVPRD-----SGG 224
Db 193 GYLSVVVVTPSSSLGTQTYICNVNHPSPNTKDKKPEPKSCDTHTCPCPAPPLAGA 252
QY 225 PEEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSEKSDAQFLTNTLLFKGFTT 284
Db 253 PS-----VPLFPPKP-----KDTLMI----- 268
QY 285 GHPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRL 344
Db 269 -----SRTPEVT-CVVVDVS----- 282
QY 345 TEEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKV 404
Db 283 HEDPEVKFNWYDVG-----VEVHNAKTKPREQ-----YNSTY---RV 317
QY 405 QRGLIVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDNTTISSTLSISLYLTTSIWMTQ 464
Db 318 VSVLTVLHQDWLNGKEY----- 334
QY 465 TPTSLLLVSAGDRVTITCKASQSVNDVAVYQKPGOSPKLLISYTSRVRAGVDPDRFSGSG 524
Db 335 -----KCKVS-----NKALPAP---IEKTISKAGQP----- 358
QY 525 YGTDFTLTSSVQAEADAAYVFCQDYNSPPTFGGKTKLEIKRADAAPTYSIIPPSSSEQLT 584
Db 359 -----REPQVYTLPPSRDEL 374
QY 585 SGGASVVCFLNFPYKIDINVKWIDGSRQNGVLNSWTDQSKDSTYSMSSTLT 639
Db 375 KNOVSLTCLVKGFYPSDIAVEMESGQPNPNYKTTTPPVLD-----DGSFFLYSKLTIV 427
QY 640 TKDEYERHNSYTCEATHK 657
Db 428 DKSRWQQNGVFCSCVMHE 445
RESULT 35
US-11-102-621-130
; Sequence 130, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 130
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-130
Query Match 23.2%; Score 817.5; DB 7; Length 447;
Best Local Similarity 32.7%; Pred. No. 6.9e-36;
Matches 217; Conservative 64; Mismatches 143; Indels 239; Gaps 18;


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; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 136
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-136

```

Query Match	23.2%	Score	816;	DB	7;	Length	446;
Best Local Similarity	30.4%	Pred. NO.	8.3e-36;				
Matches	205;	Conservative	71;	Mismatches	136;	Indels	262;
						Gaps	14;

RESULT 38
US-11-102-621-137
; Sequence 137, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Teurshita, Naoya
; APPLICANT: Tso, J. Yun

```

; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 137
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-137

```

Query Match 23.2%; Score 816; DB 7; Length 446;
Best Local Similarity 30.4%; Pred. No. 8.3e-36;
Matches 205; Conservative 70; Mismatches 137; Indels 262; Gaps 14;

RESULT 39
US-11-102-621-139
; Sequence 139, Application US/11102621
; Publication No. US20050276799A1


```
Db 303 VSVLTVLHODWLNKGEY----- 319
Qy 465 TPTSLVLSAGDRVTITCKASQSVNDVAMVYQKPGQSPKLLISYTSRVRAGVDPDRFSGSG 524
Db 320 -----KCKVS-----NKALPAP-----IEKTIKAKGP----- 343
Qy 525 YGTDFTLTISVQAEADAAYVFCQDYNSPPTFGGGTKLEIKRADAAPTIVSIFPPSSSEQLT 584
Db 344 -----REPOVVTLPSPRDELT 359
Qy 585 SGGASVVCFLNNFYPKIDNVKWKIDGSERON-----GVLNSWTDQSKDSTYMSSTLTTL 639
Db 360 KNQVSLTCLVKGYFSPSDIAVWESNGQPENNYKTTPPVLDSD-----DGSFFLYSKLTV 412
Qy 640 TKDEYERHNSYTCEATHK 657
Db 413 DKSRWQOQGNVFCSCVMHE 430

RESULT 43
US-11-102-621-133
; Sequence 133, Application US/11102621
; Publication No. US200502799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tsao, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 133
; TYPE: PRT
; LENGTH: 447
; ORGANISM: Homo sapiens
US-11-102-621-133

Query Match 23.1%; Score 814.5; DB 7; Length 447;
Best Local Similarity 31.7%; Pred. No. 9.9e-36;
Matches 215; Conservative 64; Mismatches 130; Indels 269; Gaps 18;

Qy 1 EVLOQSGDPLVKPGASVKISKASGYFTGYIMHWVKQSPGKGLWIGRIINPNNGVTL 60
Db 1 QVQLVQSGAELEKPGSSVKVSKASGYFTFTSSMINVWVKAPQGQGLEWIGRIDPSDGEVHY 60
Qy 61 NQKFKDKATLTVDKSSSTAYMELRSLTSDSAVYYCARSTMTITNYMDYWGQSTSVTVSS 120
Db 61 NQDFKDKATLTVDKSTNTAYMELSLRSDTAVYYCARGFL--PWFAD-WGQSTLVTVSS 117
Qy 121 AKTTPPSVPLAPGSAQAQNTSMVTGLCLVKGYFPEPVTVTWNSGSLSSGVHTTFAVLQSD 180
Db 118 ASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTTFAVLQSS 177
Qy 181 -LYLTSSSVTVPSSTWPSFETVTCNVAHPASSTVKDKKIVPRDS-----GG 224
Db 178 GLYSLSVSVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVBPCKDTHCTCPCPAPELGG 237
Qy 225 PSEKSEINEKDLRKSKSELOGTALGNLKIYYNKAITSSEKSAQDQFLNTLLFKGFFT 284
Db 238 PS-----VFLF-----PPKPKDQLMISR----- 255
Qy 285 GHPWYNDLLVDLSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTKACMYGGVTLHDNRL 344
Db 256 -----TPEVT-CVVVDVS----- 267
```

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Qy 345 TEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKV 404
Db 268 HEDPEVKFNWYVDG---VEVHNAKTKPREEQ-----YNSTY---RV 302
Qy 405 QRGLIVFHSESGSVSYDYLFDAGQGYPTLLRIYRDNNTTISSTLSLSLYLTYSVMTQ 464
Db 303 VSVLTVLHODWLNKGEY----- 319
Qy 465 TPTSLVLSAGDRVTITCKASQSVNDVAMVYQKPGQSPKLLISYTSRVRAGVDPDRFSGSG 524
Db 320 -----KCKVS-----NKALPAP-----IEKTIKAKGP----- 343
Qy 525 YGTDFTLTISVQAEADAAYVFCQDYNSPPTFGGGTKLEIKRADAAPTIVSIFPPSSSEQLT 584
Db 344 -----REPOVVTLPSPRDELT 359
Qy 585 SGGASVVCFLNNFYPKIDNVKWKIDGSERON-----GVLNSWTDQSKDSTYMSSTLTTL 639
Db 360 KNQVSLTCLVKGYFSPSDIAVWESNGQPENNYKTTPPVLDSD-----DGSFFLYSKLTV 412
Qy 640 TKDEYERHNSYTCEATHK 657
Db 413 DKSRWQOQGNVFCSCVLHE 430

RESULT 44
US-11-177-648-27
; Sequence 27, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBELIN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; TYPE: PRT
; LENGTH: 462
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 2A10 heavy chain humanised construct H6
US-11-177-648-27

Query Match 23.1%; Score 814.5; DB 7; Length 462;
Best Local Similarity 31.1%; Pred. No. 1e-35;
Matches 211; Conservative 65; Mismatches 129; Indels 273; Gaps 17;

Qy 1 EVLOQSGDPLVKPGASVKISKASGYFTGYIMHWVKQSPGKGLWIGRIINPNNGVTL 60
Db 20 QVQLVQSGAEVAKPGASVKVSKASGYFTTISYIMHWVRQAPGQGLEWIGININFGGTNY 79
Qy 61 NQKFKDKATLTVDKSSSTAYMELRSLTSDSAVYYCARSTMTITNYMDYWGQSTSVTVSS 120
Db 80 NEKFKSRATWTRDTSTSTAYMELSLRSDTAVYYCELG-----QGYWGQSTLVTVSS 132
Qy 121 AKTTPPSVPLAPGSAQAQNTSMVTGLCLVKGYFPEPVTVTWNSGSLSSGVHTTFAVLQSD 180
Db 133 ASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTTFAVLQSS 192
Qy 181 -LYLTSSSVTVPSSTWPSFETVTCNVAHPASSTVKDKKIVPRD-----SGG 224
Db 193 GLYSLSVSVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVBPCKDTHCTCPCPAPELAGA 252
```

QY 225 PSEKSEINEKDLKKSELOQTALGNLKOIYYNKAITSSEKSAQDLTNTLLPKGFPT 284
DB 253 PS-----VFUFPKPB-----KDTLMI-----268
QY 285 GHPWYNLLVLDLSTAAATSEYEGSSVDLYGAYGYQCAGGTNKTACMYGGVTLHDNNRL 344
DB 269 -----SRTPEVT-CVVVDVS-----282
QY 345 TEEKKVPINLWIDGKOTTPIDKVKTSKEVTVQELDLQARHYLHGKFLGYNDSDFGGKV 404
DB 283 HEDPEVKFNWYDVG---VEVHNKTKPREEQ---YNSTY---RV 317
QY 405 QRGLIVFHSSEGSTVSVDLFDAGQGVPTDLLRIYRDNTTISSTLSLSLYLTTSIVMTQ 464
DB 318 VSVLTVLHQDWLNGKEY-----334
QY 465 TPTSLLSVAGDRVTITCKASQSVNDVAMVYQKPGQSPKLLISYTSRRVAGVDPDRPSGG 524
DB 335 -----KCKVS-----NKALPAP---TEKTISKAKGP-----358
QY 525 YGTDFTLTISVQAEDAAYVFCQDYNSPPTFGGKTKLEIKRADAAPTYSIIPPSSEQLT 584
DB 359 -----REPQVYTLPPSRDEL 374
QY 585 SGGASVVCFLNNFYPKDINVKWKIDGSRQN-----GVLSNWTDDQSKDSTYSMSSTLTL 639
DB 375 KNOVSLTCLVKGFYPSDIAVEMESNGQPNYKTTTPVLDS-----DGSFFLYSKLTV 427
QY 640 TKDEYERHNSYTCETHK 657
DB 428 DKSRWQOGNVFSCSVNHE 445

RESULT 45
US-11-102-621-134
; Sequence 134, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 134
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-134

Query Match 23.1%; Score 813.5; DB 7; Length 447;
Best Local Similarity 31.7%; Pred. No. 1.1e-35;
Matches 215; Conservative 64; Mismatches 130; Indels 269; Gaps 18;
QY 1 EVLOQSGPDLVKPGASVKISCKASGYFTGYMHVVKOSPGKLEWIGRINPNNGVTLY 60
DB 1 QVQLVQSGAELKKPGASVKVSKASGYFTSSMINVVKQAPGQGLEWIGRIDPDSGEVHY 60
QY 61 NQKFKDKATLTVDKSTTAYMELRSITSESAVYYCARSTMTITNYMDYWGQGSTVTVSS 120
DB 61 NQDFKDKATLTVDKSTNTAYMELSRSEDAVYYCARGFL--PWFA--WGQGLTVTVSS 117
QY 121 AKTTPPSVPLAPGSAQAQNSMVTGLCLVKGYFPEPVTVTVNSGSISSGSGVTFPPAYLQSD 180

DB 118 ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPVTVTVMSNGALTSGVHTFPAVLQSS 177
QY 181 -LYTSSSVTVPSSTWPSSTVTCNVAHPASSTKVDKIVPRDS-----GG 224
DB 178 GLYSLSVVTVPSSSLGQTQYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 237
QY 225 PEKSEINEKDLKKSELOQTALGNLKOIYYNKAITSSEKSAQDLTNTLLPKGFPT 284
DB 238 PS-----VFUFPKPB-----PPKPKDQLMISR-----255
QY 285 GHPWYNLLVLDLSTAAATSEYEGSSVDLYGAYGYQCAGGTNKTACMYGGVTLHDNNRL 344
DB 256 -----TPEVT-CVVVDVS-----267
QY 345 TEEKKVPINLWIDGKOTTPIDKVKTSKEVTVQELDLQARHYLHGKFLGYNDSDFGGKV 404
DB 268 HEDPEVKFNWYDVG---VEVHNKTKPREEQ---YNSTY---RV 302
QY 405 QRGLIVFHSSEGSTVSVDLFDAGQGVPTDLLRIYRDNTTISSTLSLSLYLTTSIVMTQ 464
DB 303 VSVLTVLHQDWLNGKEY-----319
QY 465 TPTSLLSVAGDRVTITCKASQSVNDVAMVYQKPGQSPKLLISYTSRRVAGVDPDRPSGG 524
DB 320 -----KCKVS-----NKALPAP---TEKTISKAKGP-----343
QY 525 YGTDFTLTISVQAEDAAYVFCQDYNSPPTFGGKTKLEIKRADAAPTYSIIPPSSEQLT 584
DB 344 -----REPQVYTLPPSRDEL 359
QY 585 SGGASVVCFLNNFYPKDINVKWKIDGSRQN-----GVLSNWTDDQSKDSTYSMSSTLTL 639
DB 360 KNOVSLTCLVKGFYPSDIAVEMESNGQPNYKTTTPVLDS-----DGSFFLYSKLTV 412
QY 640 TKDEYERHNSYTCETHK 657
DB 413 DKSRWQOGNVFSCSVFHE 430

RESULT 46
US-11-102-621-138
; Sequence 138, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 138
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-138

Query Match 23.1%; Score 813; DB 7; Length 446;
Best Local Similarity 30.4%; Pred. No. 1.2e-35;
Matches 205; Conservative 70; Mismatches 137; Indels 262; Gaps 14;
QY 1 EVLOQSGPDLVKPGASVKISCKASGYFTGYMHVVKOSPGKLEWIGRINPNNGVTLY 60
DB 1 QVQLVQSGAELKKPGASVKVSKASGYFTTISYMHVVRQAPGQGLEWIGVINPRSGYTH 60
QY 61 NQKFKDKATLTVDKSTTAYMELRSITSEDAVYYCARSTMTITNYMDYWGQGSTVTVSS 120

Db 61 NOKLKD KATLTADKSASTAYMELSSLRSEDATVYCARSAAYDYDGFAYWGQGLTVTVSS 120
Qy 121 AKTTTPSVVPLAPGSAAOQNSMVTGLCKVKGYPEPEVTVTWNSGSLSSGGVHTTFAVLQSD 180
Db 121 ASKGSVFLPLACRSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTFAVLQSS 180
Qy 181 -LYTSSSVTVPSSTWPTVTCNVAHPASSTKVDKIVPR-----DSGGPSEK 228
Db 181 GLYSLSSVTVPSNFTQTYTCNVDHKPSNTKVDKVERKCCVCCPPCAPPAAPAS-- 238
Qy 229 SEBINEKDLKSELQALGNLKQIYYNSKAITSEKSAQDLTNLLFKGFFTHPW 288
Db 239 -----VFLPPPKP-----KDTLMI----- 252
Qy 289 YNDLLVDLSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMGVTLHDNNRLTEEK 348
Db 253 -----SRTPVET-CVVVDVS-----HEDP 270
Qy 349 KVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLGNSDSFGKVGQGL 408
Db 271 EVQFNWYVDG-----VEVHNAKTKPRE----- 292
Qy 409 IVFHSSEGSTVSDLDFAQOQYPTLLRIYRDNTTISSTLSLSLYLYTTSIYVMTQTPS 468
Db 293 -----EQFNSTFRVSVLTVHQD----- 311
Qy 469 LLVSGADRVTITCKASQSVNDVAVYQKQSPKLLISYTSRYAGVDPDRFSGSGVGT 528
Db 312 -----WLNKGEYK-----KVNKGLPLAP 330
Qy 529 FTLTSSVQAEADAAYVFCQDYNPSPTFGGKTKLEIKRAADAAPTISFPSSBQLTSGGA 588
Db 331 IEKTISSKTKGQ-----PREQVTVLPPSREEMTKNOV 362
Qy 589 SVVCFPLNFYPKDINVKWKIDGSRQN-----GVLSWTDQDSDKSTYSMSSTLTITKDE 643
Db 363 SLTCLVKGFYPSDIAVEWESNGQPENNYKTPPMLDS-----DGSFFLYSKLTVDKSR 415
Qy 644 YERHNSVTCETHK 657
Db 416 WQGNVFCSVLHE 429

RESULT 47
US-11-102-621-132
; Sequence 132, Application US/11102621
; Publication No. US2005027679A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Taurushita, Naoya
; APPLICANT: Tsao, J. Yun
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 132
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-132

Query Match 23.1%; Score 812.5; DB 7; Length 447;
Best Local Similarity 32.7%; Pred. No. 1.3e-35;
Matches 217; Conservative 62; Mismatches 145; Indels 239; Gaps 18;

Qy 1 EVOLQSGPDLVKPGASVKISKASGYSTGYMHVWVKSPGKGLWIGRINPNNGVTLY 60
Db 1 QVOLVQSGAELKKPGSVKSCASGYIFTSSINWVKQAPGQGLEWIGRIPDSGEVHY 60

Qy 61 NQKFKDKATLTVDKSTTAYMELRSLTSEDSAVVYCARSTMTITNYVMDYWGQGTSTVTVSS 120
Db 61 NQDFDKATLTVDKSTNTAYMELSSLRSEDATVYCARGLF--PWFAD-WGQGLTVTVSS 117

Qy 121 AKTTTPSVVPLAPGSAAOQNSMVTGLCKVKGYPEPEVTVTWNSGSLSSGGVHTTFAVLQSD 180
Db 118 ASKGSVFLPLACRSRSTSGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTFAVLQSS 177

Qy 181 -LYTSSSVTVPSSTWPTVTCNVAHPASSTKVDKIVPRDSDGSPSEKSENEKDLRK 239
Db 178 GLYSLSSVTVPSLSLGTQTYICNVNHPKPSNTKVDKVPKSC----- 220

Qy 240 KSELQALGNLKQIYYNSKAITSEKSAQDLTNLLFKGFFTHPWINDLLVDLQST 299
Db 221 -----DKHTCPKPAPELLGGPSVF--LFPKPP--KDTLM----- 252

Qy 300 AATSEYEGSSVDLYGAYGYQCAGGTPNKTACMGVTLHDNNRLTEKKVPINLWIDGK 359
Db 253 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVDG- 281

Qy 360 QTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLGNSDSFGKVGORGLIVFHSSEGSTV 419
Db 282 ---VEVHNAKTKPREQ-----YNSTY---RVSVSLTVLHQDWLNGK 317

Qy 420 SYDLFDAQOQYPTLLRIYRDNTTISSTLSLSLYLYTTSIYVMTQTPSLVSGADRVTI 479
Db 318 EY----- 319

Qy 480 TKCASQSVNDVAVYQKQSPKLLISYTSRYAGVDPDRFSGSGYGTDTLTSSVQAE 539
Db 320 KCKVS-----NKALPAP--IEKTISSKAKGP----- 343

Qy 540 DAAVYFCQDYNPSPTFGGKTKLEIKRAADAAPTISFPSSBQLTSGGASVVCFLNFPY 599
Db 344 -----REPOVYTLPPSRDELTKNQVSLTCLVKGFY 374

Qy 600 KOINVKWKIDGSRQN-----GVLSWTDQDSDKSTYSMSSTLTITKDEYERHNSYTCFA 654
Db 375 SDIAVEWESNGQPENNYKTPPMLDS-----DGSFFLYSKLTVDKSRWQGNVFCSV 427

Qy 655 THK 657
Db 428 LHE 430

RESULT 48
US-11-177-648-92
; Sequence 92, Application US/11177648
; Publication No. US20060029603A1
; GENERAL INFORMATION:
; APPLICANT: Jonathon Henry ELLIS
; APPLICANT: Paul Andrew HAMBELIN
; APPLICANT: Paul Alexander WILSON
; APPLICANT: Alan Peter LEWIS
; TITLE OF INVENTION: IMMUNOGLOBULINS
; FILE REFERENCE: PB60608-2
; CURRENT APPLICATION NUMBER: US/11/177,648
; CURRENT FILING DATE: 2005-07-06
; PRIOR APPLICATION NUMBER: PCT/GB2004/005325
; PRIOR FILING DATE: 2004-12-20
; PRIOR APPLICATION NUMBER: GB0329711.6
; PRIOR FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: GB0329684.5
; PRIOR FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 462
; TYPE: PRT


```
Db 359 -----REPOVYTLPPSRDEL 374
QY 585 SGASVVCFLNNFYPKIDNWKIDGSRQN-----GVLSNWTDDQSDKSTYSMSSTLTL 639
Db 375 KNQVSLTCLVKFGFYPDAVWESNGQPNKYKTPPVLDSDSGSFLYSKLTAV 427
QY 640 TKDEYERHNSYCEATHK 657
Db 428 DXSRWQOGNVPFSCVMHE 445

RESULT 52
US-11-120-338-22
; Sequence 22, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IQBAL S.
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IQBAL S.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 22
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-120-338-22

Query Match 22.7%; Score 800; DB 7; Length 451;
Best Local Similarity 31.4%; Pred. No. 5.6e-35;
Matches 209; Conservative 65; Mismatches 153; Indels 238; Gaps 17;

QY 1 EVLOQSGPDLVKPGASVKISCKASGYSTGYMHVWVKSPGKLEWIGRIINPNNGVTLY 60
Db 1 EVQLVESGGLVQPGGSLRLSCAASGFTFTSYNMHWVRQAPGKLEWVGAIYPGNGDTSY 60
QY 61 NQKFKDKATLTVDKSTTHAYMELRLSTSDSAVYICARSTMTIN--YVMDYWGQGTSTV 118
Db 61 NQKFKGRFTISVDKSKNTLYLQMSLRADTAIVYCARVYVYSNSYWFYDVMGQGLVT 120
QY 119 SSAKTTTPPSVYPLAPGSAATNSMTVLGCLVKGYRPEPTVTWNSGSLSSGVHTFPV 178
Db 121 SSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFP 180
QY 179 SD-LYTLSSSVTPSPSTWSETVTCNVAHPASTKVDKIKVPRDGGPSEKSEINEKOL 237
Db 181 SSGLYSLSSVTPSPSSSLGTQYICNVNHPKNTKVDKKEPKSC-----225
QY 238 RKXSELQGTALGNLKOIYYNSKAITSSSEKSDOFLNTLLKGFTHGPHWYNLDLVLG 297
Db 226 -----DKTHTCPPCPAPELGGPSVF--LPPPKP--KDTLM---257
QY 298 STAATSEYEGSSVDLYGAYGYQCAGGTGPKTACMYGGVTLHDNNRLTEKKVPINLWID 357
Db 258 -----ISRTEVT-CVVVDVS-----HEDPEVKFNWYVD 285
QY 358 GKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGKQGLIVFHSSEGS 417
Db 286 G-----VEVHNATKPREEQ-----YNSTY---RWVSVLTVLHQDWLN 320
QY 418 TVSYDLFDAGQGPDTLLRIYRDNTTISSTLSLSLYLTTSIVMTQTPTSLLSVSGDRV 477
Db 321 GKEY-----324
QY 478 TITCKASQSVNDVAWYQKPGSPKLLISYTSRYAGVPDRFSGSGYGTDTLTISVQ 537
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Db 325 --CKKVS-----NKALPAP---TEKTSKAKGP-----348
QY 538 AEDAAVYFCQDYNSPPTFGGTGKLEIKRADAPTYSIEPPSSEQLTSGASVVCFLNNF 597
Db 349 -----REPOVYTLPPSRDEMTKNQVSLTCLVKGF 377
QY 598 YPKDINVWKIDGSRQN-----GVLSNWTDDQSDKSTYSMSSTLTLTKDEYERHNSYTC 652
Db 378 YPSDIAVWESNGQPNKYKTPPVLDSDSGSFLYSKLTVDKSRWQOGNVPFSC 430
QY 653 EATHK 657
Db 431 SVMHE 435

RESULT 53
US-11-120-338-14
; Sequence 14, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IQBAL S.
; APPLICANT: WALICKE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 14
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-120-338-14

Query Match 22.7%; Score 800; DB 7; Length 452;
Best Local Similarity 31.4%; Pred. No. 5.6e-35;
Matches 209; Conservative 65; Mismatches 153; Indels 238; Gaps 17;

QY 1 EVLOQSGPDLVKPGASVKISCKASGYSTGYMHVWVKSPGKLEWIGRIINPNNGVTLY 60
Db 1 EVQLVESGGLVQPGGSLRLSCAASGFTFTSYNMHWVRQAPGKLEWVGAIYPGNGDTSY 60
QY 61 NQKFKDKATLTVDKSTTHAYMELRLSTSDSAVYICARSTMTIN--YVMDYWGQGTSTV 118
Db 61 NQKFKGRFTISVDKSKNTLYLQMSLRADTAIVYCARVYVYSNSYWFYDVMGQGLVT 120
QY 119 SSAKTTTPPSVYPLAPGSAATNSMTVLGCLVKGYRPEPTVTWNSGSLSSGVHTFPV 178
Db 121 SSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFP 180
QY 179 SD-LYTLSSSVTPSPSTWSETVTCNVAHPASTKVDKIKVPRDGGPSEKSEINEKOL 237
Db 181 SSGLYSLSSVTPSPSSSLGTQYICNVNHPKNTKVDKKEPKSC-----225
QY 238 RKXSELQGTALGNLKOIYYNSKAITSSSEKSDOFLNTLLKGFTHGPHWYNLDLVLG 297
Db 226 -----DKTHTCPPCPAPELGGPSVF--LPPPKP--KDTLM---257
QY 298 STAATSEYEGSSVDLYGAYGYQCAGGTGPKTACMYGGVTLHDNNRLTEKKVPINLWID 357
Db 258 -----ISRTEVT-CVVVDVS-----HEDPEVKFNWYVD 285
QY 358 GKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGKQGLIVFHSSEGS 417
Db 286 G-----VEVHNATKPREEQ-----YNSTY---RWVSVLTVLHQDWLN 320
QY 418 TVSYDLFDAGQGPDTLLRIYRDNTTISSTLSLSLYLTTSIVMTQTPTSLLSVSGDRV 477
Db 321 GKEY-----324
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QY 358 GKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQGRGLIVFHSSEGS 417
Db 286 G-----VEVHNAKTKPREQ-----YNSTY---RVSVLTVLHQDWLN 320
QY 418 TVSYDLFDAQGOYPTDLLRIYRDNNTTISSTLSLSLYLTTISVMTQTPTSLLSVAGDRV 477
Db 321 GKXY-----
QY 478 TITCKASQSVSNDAVYQKPGQPKLLISYTSRRYAGVDPDRFSGSGYGTDFLTITISSVQ 537
Db 325 --KCKVS-----NKALPAP---IEKTIKAKGQP----- 348
QY 538 AEDAAVYFCQDYNSPPTFGGKLEIKRADAAPTVSIPIPPSSEQLTSGASVVCFLNPF 597
Db 349 -----REPQVYTLPPSREEMTKNQVSLTCLVKGF 377
QY 598 YPKDINVKWKIDGSRQN-----GVLNSWTDQDSKDYSTYSMSSTLTLTCKDEYERHNSYTC 652
Db 378 YPSDIAVESNGQPNENYKTTTPPVLDS-----DGSFFLYSKLTVDKSRWQGNVFSC 430
QY 653 EATHK 657
Db 431 SVMHE 435

RESULT 56
US-11-143-077-14
; Sequence 14, Application US/11143077
; Publication No. US20060024295A1
; GENERAL INFORMATION:
; APPLICANT: Brunetta, Paul G.
; TITLE OF INVENTION: METHOD FOR TREATING LUPUS
; FILE REFERENCE: P2133R1
; CURRENT APPLICATION NUMBER: US/11/143,077
; PRIOR FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/577,235
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/617,997
; PRIOR FILING DATE: 2004-10-11
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 14
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-143-077-14

Query Match 22.7%; Score 800; DB 7; Length 452;
Best Local Similarity 31.4%; Pred. No. 5.6e-35;
Matches 209; Conservative 65; Mismatches 153; Indels 238; Gaps 17;

QY 1 EVOLQSGPDLVKPGASVKISKASGYSTGYGMHWKQSPGKLEWIGRIINPNNGVTL 60
Db 1 EVOLVESGGLVQPGGSLRLSCAASGYFTSYNMHWVRQAPGKLEWVGAIYPGNGDTSY 60
QY 61 NQKFKDKATLVDSKSTTAYMELRSITSDSAVYICARSTMITN--YVMDYWGQGTSTV 118
Db 61 NQKFKGRFTISVDKSKNTLYLQWNSLRAEDTAVYICARVYVYNSYWFYDMWGQGLTV 120
QY 119 SSAKTTTPSVYPLAPGSAATNSMVTLCGLVKGYFPPEVTVTVNWSGSLSGVHTFPV 178
Db 121 SSASTKGPVFPPLAPSKSTSGGTAALGCLVKDYFPPEVTVTVNWSGALTSGVHTFP 180
QY 179 SD--LYTLSSSVTVPSSTWPSSEVTCNVAPASSTKVDKIVPRDSGGPSEKSEINE 237
Db 181 SSGLYSLSSVTVPSSSLGTQTYICNVNHPKSTKVDKIVPRDSGGPSEKSEINEKOL 225
QY 238 RKKSELOQTALGNLKQIYYNKAITSSEKSAQDFLTNTLLFKGFTTGHFWYNDLLVD 297
Db 226 -----DKTHTCPCPAPPELLGGPSVF--LPFPKP--KDTLM-- 257
QY 298 STAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTVLHDNRLTEKKVPINLWID 357
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Db 258 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVD 285
QY 358 GKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQGRGLIVFHSSEGS 417
Db 286 G-----VEVHNAKTKPREQ-----YNSTY---RVSVLTVLHQDWLN 320
QY 418 TVSYDLFDAQGOYPTDLLRIYRDNNTTISSTLSLSLYLTTISVMTQTPTSLLSVAGDRV 477
Db 321 GKXY-----
QY 478 TITCKASQSVSNDAVYQKPGQPKLLISYTSRRYAGVDPDRFSGSGYGTDFLTITISSVQ 537
Db 325 --KCKVS-----NKALPAP---IEKTIKAKGQP----- 348
QY 538 AEDAAVYFCQDYNSPPTFGGKLEIKRADAAPTVSIPIPPSSEQLTSGASVVCFLNPF 597
Db 349 -----REPQVYTLPPSREEMTKNQVSLTCLVKGF 377
QY 598 YPKDINVKWKIDGSRQN-----GVLNSWTDQDSKDYSTYSMSSTLTLTCKDEYERHNSYTC 652
Db 378 YPSDIAVESNGQPNENYKTTTPPVLDS-----DGSFFLYSKLTVDKSRWQGNVFSC 430
QY 653 EATHK 657
Db 431 SVMHE 435

RESULT 57
US-11-106-820-25
; Sequence 25, Application US/11106820
; Publication No. US20060002930A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G
; TITLE OF INVENTION: Treatment of Disorders
; FILE REFERENCE: P2102R1
; CURRENT APPLICATION NUMBER: US/11/106,820
; PRIOR FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,227
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/565,098
; PRIOR FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 25
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-106-820-25

Query Match 22.7%; Score 800; DB 7; Length 471;
Best Local Similarity 31.4%; Pred. No. 5.8e-35;
Matches 209; Conservative 65; Mismatches 153; Indels 238; Gaps 17;

QY 1 EVOLQSGPDLVKPGASVKISKASGYSTGYGMHWKQSPGKLEWIGRIINPNNGVTL 60
Db 20 EVOLVESGGLVQPGGSLRLSCAASGYFTSYNMHWVRQAPGKLEWVGAIYPGNGDTSY 79
QY 61 NQKFKDKATLVDSKSTTAYMELRSITSDSAVYICARSTMITN--YVMDYWGQGTSTV 118
Db 80 NQKFKGRFTISVDKSKNTLYLQWNSLRAEDTAVYICARVYVYNSYWFYDMWGQGLTV 139
QY 119 SSAKTTTPSVYPLAPGSAATNSMVTLCGLVKGYFPPEVTVTVNWSGSLSGVHTFPV 178
Db 140 SSASTKGPVFPPLAPSKSTSGGTAALGCLVKDYFPPEVTVTVNWSGALTSGVHTFP 199
QY 179 SD--LYTLSSSVTVPSSTWPSSEVTCNVAPASSTKVDKIVPRDSGGPSEKSEINE 237
Db 200 SSGLYSLSSVTVPSSSLGTQTYICNVNHPKSTKVDKIVPRDSGGPSEKSEINEKOL 244
QY 238 RKKSELOQTALGNLKQIYYNKAITSSEKSAQDFLTNTLLFKGFTTGHFWYNDLLVD 297
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Db      245  -----DKTHTCPPCPAPPELLGGPSVF--LPPPKP--KDTLM-- 276
QY      298  STAATSEYEGSSVDLYGAYGYQCAGGTGNKTKACMYGGVTLHDNNRLTEKKVPIINLWID 357
Db      277  -----ISRTPEVT--CVVVDVS-----HEDPEVKFNWYVD 304
QY      358  GKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFLGYNDSFGGKVQVGLIIVFHSSEGS 417
Db      305  G-----VEVHNAKTKPREEQ-----YNSTY---RVVSVLTVLHQDWLNL 339
QY      418  TVSYDLFDAAGQVPTDLLRIYRDNNTTSSLSLSLYLTTISVMTQTPTSSLVSAGDRV 477
Db      340  GKEY-----ISRTPEVT--CVVVDVS-----HEDPEVKFNWYVD 343
QY      478  TITCKASQSVNDVAVYQKPGOSPKLLISYTSRVRAGVDPDRFSGSGYGTDTLTITSSVQ 537
Db      344  --KCKVS-----NKALPAP---IEKTIKAKGP----- 367
QY      538  AEDAAVYFCQDYNPPTFGGKTKLEIKRADAAPTYSIFPPSSEQLTSGGASVVCFLNPF 597
Db      368  -----REPQVYTLPPSREEMTKNQVSLTCLVKGF 396
QY      598  YPKDINVKKIDGSERON-----GVLSNWTDDQSKDSTYSMSSTLTITKDEYERHNSYTC 652
Db      397  YPSDIAVEWESNGQPENNYKTPPPVLDS-----DGSFFLYSKLTVDKSRWQGNVFSC 449
QY      653  EATHK 657
Db      450  SVMHE 454

RESULT 58
US-11-190-364-22
; Sequence 22, Application US/11190364
; Publication No. US20060024300A1
; GENERAL INFORMATION:
; APPLICANT: Adams ET AL.
; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
; FILE REFERENCE: P1990R3C1P1
; CURRENT APPLICATION NUMBER: US/11/190,364
; CURRENT FILING DATE: 2005-07-26
; PRIOR APPLICATION NUMBER: US 60/434,115
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/526,163
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: PCT/US03/40426
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 11/147,780
; PRIOR FILING DATE: 2005-06-07
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 22
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-190-364-22

Query Match      22.7%; Score 800; DB 7; Length 471;
Best Local Similarity 31.4%; Pred. No. 5.8e-35;
Matches 209; Conservative 65; Mismatches 153; Indels 238; Gaps 17;

QY      1  EVLOQSGDPLVKPGASVKISKASGYSTGYIMHWVKQSPGKLEWIGRINPNNGVTLY 60
Db      20  EVLVESGGGLVQPGGSLRLSCAASGYTFYSYNHWVRQAPGKLEWVGAIYFNGDTSY 79
QY      61  NQKFKDKATLTVDKSTTAYMELRLSTSDSAVYYCARSTMITN--YVMDYWGQGSVTY 118
Db      80  NQKFKGRFTISVDKSKNTLYLQMSLRAEDTAVYCARVYVYSNYSYWFYDVMWGQGLTVT 139
QY      119  SSAKTPPSVYPLAPGSAAGTNSMTLGLCLVKGYFPEPVTVTVNSGSLSSGTVHTFPAVLQ 178
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Db      140  SSASTKGPSVFPLAAPSSTSGTAAALGCLVKDYFPEPVTVTVNSGALTSGVHTFPAVLQ 199
QY      179  SD--LYTLSSSVTPSPSTWSPSETVTCNVAHPASSTKVDKIKIVPRDSGGPSEKSEINEKDL 237
Db      200  SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSC----- 244
QY      238  RKKSELQGTALGNLKOIYYNNSKAITSSSEKSDAQFLTNLLFKGFTTGHWPYNDLLVDLG 297
Db      245  -----DKTHTCPPCPAPPELLGGPSVF--LPPPKP--KDTLM-- 276
QY      298  STAATSEYEGSSVDLYGAYGYQCAGGTGNKTKACMYGGVTLHDNNRLTEKKVPIINLWID 357
Db      277  -----ISRTPEVT--CVVVDVS-----HEDPEVKFNWYVD 304
QY      358  GKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFLGYNDSFGGKVQVGLIIVFHSSEGS 417
Db      305  G-----VEVHNAKTKPREEQ-----YNSTY---RVVSVLTVLHQDWLNL 339
QY      418  TVSYDLFDAAGQVPTDLLRIYRDNNTTSSLSLSLYLTTISVMTQTPTSSLVSAGDRV 477
Db      340  GKEY-----ISRTPEVT--CVVVDVS-----HEDPEVKFNWYVD 343
QY      478  TITCKASQSVNDVAVYQKPGOSPKLLISYTSRVRAGVDPDRFSGSGYGTDTLTITSSVQ 537
Db      344  --KCKVS-----NKALPAP---IEKTIKAKGP----- 367
QY      538  AEDAAVYFCQDYNPPTFGGKTKLEIKRADAAPTYSIFPPSSEQLTSGGASVVCFLNPF 597
Db      368  -----REPQVYTLPPSREEMTKNQVSLTCLVKGF 396
QY      598  YPKDINVKKIDGSERON-----GVLSNWTDDQSKDSTYSMSSTLTITKDEYERHNSYTC 652
Db      397  YPSDIAVEWESNGQPENNYKTPPPVLDS-----DGSFFLYSKLTVDKSRWQGNVFSC 449
QY      653  EATHK 657
Db      450  SVMHE 454

RESULT 59
US-11-120-338-15
; Sequence 15, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IOBAL S.
; APPLICANT: WALICKE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 15
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-120-338-15

Query Match      22.7%; Score 798; DB 7; Length 452;
Best Local Similarity 30.8%; Pred. No. 7.1e-35;
Matches 207; Conservative 69; Mismatches 144; Indels 252; Gaps 17;

QY      1  EVLOQSGDPLVKPGASVKISKASGYSTGYIMHWVKQSPGKLEWIGRINPNNGVTLY 60
Db      1  EVLVESGGGLVQPGGSLRLSCAASGYTFYSYNHWVRQAPGKLEWVGAIYFNGDTSY 60
QY      61  NQKFKDKATLTVDKSTTAYMELRLSTSDSAVYYCARSTMITN--YVMDYWGQGSVTY 118
Db      61  NQKFKGRFTISVDKSKNTLYLQMSLRAEDTAVYCARVYVYSNYSYWFYDVMWGQGLTVT 120
```

QY 119 SSAKTPPSVYPLAPGSAQAQTNMWTLCGLVKGYPPEPVTVTWNSGSLSSGVHTTTPAVLQ 178
Db 121 SSAKTPPSVYPLAPGSAQAQTNMWTLCGLVKGYPPEPVTVTWNSGSLSSGVHTTTPAVLQ 180
QY 179 SD-LYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKVDDKIIVPRDSDGGPSEKSEINEKOL 237
Db 181 SGLVSLSSVTVPSSTWPSSTWPSSETVTCNVAHPASSTKVDDKIIVPRDSDGGPSEKSEINEKOL 225
QY 238 RKKSELQGTALGNLQIYYVNSKAITSSSEKSDAQFLNTLLFKGFFTHGHPWYNDLLVDLG 297
Db 226 -----DKTHCTPCPCAPPELLGGPSVF--LPPKP--KDTLM--- 257
QY 298 STAATSEYEGSSVDLYGAYGYQCAGGTPNKACTMYGVTLLHNNRLTEKKVPIINLWID 357
Db 258 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVD 285
QY 411 FHSSEGSTVSYDLFDAQGYQYPTDLLRIYRDNTTISSTLSLSISLYLYTTTSIVMTQTPTSL 470
Db 323 -----EY----- 324
QY 471 VSAGDRVTITCKASQSVNDVAWYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDTFT 530
Db 325 -----KCKVS-----NKALPAP---IAATISKAKGQP----- 348
QY 531 LTISSVQAEDAAYVFCQDYNSPPTFGGKLEIKRADAAPTIVSIPPPSSEQLTSGGASV 590
Db 349 -----REPQYVTLPPBREEMTKNOVSL 370
QY 591 VCFLNFPKIDINVKWKIDGSRQN-----GVLSNMTDQDSKDYMSSTLTLTKEDEYE 645
Db 371 TCLVKGFPYSDIAVESNGQPNVKTTPPVLDSD-----DGSFFLYSKLTVDKSRWQ 423
QY 646 RHNSYTCEATHK 657
Db 424 QGNVFCSCVMHE 435

RESULT 60
US-11-107-028-33
; Sequence 33, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
; APPLICANT: CHAN, ANDREW C.
; APPLICANT: GONG, QIAN
; APPLICANT: MARTIN, FLAVIUS
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion
; FILE REFERENCE: P2112R1
; CURRENT APPLICATION NUMBER: US/11/107,028
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,263
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 33
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-107-028-33

Query Match 22.7%; Score 798; DB 7; Length 452;
Best Local Similarity 30.8%; Pred. No. 7.1e-35;
Matches 207; Conservative 69; Mismatches 144; Indels 252; Gaps 17;

QY 1 EVQLQQSGPDLVRPGASVKISKASGYSTFGYYMHVWKQSPGKLEWIGRINPNNGVTLY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYTFSTYNHNVWRVAPGKLEWVGAIYPCNGDTSY 60

QY 61 NOKFKDKATLTVDKSGTSTAYMELRSLTSEDSAVVYCARSTMITN--YVMDYMGQGTSTV 118
Db 61 NOKFKGRITISVDKSKNTLYLQMNLSRAEDTAVVYCARVVVYSNSWYEDVWGQGLTVIV 120
QY 119 SSAKTPPSVYPLAPGSAQAQTNMWTLCGLVKGYPPEPVTVTWNSGSLSSGVHTTTPAVLQ 178
Db 121 SSAKTPPSVYPLAPGSAQAQTNMWTLCGLVKGYPPEPVTVTWNSGSLSSGVHTTTPAVLQ 180
QY 179 SD-LYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKVDDKIIVPRDSDGGPSEKSEINEKOL 237
Db 181 SGLVSLSSVTVPSSTWPSSTWPSSETVTCNVAHPASSTKVDDKIIVPRDSDGGPSEKSEINEKOL 225
QY 238 RKKSELQGTALGNLQIYYVNSKAITSSSEKSDAQFLNTLLFKGFFTHGHPWYNDLLVDLG 297
Db 226 -----DKTHCTPCPCAPPELLGGPSVF--LPPKP--KDTLM--- 257
QY 298 STAATSEYEGSSVDLYGAYGYQCAGGTPNKACTMYGVTLLHNNRLTEKKVPIINLWID 357
Db 258 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVD 285
QY 358 GKQTTVPIDKVKTSKEV-----TVQELDLQARHYLHGKFGLYNSDSFGGKVQORGLIV 410
Db 286 G-----VEVHNAKTKPREEQYNATYRVVSVLTVLHQDWLNGK----- 322
QY 411 FHSSEGSTVSYDLFDAQGYQYPTDLLRIYRDNTTISSTLSLSISLYLYTTTSIVMTQTPTSL 470
Db 323 -----EY----- 324
QY 471 VSAGDRVTITCKASQSVNDVAWYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDTFT 530
Db 325 -----KCKVS-----NKALPAP---IAATISKAKGQP----- 348
QY 531 LTISSVQAEDAAYVFCQDYNSPPTFGGKLEIKRADAAPTIVSIPPPSSEQLTSGGASV 590
Db 349 -----REPQYVTLPPBREEMTKNOVSL 370
QY 591 VCFLNFPKIDINVKWKIDGSRQN-----GVLSNMTDQDSKDYMSSTLTLTKEDEYE 645
Db 371 TCLVKGFPYSDIAVESNGQPNVKTTPPVLDSD-----DGSFFLYSKLTVDKSRWQ 423
QY 646 RHNSYTCEATHK 657
Db 424 QGNVFCSCVMHE 435

RESULT 61
US-11-106-820-28
; Sequence 28, Application US/11106820
; Publication No. US20060002930A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G
; APPLICANT: SEWELL, KATHRYN L.
; TITLE OF INVENTION: Treatment of Disorders
; FILE REFERENCE: P2102R1
; CURRENT APPLICATION NUMBER: US/11/106,820
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,227
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/565,098
; PRIOR FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 28
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-106-820-28

Query Match 22.7%; Score 798; DB 7; Length 452;
Best Local Similarity 30.8%; Pred. No. 7.1e-35;
Matches 207; Conservative 69; Mismatches 144; Indels 252; Gaps 17;

QY 1 EVLOQSGPDLVKPGASVKISKASGYSFTGYVMHWKQSPGKLEWIGRINPNNGVTLY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTSYNMHWVRQAPGKLEWVGAIYFGNGDTSY 60
QY 61 NQKFKDKATLTVDKSSSTTAYMELSLTSEDSAVVYCARSTMITN--YVMDYWGQGSVTY 118
Db 61 NQKFKGRFTISVDKSKNTLYLQWNSLRAEDTAVYCARVYVYNSYVYFVWVGQGLTVTV 120
QY 119 SSAKTTTPSPVYPLAPGSAAGTNSMTLGLCLVKGYFPEPVPTVTWNSGSLSSGVHTFFPAVLQ 178
Db 121 SSAATKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPVTVSWNSGALTSVGHVTFPAVLQ 180
QY 179 SD-LYTLSSSVTPSPSTWPSSETVTCNVAPASSTKVDKIVPRDSDGSPSEKSEINEKDL 237
Db 181 SSGLYSLSSVTVFPSSSLGTQTYICNVNHPKPSNTKVDKKEPKSC----- 225
QY 238 RKSELOQTALGNLKOIYYNNSKAITSSSEKSAQDLTNTLLFKGFTTGHWPYNDLLVDLG 297
Db 226 -----DKHTCCPPCPAPPELLGGPSVF--LPFPKP--KDTLM--- 257
QY 298 STAATSEYEGSSVDLYGAYGYQCAGGTPNKTACTMYGGVTLHDNRLTEKKVPINLWID 357
Db 258 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVD 285
QY 358 GKQTTVPIDKVTSSKEV-----TVQELDLQARHYLHGKFGLYNSDSFGGKVQVRLIV 410
Db 286 G-----VEVHNKTKPREEQNATYRVVSVLTVLHQDLNKG----- 322
QY 411 FHSSEGSTVSYDLFDAQGYPDTLRLIYRDNTTISSTLSISLYLYTTSIVMTQTPTSLL 470
Db 323 -----EY----- 324
QY 471 VSAGDRVTITCKASQSVNDVAVYQKPGQSPKLLISYTSRVRAGVDPDRFSGSGYGTDF 530
Db 325 -----KCKVS-----NKALPAP--IAATISKAKGP----- 348
QY 531 LTISVQAEADAAYFCQDYNPSPTFGGKTKLEIKRADAAPTYSIFPPSSEQLTSGASV 590
Db 349 -----REPQVYTLPPSREEMTKNQVSL 370
QY 591 VCFLNFPYKIDINVKWKIDGSRQN-----GVLSNWTQDQSKDSTYSMSSTLTLTDEYE 645
Db 371 TCLVKGFPSPDIWESNGQPNKYKTPPVLDLSD-----DGSFPLYSKLTVDKSRWQ 423
QY 646 RHNSYTCETHK 657
Db 424 QGNVFCSCVMHE 435

RESULT 62
US-11-143-077-15
; Sequence 15, Application US/11143077
; Publication No. US20060024295A1
; GENERAL INFORMATION:
; APPLICANT: Brunetta, Paul G.
; TITLE OF INVENTION: METHOD FOR TREATING LUPUS
; FILE REFERENCE: P2133R1
; CURRENT APPLICATION NUMBER: US/11/143,077
; PRIOR FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/577,235
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/617,997
; PRIOR FILING DATE: 2004-10-11
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 15
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-143-077-15

Query Match 22.7%; Score 798; DB 7; Length 452;

Best Local Similarity 30.8%; Pred. No. 7.1e-35;
Matches 207; Conservative 69; Mismatches 144; Indels 252; Gaps 17;
QY 1 EVLOQSGPDLVKPGASVKISKASGYSFTGYVMHWKQSPGKLEWIGRINPNNGVTLY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTSYNMHWVRQAPGKLEWVGAIYFGNGDTSY 60
QY 61 NQKFKDKATLTVDKSSSTTAYMELSLTSEDSAVVYCARSTMITN--YVMDYWGQGSVTY 118
Db 61 NQKFKGRFTISVDKSKNTLYLQWNSLRAEDTAVYCARVYVYNSYVYFVWVGQGLTVTV 120
QY 119 SSAKTTTPSPVYPLAPGSAAGTNSMTLGLCLVKGYFPEPVPTVTWNSGSLSSGVHTFFPAVLQ 178
Db 121 SSAATKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPVTVSWNSGALTSVGHVTFPAVLQ 180
QY 179 SD-LYTLSSSVTPSPSTWPSSETVTCNVAPASSTKVDKIVPRDSDGSPSEKSEINEKDL 237
Db 181 SSGLYSLSSVTVFPSSSLGTQTYICNVNHPKPSNTKVDKKEPKSC----- 225
QY 238 RKSELOQTALGNLKOIYYNNSKAITSSSEKSAQDLTNTLLFKGFTTGHWPYNDLLVDLG 297
Db 226 -----DKHTCCPPCPAPPELLGGPSVF--LPFPKP--KDTLM--- 257
QY 298 STAATSEYEGSSVDLYGAYGYQCAGGTPNKTACTMYGGVTLHDNRLTEKKVPINLWID 357
Db 258 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVD 285
QY 358 GKQTTVPIDKVTSSKEV-----TVQELDLQARHYLHGKFGLYNSDSFGGKVQVRLIV 410
Db 286 G-----VEVHNKTKPREEQNATYRVVSVLTVLHQDLNKG----- 322
QY 411 FHSSEGSTVSYDLFDAQGYPDTLRLIYRDNTTISSTLSISLYLYTTSIVMTQTPTSLL 470
Db 323 -----EY----- 324
QY 471 VSAGDRVTITCKASQSVNDVAVYQKPGQSPKLLISYTSRVRAGVDPDRFSGSGYGTDF 530
Db 325 -----KCKVS-----NKALPAP--IAATISKAKGP----- 348
QY 531 LTISVQAEADAAYFCQDYNPSPTFGGKTKLEIKRADAAPTYSIFPPSSEQLTSGASV 590
Db 349 -----REPQVYTLPPSREEMTKNQVSL 370
QY 591 VCFLNFPYKIDINVKWKIDGSRQN-----GVLSNWTQDQSKDSTYSMSSTLTLTDEYE 645
Db 371 TCLVKGFPSPDIWESNGQPNKYKTPPVLDLSD-----DGSFPLYSKLTVDKSRWQ 423
QY 646 RHNSYTCETHK 657
Db 424 QGNVFCSCVMHE 435

RESULT 63
US-11-106-820-27
; Sequence 27, Application US/11106820
; Publication No. US20060002930A1
; GENERAL INFORMATION:
; APPLICANT: Brunetta, Paul G.
; APPLICANT: SEWELL, KATHRYN L.
; TITLE OF INVENTION: Treatment of Disorders
; FILE REFERENCE: P2102R1
; CURRENT APPLICATION NUMBER: US/11/106,820
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,227
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/565,098
; PRIOR FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 27
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:

```
; OTHER INFORMATION: sequence is synthesized
US-11-106-820-27

Query Match      22.7%; Score 798; DB 7; Length 471;
Best Local Similarity 30.8%; Pred. No. 7.4e-35;
Matches 207; Conservative 69; Mismatches 144; Indels 252; Gaps 17;

QY 1 EVQLQSGDPLVKPGASVKISKASGYSTGYMHVWVQSPGKGLEWIGRIINPNNGVTLV 60
DB 20 EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHWVRQAPGKLEWVGAIIYPGNGDTSY 79
QY 61 NQKFKDKATLTVDKSTTAYMELRLSLSDSAVYYCARSTMTITN--YVMDYMGQGTSTV 118
DB 80 NQKFKGRFTISVDKSKNTLYLQWNSLRADTAVYYCARVYVYNSWYFDVWGQGLTVV 139
QY 119 SSAKTPPSVYPLAPGSAATQNSMTVLCGLVKGYPPEPVTVTWNSGSLSSGVHTFPVAVLQ 178
DB 140 SSAATKGPSVFPPLAPGSKTSGTAAALGCLVKDYFPPEVTVSWNSGALTSGVHTFPVAVLQ 199
QY 179 SD-LYTLSSVTVPSSTWPSSETVTCNVAHPASSTKVDKIVPRDSDGPPSEKSEINEKDL 237
DB 200 SSGLYSLSSVTVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSC----- 244
QY 238 RKKSELQGTALGNLQIYYVNSKAITSEKSDAQFLTNTLLFKGFTGHPWYNDLLVDLG 297
DB 245 -----DKTHTCPCPAPPELLGGPSV--LPFPPK--KDTLM--- 276
QY 298 STAATSEYEGSSVDLYGAYGYQCAGTPNKTACMYGGVTLHDNNRLTBEKKVPINLWID 357
DB 277 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVD 304
QY 358 GKQTTVPIDKVKTSKEV-----TVQELDLQARHYLHGKFGLYNSDSFGGKVGQGLIV 410
DB 305 G-----VEVHNAKTKPREEQYNATYRVVSVLTVLHODWLNK----- 341
QY 411 FHSSEGSTVSYDLFDAQGYQPDTLRLIYRDNTTISSTLSLSLYLTVTSIVMTQTPTSL 470
DB 342 -----EY----- 343
QY 471 VSAGDRVTITCKASQSVNDVAWYQKPGQSKLLISYTSRYAGVDPDRFSGSGYGTDT 530
DB 344 -----CKKVS-----NKALPAP---IAATISKAKGP----- 367
QY 531 LTISSVQAEDAAVYFCQDYNSPPTFGGKTKLEIKRADAAPTYSIFPPSSEQLTSGASV 590
DB 368 -----REPQVYTLPPSREEMTKNQVSL 389
QY 591 VCLNNFYPKDINVKWKIDGSRQN-----GVLNSMTDQDSKDYSTYSMSSTLTLTCKDEYE 645
DB 390 TCLVKGFPYSDIAVENESNGQPNYKTTTPVLDS-----DGSFFLYSKLTVDKSRWQ 442
QY 646 RHNSYTCEATHK 657
DB 443 QGNVFSCSVNME 454

RESULT 64
US-11-190-364-23
; Sequence 23, Application US/11190364
; Publication No. US20060024300A1
; GENERAL INFORMATION:
; APPLICANT: Adams ET AL.
; TITLE OF INVENTION: Immunoglobulin Variants and Uses Thereof
; FILE REFERENCE: P19903C1P1
; CURRENT APPLICATION NUMBER: US/11/190,364
; CURRENT FILING DATE: 2005-07-26
; PRIOR APPLICATION NUMBER: US 60/434,115
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/526,163
; PRIOR FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: PCT/US03/40426
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 11/147,780
;

; PRIOR FILING DATE: 2005-06-07
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 23
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-190-364-23

Query Match      22.7%; Score 798; DB 7; Length 471;
Best Local Similarity 30.8%; Pred. No. 7.4e-35;
Matches 207; Conservative 69; Mismatches 144; Indels 252; Gaps 17;

QY 1 EVQLQSGDPLVKPGASVKISKASGYSTGYMHVWVQSPGKGLEWIGRIINPNNGVTLV 60
DB 20 EVQLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHWVRQAPGKLEWVGAIIYPGNGDTSY 79
QY 61 NQKFKDKATLTVDKSTTAYMELRLSLSDSAVYYCARSTMTITN--YVMDYMGQGTSTV 118
DB 80 NQKFKGRFTISVDKSKNTLYLQWNSLRADTAVYYCARVYVYNSWYFDVWGQGLTVV 139
QY 119 SSAKTPPSVYPLAPGSAATQNSMTVLCGLVKGYPPEPVTVTWNSGSLSSGVHTFPVAVLQ 178
DB 140 SSAATKGPSVFPPLAPGSKTSGTAAALGCLVKDYFPPEVTVSWNSGALTSGVHTFPVAVLQ 199
QY 179 SD-LYTLSSVTVPSSTWPSSETVTCNVAHPASSTKVDKIVPRDSDGPPSEKSEINEKDL 237
DB 200 SSGLYSLSSVTVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSC----- 244
QY 238 RKKSELQGTALGNLQIYYVNSKAITSEKSDAQFLTNTLLFKGFTGHPWYNDLLVDLG 297
DB 245 -----DKTHTCPCPAPPELLGGPSV--LPFPPK--KDTLM--- 276
QY 298 STAATSEYEGSSVDLYGAYGYQCAGTPNKTACMYGGVTLHDNNRLTBEKKVPINLWID 357
DB 277 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVD 304
QY 358 GKQTTVPIDKVKTSKEV-----TVQELDLQARHYLHGKFGLYNSDSFGGKVGQGLIV 410
DB 305 G-----VEVHNAKTKPREEQYNATYRVVSVLTVLHODWLNK----- 341
QY 411 FHSSEGSTVSYDLFDAQGYQPDTLRLIYRDNTTISSTLSLSLYLTVTSIVMTQTPTSL 470
DB 342 -----EY----- 343
QY 471 VSAGDRVTITCKASQSVNDVAWYQKPGQSKLLISYTSRYAGVDPDRFSGSGYGTDT 530
DB 344 -----CKKVS-----NKALPAP---IAATISKAKGP----- 367
QY 531 LTISSVQAEDAAVYFCQDYNSPPTFGGKTKLEIKRADAAPTYSIFPPSSEQLTSGASV 590
DB 368 -----REPQVYTLPPSREEMTKNQVSL 389
QY 591 VCLNNFYPKDINVKWKIDGSRQN-----GVLNSMTDQDSKDYSTYSMSSTLTLTCKDEYE 645
DB 390 TCLVKGFPYSDIAVENESNGQPNYKTTTPVLDS-----DGSFFLYSKLTVDKSRWQ 442
QY 646 RHNSYTCEATHK 657
DB 443 QGNVFSCSVNME 454

RESULT 65
US-11-183-205-56
; Sequence 56, Application US/11183205
; Publication No. US20060030521A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Bowe, Caryn
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; APPLICANT: Hakes, David
; APPLICANT: Chen, xi
; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
; FILE REFERENCE: 040853-01-5052-US01
; CURRENT APPLICATION NUMBER: US/11/183,205
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 11/183,205
; PRIOR FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 60/334,233
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/334,301
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: PCT/US2002/032263
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 10/287,994
; PRIOR FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 56
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-183-205-56

Query Match      22.6%; Score 794.5; DB 7; Length 448;
Best Local Similarity 32.1%; Pred. No. 1.1e-34;
Matches 213; Conservative 63; Mismatches 149; Indels 239; Gaps 18;

QY 1 EVLOQSGDPLVPGASVKISCKASGYSTGYMHVWKQSPGKLEWIGRINPNNGVTLY 60
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB 1 QVQLVQSGAEVKPGSSVKVSKASGVAFTNLYIEWRQAPGQGLEWIGVLYPGSGGTNY 60
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 61 NQKPKDKATLTVDKSSTAYMELRLSTSDSAVYYCARSTMIINY-VMDYWGQGTSTVTS 119
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB 61 NEKPKGRVTLTVDESTNTAYMELSSRLSRSDTAVYFCARRD--GNYGMFAYWGQGTIVTS 118
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 120 SAKTTTPSVYPLAPGSAATNSMVTLCGLVKGYPPEPTVTWNSGSLSGVHTFPVQLQS 179
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB 119 SASAKGSPVFPPLAPSSKSTGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQ 178
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 180 D-LYTLSSSVTPSSSTWPSSETVTCNVAHPASSTKVDKIKVPRDSGGPSEKSEINEKDLR 238
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB 179 SGLYSLSVVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSC-----222
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 239 KKSELOQTALGNLKQIYYNNSKAITSEKSAQDQFLNTLLFKGFFTGHPWYNDLLVDLGS 298
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB 223 -----DKHTCTPCPAPPELLGGPSVF--LFPPKP--KDTLM---254
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 299 TAATSEYEGSSVDLYGAYGYOCAGGTGPNKTCMYGGVTLHDNNRLTEKKVPINLWIDG 358
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB 255 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVD 283
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 359 KQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVGQVRLIVFHSSEGST 418
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB 284 -----VEVHNKATKPREEQ-----YNSTY---RVVSVLTVLHQDWLNG 318
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 419 VSYDLFDAQOQVPTLLRIYRDNTTISSTSLSLSYLYTTSIVMTQPTPTSLLSAGDRV 478
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB 319 KEY-----321
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 479 ITCASQSVSNDAWYQKPGQSPKLLISYTSRYAGVDPFSGSGVGTDFTLTISVQA 538
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB 322 -KCVS-----NKAIPAP---IEKTIKAKQGP-----345
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||

RESULT 66
US-11-107-028-45
; Sequence 45, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
; APPLICANT: CHAN, ANDREW C.
; APPLICANT: GONG, QIAN
; APPLICANT: MARTIN, FLAVIUS
; TITLE OF INVENTION: Method for Augmenting B Cell Depletion
; FILE REFERENCE: P2112R1
; CURRENT APPLICATION NUMBER: US/11/107,028
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,263
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 45
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-107-028-45

Query Match      22.5%; Score 793; DB 7; Length 452;
Best Local Similarity 30.7%; Pred. No. 1.3e-34;
Matches 206; Conservative 69; Mismatches 145; Indels 252; Gaps 17;

QY 1 EVLOQSGDPLVPGASVKISCKASGYSTGYMHVWKQSPGKLEWIGRINPNNGVTLY 60
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB 1 EVQLVESGGLVQPGGSLRLSCAASGYTFTSYNMHWVRQAPGKLEWVGAIYPGNGATSY 60
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 61 NQKPKDKATLTVDKSSTAYMELRLSTSDSAVYYCARST--MITNVMDYWGQGTSTV 118
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB 61 NQKPKGRFTISVDKSKNTLYLQWNSLRADETAIVYCARVYVYASVYFDWVGQGLTV 120
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 119 SSAKTTTPSVYPLAPGSAATNSMVTLCGLVKGYPPEPTVTWNSGSLSGVHTFPVQLQ 178
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB 121 SSASTKGPSVFPPLAPSSKSTGGTAALGCLVKDYFPEPTVSMNSGALTSGVHTFPAVLQ 180
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 179 SD-LYTLSSSVTPSSSTWPSSETVTCNVAHPASSTKVDKIKVPRDSGGPSEKSEINEKDL 237
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB 181 SGLYSLSVVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSC-----225
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 238 RKKSELQGTALGNLKQIYYNNSKAITSEKSAQDQFLNTLLFKGFFTGHPWYNDLLVDLG 297
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB 226 -----DKHTCTPCPAPPELLGGPSVF--LFPPKP--KDTLM---257
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 298 STAATSEYEGSSVDLYGAYGYOCAGGTGPNKTCMYGGVTLHDNNRLTEKKVPINLWID 357
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB 258 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVD 285
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 358 GKQTTVPIDKVKTSKKEV-----TVQELDLQARHYLHGKFGLYNSDSFGGKVGQVRLIV 410
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB 286 G-----VEVHNKATKPREEQNATYRVVSVLTVLHQDWLNG-----322
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
QY 411 FHSSEGSTVSYDLFDAQOQVPTLLRIYRDNTTISSTSLSLSYLYTTSIVMTQPTPTSL 470
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
DB 323 -----EY-----324
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
```

QY 471 VSAGDRVTITCKASQSVNDVAVYQOKPGOSPKLLISYTSRYSRYAGVDPDRFSGSGYGTDTT 530
Db 325 -----KCKVS-----NKALPAP-----IAATISKAKGP----- 348
QY 531 LTISSVQAEADAAYFYCQDYNSPPTFGGGTKLEIKRADAAPTVISIFPPSSSEQLTSGGASV 590
Db 349 -----EQYAST-YRVVSVLTVLHQDWLNGKEY-----REQVYTLPPSREEMTKNQVSL 370
QY 591 VCFLNPFYPKDINVKWKIDGSRQN-----GVLSNWTQDQSKDSTYSMSSTLTTLTKDEYVE 645
Db 371 TCLVKGFPSPDIAVEWESNGQPNKYKTPPVLDSE-----DGSFFLYSKLTVDKSRMQ 423
QY 646 RNSYTCETHK 657
Db 424 QGNVFCSCVMHE 435

RESULT 67
US-11-158-505-16
; Sequence 16, Application US/111158505
; Publication No. US20060002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; PRIOR FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 16
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: antibody heavy chain construct
US-11-158-505-16

Query Match 22.5%; Score 792; DB 7; Length 448;
Best Local Similarity 31.5%; Pred. No. 1.4e-34;
Matches 209; Conservative 67; Mismatches 149; Indels 238; Gaps 17;

QY 1 EVOLQSGPDLVKPGASVKISKASGYSTGYVMHWKSPGKLEWIGRINPNNGVTLY 60
Db 1 QVOLVSGAEVKKPGASVKSCASGYTTAYVISWRQAPGQGLEWMGEIYPGSSSY 60
QY 61 NQKFKDKATLVTDKSSTTAYMELRSLTSDSAVYYCARSTMTITNYNDYWGQGTSTVTS 120
Db 61 NEKFKGRVTWTRDTSTSTVYMLSLRSEDATVYYCARSGDGSRFV--YWGQGTSTVTS 118
QY 121 AKTTPSPVPLAPGSAQAQNSMTVLGCLVKGYFPEPVTVTVNSGSLSSGVHPTPAVLQSD 180
Db 119 ASTKGSPVPLAPSSKSTSGTAAALCLVKDYFPEPVTVTVNSGALTSGVHTTTPAVLQSS 178
QY 181 -LVTLSSSVTPSPSTWPSSETVTCNVAHPASSTKVDKKIIPRDSGGPSEKSEENEDLRK 239
Db 179 GLYSLSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSC----- 221
QY 240 KSELOGTALGNLQKIYYNSKAITSEKSDAQFLTNTLLFKGFFTGHWPYNLDLLVGLST 299
Db 222 -----DKHTCCPCAPPELLGGPSVF--LFPKPK--KDTLM----- 253
QY 300 AATSEYEGSSVDLYGAYGYQCAGGTPTNKACMYGVTLLHDNRLTEKKYVPINLWDGK 359
Db 254 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVDG-- 282
QY 360 QTTVPIDKVKTSKEVTVQELDQARHLYHGKFLYNSDSFGKVGQRGLIVFHSSEGSTV 419

Db 283 ---VEVHNAKTPRE----- 294
QY 420 SYDLFDAQQYQDPTLLRIYRDNTTISSTLSLSLYLYTTSIVMTQTPTSLLSAGDRVTI 479
Db 295 -----EQYAST-YRVVSVLTVLHQDWLNGKEY----- 320
QY 480 TCKASQSVNDVAVYQOKPGOSPKLLISYTSRYSRYAGVDPDRFSGSGYGTDTTLLISSVQAE 539
Db 321 KCKVS-----NKALPAP-----IETISKAKGP----- 344
QY 540 DAAVFCQDYNSPPTFGGGTKLEIKRADAAPTVISIFPPSSSEQLTSGGASVVCFLNNFYP 599
Db 345 -----REQVYTLPPSRDELTKNQVSLTCLVKGFYP 375
QY 600 KDINVKWKIDGSRQN-----GVLSNWTQDQSKDSTYSMSSTLTTLTKDEYERHNSITCEA 654
Db 376 SDIAVEWESNGQPNKYKTPPVLDSE-----DGSFFLYSKLTVDKSRMQGNVFCSCV 428
QY 655 THK 657
Db 429 MHE 431

RESULT 68
US-11-158-505-32
; Sequence 32, Application US/111158505
; Publication No. US20060002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAWN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; FILE REFERENCE: TLN-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; PRIOR FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 32
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: heavy chain construct
US-11-158-505-32

Query Match 22.5%; Score 792; DB 7; Length 448;
Best Local Similarity 31.5%; Pred. No. 1.4e-34;
Matches 209; Conservative 67; Mismatches 149; Indels 238; Gaps 17;

QY 1 EVOLQSGPDLVKPGASVKISKASGYSTGYVMHWKSPGKLEWIGRINPNNGVTLY 60
Db 1 QVOLVSGAEVKKPGASVKSCASGYTTAYVISWRQAPGQGLEWMGEIYPGSSSY 60
QY 61 NQKFKDKATLVTDKSSTTAYMELRSLTSDSAVYYCARSTMTITNYNDYWGQGTSTVTS 120
Db 61 NEKFKGRVTWTRDTSTSTVYMLSLRSEDATVYYCARSGDGSRFV--YWGQGTSTVTS 118
QY 121 AKTTPSPVPLAPGSAQAQNSMTVLGCLVKGYFPEPVTVTVNSGSLSSGVHPTPAVLQSD 180
Db 119 ASTKGSPVPLAPSSKSTSGTAAALCLVKDYFPEPVTVTVNSGALTSGVHTTTPAVLQSS 178
QY 181 -LVTLSSSVTPSPSTWPSSETVTCNVAHPASSTKVDKKIIPRDSGGPSEKSEENEDLRK 239
Db 179 GLYSLSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEPKSC----- 221
QY 240 KSELOGTALGNLQKIYYNSKAITSEKSDAQFLTNTLLFKGFFTGHWPYNLDLLVGLST 299

Db 222 -----DKHTCCPPCAPPELLGGPSVF--LPPPKP--KOTLM----- 253
QY 300 AATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTEEEKVPIINLWIDGK 359
Db 254 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYDVG- 282
QY 360 QTTVPIDKVKTSKEVTVQBELDIQARHYLHGKFGLYNSDFGKVGQRLIVFHSSEGSTV 419
Db 283 ---VEVHNKTKPRE----- 294
QY 420 SYDLFDAQGOYPTLLRIYRDNTTISSTLSISLYLYTTTSIVMTQPTSLVSGDRVTI 479
Db 295 -----EYAST-YRVSVLTVLHQDWLNGKEY----- 320
QY 480 TCKASQSVNDVAVYQOQPGQPKLLISYTSRYAGVDPFRFGSGYGTDTFTLTATISSVQAE 539
Db 321 KCKVS-----NKALPAP--LEKTSKAKGQP----- 344
QY 540 DAAVYFCQDYNPPPTFGGQTKLEIKRADAAPTYSIPPPSSEQLTSGGASVVCFLNFPY 599
Db 345 -----REPQVYTLPPSRDELTKNQVSLTCLVRGFPY 375
QY 600 KDINVKWKIDGSRQN-----GVLSNWTDDQSDKSTYSMSLTLTCKDEYERHNSYTCFA 654
Db 376 SDIAYEWESNGQPENNYKTTTPPVLDSE-----DGSFFLYSKLTVDKSRWQOQGNVFSV 428
QY 655 THK 657
Db 429 MHE 431

RESULT 69

US-11-120-338-25
; Sequence 25, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IQBAL S.
; APPLICANT: WALICKE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P20792
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 25
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-120-338-25

Query Match 22.5%; Score 792; DB 7; Length 451;
Best Local Similarity 30.5%; Pred. No. 1.4e-34;
Matches 205; Conservative 70; Mismatches 145; Indels 252; Gaps 17;

QY 1 EVOLQSGDPLVKPGASVKISKASGYSTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 60
Db 1 EVOLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHWVRQAPGKLEWVGAIYFGNGATSY 60
QY 61 NQKFKDKATLTVDKSTTAYMELRSITSEDSAVYYCARSTMIT--NYVMDYWGQGSVTV 118
Db 61 NQKFKGRFTISVDKSKNTLYLQWNSLRADTAIVYCARVYYSRYRYFDVWGQGLTVTV 120
QY 119 SSAKTTTPPSVYPLAPGSAQTNSMVTLCGLVKGYFPPEVTVTNWNSGLSSGVHTTFAVLQ 178
Db 121 SSASTKGPSVFPPLAPSSKTSFGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTTFAVLQ 180
QY 179 SD-LYTLSSSVTVPSSTWSESTVTCNVAHPASTKVDKLVPRDSDGPGSEKSEINEKDL 237
Db 181 SSGLYSLSSVTVTPSSSLGQTQYICNVNHPKPSNTKVDKKEPKSC----- 225

QY 238 RKKSELQGTALGNLKOIYYNSKAITSSSEKSAQDLFTNTLLFKGFFTHGFWYNDLLVDLG 297
Db 226 -----DKHTCCPPCAPPELLGGPSVF--LPPPKP--KOTLM----- 257
QY 298 STRATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTEEEKVPIINLWID 357
Db 258 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYD 285
QY 358 GKQTTVPIDKVKTSKEV-----TVQELDLQARHYLHGKFGLYNSDFGKVGQRLIV 410
Db 286 G-----VEVHNKTKPREEQYNATYRVSVLTVLHQDWLNGK----- 322
QY 411 FHSSEGSTVSYDLFDAQGOYPTLLRIYRDNTTISSTLSISLYLYTTTSIVMTQPTSL 470
Db 323 -----EY----- 324
QY 471 VSAGDRVTITCKASQSVNDVAVYQOQPGQPKLLISYTSRYAGVDPFRFGSGYGTDTFT 530
Db 325 -----KCKVSNAAL-----PAP--IAATISKAKGQP----- 348
QY 531 LTISSVQAEADAAVYFCQDYNPPPTFGGQTKLEIKRADAAPTYSIPPPSSEQLTSGGASV 590
Db 349 -----REPQVYTLPPSRDELTKNQVSLTCLVRGFPY 370
QY 591 VCFLNFPYPKDINVKWKIDGSRQN-----GVLSNWTDDQSDKSTYSMSLTLTCKDEYE 645
Db 371 TCLVKGFPYSDIAYEWESNGQPENNYKTTTPPVLDSE-----DGSFFLYSKLTVDKSRWQ 423
QY 646 RHNSYTCETHK 657
Db 424 QGNVFSVSMHE 435

RESULT 70

US-11-143-077-22
; Sequence 22, Application US/11143077
; Publication No. US20060024295A1
; GENERAL INFORMATION:
; APPLICANT: Brunetta, Paul G.
; TITLE OF INVENTION: METHOD FOR TREATING LUPUS
; FILE REFERENCE: P2133R1
; CURRENT APPLICATION NUMBER: US/11/143,077
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US 60/577,235
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/617,997
; PRIOR FILING DATE: 2004-10-11
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 22
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-11-143-077-22

Query Match 22.5%; Score 792; DB 7; Length 451;
Best Local Similarity 30.5%; Pred. No. 1.4e-34;
Matches 205; Conservative 70; Mismatches 145; Indels 252; Gaps 17;

QY 1 EVOLQSGDPLVKPGASVKISKASGYSTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 60
Db 1 EVOLVESGGGLVQPGGSLRLSCAASGYTFTSYNMHWVRQAPGKLEWVGAIYFGNGATSY 60
QY 61 NQKFKDKATLTVDKSTTAYMELRSITSEDSAVYYCARSTMIT--NYVMDYWGQGSVTV 118
Db 61 NQKFKGRFTISVDKSKNTLYLQWNSLRADTAIVYCARVYYSRYRYFDVWGQGLTVTV 120
QY 119 SSAKTTTPPSVYPLAPGSAQTNSMVTLCGLVKGYFPPEVTVTNWNSGLSSGVHTTFAVLQ 178
Db 121 SSASTKGPSVFPPLAPSSKTSFGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTTFAVLQ 180


```
QY 1 EVLOQSGDLVKPGASVKISKASGYSTGYVMHWKOSPGLGLEWIGRIINPNNGVTLV 60
Db 1 EVOLVESGGGLVQPGGSLRLSCLASGYTFTSYNMHWVRQAPGKLEWVGAIYFGNGATSY 60
QY 61 NQKFKDKATLTVDKSKSTTAYMELRLSITSDSAVYICARSTMIT--NYVMNDYWGQGTSTVTV 118
Db 61 NQKFKGRFTISVDKSKNTLYLQWNSLRAEDTAVYICARVYVYSYRYWYFDVWGQGLTVTV 120
QY 119 SSKAKTTPPSVYPLAPGSAQAQNSMTVLGCLVKGYPPEPTVTWNSSGLSSGVHTTFAVLQ 178
Db 121 SSASTKGPSPVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTTFAVLQ 180
QY 179 SD-LYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKVDKIVPRDSGGPSEKSEINEKOL 237
Db 181 SSGLYSLSSVTVPSSSLGTQTYICNVNHPKSNTRKVDKKEPKSC----- 225
QY 238 RKKSELQGTALGNLKIYYNNSKAITSSSEKSDAQFLTNLLFKGFTTGHFWYNDLLVDLG 297
Db 226 -----DKHTCTPCPCPAPELLGGPSVF--LPPPKP--KDTLM--- 257
QY 298 STAATSEYEGSSVDLYGAYGYQCAGGTENKACMYGGVTLHDNNRLTBEKKVPIINLWID 357
Db 258 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVD 285
QY 358 GKQTTVPIDKVKTSKEV-----TVQELDLQARHYLHGKFGLYNSDSFGGKVQGRGLIV 410
Db 286 G-----VEVHNKTKPREEQYNATYRVVSVTLVHQDWLNGK----- 322
QY 411 FHSSEGSTVSYDLFDAQGOYPTDLLRIYRDNTTISSTLSLSISLYLTVTSIVMTQTPTSLL 470
Db 323 -----EY----- 324
QY 471 VSAGDRVTITCKASQSVNDVAWYQKPGQSPKLLISYTSRRYAGVDPDRFSGSGYGTDTFT 530
Db 325 -----KCKVSNAAL-----PAP---IAATISKAKGP----- 348
QY 531 LTISVQAEDAAVYFCQDYNPPTFGGKTKLEIKRADAAPTVISIPPPSEQLTSGGASV 590
Db 349 -----REPOVYTLPPSREEMTKNQVSL 370
QY 591 VCFLNFPKIDINVKWKIDGSRQN-----GVLSNMTDQDSKDYTSMSSTLTLTCKEY 645
Db 371 TCLVKGFPSPDI AVEWESNGQPENNYKTTTPVLDL-----DGSFPLYSKLTVDKSRWQ 423
QY 646 RHNSYTCEATHK 657
Db 424 QGNVFSCSVWHE 435
```

RESULT 75

```
US-11-106-820-30
; Sequence 30, Application US/11106820
; Publication No. US20060002930A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G
; APPLICANT: SEWELL, KATHRYN L.
; TITLE OF INVENTION: Treatment of Disorders
; FILE REFERENCE: P2102R1
; CURRENT APPLICATION NUMBER: US/11/106,820
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,227
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/565,098
; PRIOR FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 45
; SEQ ID NO 30
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-106-820-30
```

```
Query Match 22.5%; Score 792; DB 7; Length 452;
Best Local Similarity 30.5%; Pred.No.1.4e-34;
Matches 205; Conservative 70; Mismatches 145; Indels 252; Gaps 17;
QY 1 EVLOQSGDLVKPGASVKISKASGYSTGYVMHWKOSPGLGLEWIGRIINPNNGVTLV 60
Db 1 EVOLVESGGGLVQPGGSLRLSCLASGYTFTSYNMHWVRQAPGKLEWVGAIYFGNGATSY 60
QY 61 NQKFKDKATLTVDKSKSTTAYMELRLSITSDSAVYICARSTMIT--NYVMNDYWGQGTSTVTV 118
Db 61 NQKFKGRFTISVDKSKNTLYLQWNSLRAEDTAVYICARVYVYSYRYWYFDVWGQGLTVTV 120
QY 119 SSKAKTTPPSVYPLAPGSAQAQNSMTVLGCLVKGYPPEPTVTWNSSGLSSGVHTTFAVLQ 178
Db 121 SSASTKGPSPVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTTFAVLQ 180
QY 179 SD-LYTLSSSVTVPSSTWPSSETVTCNVAHPASSTKVDKIVPRDSGGPSEKSEINEKOL 237
Db 181 SSGLYSLSSVTVPSSSLGTQTYICNVNHPKSNTRKVDKKEPKSC----- 225
QY 238 RKKSELQGTALGNLKIYYNNSKAITSSSEKSDAQFLTNLLFKGFTTGHFWYNDLLVDLG 297
Db 226 -----DKHTCTPCPCPAPELLGGPSVF--LPPPKP--KDTLM--- 257
QY 298 STAATSEYEGSSVDLYGAYGYQCAGGTENKACMYGGVTLHDNNRLTBEKKVPIINLWID 357
Db 258 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVD 285
QY 358 GKQTTVPIDKVKTSKEV-----TVQELDLQARHYLHGKFGLYNSDSFGGKVQGRGLIV 410
Db 286 G-----VEVHNKTKPREEQYNATYRVVSVTLVHQDWLNGK----- 322
QY 411 FHSSEGSTVSYDLFDAQGOYPTDLLRIYRDNTTISSTLSLSISLYLTVTSIVMTQTPTSLL 470
Db 323 -----EY----- 324
QY 471 VSAGDRVTITCKASQSVNDVAWYQKPGQSPKLLISYTSRRYAGVDPDRFSGSGYGTDTFT 530
Db 325 -----KCKVSNAAL-----PAP---IAATISKAKGP----- 348
QY 531 LTISVQAEDAAVYFCQDYNPPTFGGKTKLEIKRADAAPTVISIPPPSEQLTSGGASV 590
Db 349 -----REPOVYTLPPSREEMTKNQVSL 370
QY 591 VCFLNFPKIDINVKWKIDGSRQN-----GVLSNMTDQDSKDYTSMSSTLTLTCKEY 645
Db 371 TCLVKGFPSPDI AVEWESNGQPENNYKTTTPVLDL-----DGSFPLYSKLTVDKSRWQ 423
QY 646 RHNSYTCEATHK 657
Db 424 QGNVFSCSVWHE 435
```

Search completed: February 15, 2006, 20:39:04
Job time : 38.3359 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 15, 2006, 20:08:10 ; Search time 69.7713 Seconds

(without alignments)
1467.298 Million cell updates/sec

Title: US-09-900-766-7

Perfect score: 1238

Sequence: 1 SRKSEINBKDLKKSELR.....RDNKTINSENLHLDLYTT 233.

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 300 summaries

Database :

A_Geneseq_21.*

1: Geneseqp1990s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1238	100.0	233	6	Abp58456 Staphyloc
2	1238	100.0	257	4	Aau14103 Peptide s
3	1238	100.0	257	6	Abol10268 S. aureus
4	1238	100.0	257	8	Adf89830 Staphyloc
5	1224	98.9	230	4	Aab67339 Staphyloc
6	1222	98.7	245	2	Aaw35374 Staphyloc
7	1210	97.7	233	6	Abp58457 Engineere
8	1202	97.1	245	2	Aaw35375 Staphyloc
9	1188	96.0	248	6	Abu79072 S. aureus
10	1188	96.0	248	7	Adf43296 Staphyloc
11	1188	96.0	248	9	Aea02990 Staphyloc
12	1179	95.2	230	2	AAR45012 Staphyloc
13	1175	94.9	230	5	Abb76235 Staphyloc
14	1156	93.4	230	2	AAR13204 Staphyloc
15	1107	89.4	233	6	Abp58455 Engineere
16	1107	89.4	672	6	Abp58454 Engineere
17	1035	83.6	233	2	AAR13203 Staphyloc
18	1023	82.6	233	6	Abp58458 Staphyloc
19	1023	82.6	257	4	Aau14104 Peptide s
20	1023	82.6	257	6	Abol10269 S. aureus
21	1023	82.6	257	7	Add44368 Staphyloc
22	1023	82.6	257	8	Adhl10956 Enterotox
23	1023	82.6	257	9	Advll1662 Staphyloc
24	1023	82.6	301	9	Aeb13483 EGF-SEA I

25	1023	82.6	369	9	AEB13485	Aeb13485 VEGF-SEA
26	1019	82.3	233	2	AAW06738	Aaw06738 Staphyloc
27	1019	82.3	233	8	ADI95318	Adi95318 OsPF-rela
28	1016	82.1	233	2	AAW35373	Aaw35373 Staphyloc
29	1016	82.1	233	4	AAW67338	Aaw67338 Staphyloc
30	1013	81.8	233	2	AAR45011	Aar45011 Staphyloc
31	1013	81.8	257	6	ABU79068	Abu79068 S. aureus
32	1013	81.8	257	7	ADF43288	Adf43288 Staphyloc
33	1013	81.8	257	9	AEA02982	Aea02982 Staphyloc
34	1004	81.1	233	5	ABB76234	Abb76234 Staphyloc
35	1000	80.8	257	5	ABB79501	Abb79501 Staphyloc
36	1000	80.8	257	6	ABU10081	Abu10081 Staphyloc
37	1000	80.8	257	7	ABU62324	Abu62324 S. aureus
38	1000	80.8	257	7	AAE37676	Aae37676 Protein #
39	1000	80.8	257	9	ADY93171	Ady93171 Bacterial
40	996	80.5	233	3	AAV54463	Aay54463 Amino aci
41	996	80.5	233	5	ABB79502	Abb79502 Staphyloc
42	996	80.5	233	6	ABU10082	Abu10082 Staphyloc
43	996	80.5	233	7	ABU62325	Abu62325 S. aureus
44	996	80.5	233	7	AAE37677	Aae37677 Protein #
45	996	80.5	233	9	ADY93173	Ady93173 Bacterial
46	992	80.1	233	6	ABU10099	Abu10099 Staphyloc
47	991	80.0	231	8	ADF89824	Adf89824 Staphyloc
48	987	79.7	233	6	ABU10098	Abu10098 Staphyloc
49	987	79.4	257	3	AAV70102	Aay70102 Staphyloc
50	978	79.0	233	3	AAV70103	Aay70103 Mutant St
51	830	67.0	268	8	ADF89835	Adf89835 Staphyloc
52	663	53.6	258	6	ABU79071	Abu79071 S. aureus
53	663	53.6	258	7	ADF43294	Adf43294 Staphyloc
54	663	53.6	258	8	ADF89829	Adf89829 Staphyloc
55	663	53.6	258	9	AEA02988	Aea02988 Staphyloc
56	657	53.1	228	2	AAW45013	Aar45013 Staphyloc
57	657	53.1	228	4	AAW67340	Aaw67340 Staphyloc
58	657	53.1	228	5	ABB76236	Abb76236 Staphyloc
59	649	52.4	228	2	AAR13205	Aar13205 Staphyloc
60	523	42.2	203	6	ABP58459	Abp58459 Staphyloc
61	492.5	39.8	250	6	ABM70958	Abm70958 Staphyloc
62	457	36.9	82	6	ABU10091	Abu10091 Bacterial
63	457	36.9	82	7	ABU62338	Abu62338 S. aureus
64	457	36.9	82	9	ADY93188	Ady93188 Staphyloc
65	399	32.2	82	6	ABU10089	Abu10089 Bacterial
66	399	32.2	82	7	ABU62336	Abu62336 S. aureus
67	399	32.2	82	9	ADY93186	Ady93186 Staphyloc
68	370	29.9	91	2	AAW24299	Aaw24299 Staphyloc
69	366	29.6	217	6	ABP58460	Abp58460 Staphyloc
70	366	29.6	217	8	ADF89833	Adf89833 Staphyloc
71	339.5	27.4	242	8	ADF89834	Adf89834 Staphyloc
72	337	27.2	240	8	ADF89837	Adf89837 Staphyloc
73	336.5	27.2	259	5	ABP29357	Abp29357 Streptoco
74	320	25.8	239	8	ADF89838	Adf89838 Staphyloc
75	319.5	25.8	242	8	ADF89832	Adf89832 Staphyloc
76	310	25.0	242	8	ADF89836	Adf89836 Staphyloc
77	300.5	24.3	266	6	ABU79069	Abu79069 S. aureus
78	300.5	24.3	266	7	ABG75015	Abg75015 S. aureus
79	300.5	24.3	266	9	ADF43290	Adf43290 Staphyloc
80	300.5	24.3	266	9	AEA02984	Aea02984 Staphyloc
81	300	24.2	255	2	AAW06737	Aaw06737 Staphyloc
82	299.5	24.2	238	8	ADP89825	Adp89825 Staphyloc
83	299.5	24.2	239	2	AAW64647	Aaw64647 Synthetic
84	299.5	24.2	239	4	AAW67341	Aaw67341 Staphyloc
85	299.5	24.2	239	7	ABG75016	Abg75016 Unidentif
86	299.5	24.2	239	8	ADL14247	Adl14247 Wild type
87	297.5	24.0	239	8	ADS87876	Ads87876 Staphyloc
88	297.5	24.0	239	9	ADY63818	Ady63818 Staphyloc
89	297.5	24.0	251	2	AAW12153	Aaw12153 Streptoco
90	297.5	24.0	266	7	ABU62455	Abu62455 S. aureus
91	296.5	23.9	221	2	AAR13209	Aar13209 Streptoco
92	296.5	23.9	221	2	AAR45017	Aar45017 Staphyloc
93	296.5	23.9	221	5	ABB76240	Abb76240 Staphyloc
94	296.5	23.9	239	8	ADS87891	Ads87891 Staphyloc
95	296.5	23.9	239	9	ADY63819	Ady63819 S. aureus
96	296.5	23.9	251	2	AAW12151	Aaw12151 Streptoco
97	295.5	23.9	259	8	ADS87887	Ads87887 Staphyloc

98	295.5	23.9	251	2	AAW12150	Aaw12150 Streptoco	171	279.5	22.6	238	4	AA567343	Aab67343 Staphyloc
99	295.5	23.9	251	8	ADP89839	Adf89839 Streptoco	172	279.5	22.6	238	5	AB576239	Abb76239 Staphyloc
100	294.5	23.8	251	8	ADS87890	Ads87890 Staphyloc	173	276.5	22.3	228	4	AAG63856	Aag63856 Amino aci
101	294.5	23.8	251	2	AAW12154	Aaw12154 Streptoco	174	276.5	22.3	238	2	AA13208	Aar13208 Staphyloc
102	294.5	23.8	251	2	AAW12146	Aaw12146 Streptoco	175	276.5	22.3	239	2	AA106258	Aay06258 Staphyloc
103	294.5	23.8	251	2	AAW12097	Aaw12097 Streptoco	176	276.5	22.3	239	2	AA106257	Aay06257 Staphyloc
104	294.5	23.8	251	2	AAW12147	Aaw12147 Streptoco	177	276.5	22.3	240	6	ABG71373	Abg71373 Staphyloc
105	294.5	23.8	251	2	AAW12148	Aaw12148 Streptoco	178	276.5	22.3	240	6	ABG71374	Abg71374 Staphyloc
106	294.5	23.8	251	2	AAW59780	Aaw59780 Amino aci	179	276.5	22.3	240	6	AB70859	Aeb70859 Staphyloc
107	293.5	23.7	239	2	AAW59780	Aaw59780 Amino aci	180	276.5	22.3	240	9	AB70858	Aeb70858 Staphyloc
108	293.5	23.7	239	8	ADY06234	Aay06234 Staphyloc	181	276.5	22.3	265	3	AA170105	Aay70105 Mutant St
109	293.5	23.7	239	8	ADY06234	Aay06234 Staphyloc	182	276.5	22.3	265	3	AA170105	Aay70105 Mutant St
110	293.5	23.7	240	6	ABG71370	Abg71370 Staphyloc	183	269.5	21.8	236	9	AB70860	Aeb70860 Staphyloc
111	293.5	23.7	240	9	AB70855	Aeb70855 Staphyloc	184	267.5	21.6	239	2	AA13207	Aar13207 Staphyloc
112	293.5	23.7	266	5	AB79503	Abb79503 Staphyloc	185	267.5	21.6	239	2	AA13207	Aar13207 Staphyloc
113	293.5	23.7	266	6	ABU10083	Abu10083 Staphyloc	186	267.5	21.6	239	5	AB76238	Abb76238 Staphyloc
114	293.5	23.7	266	7	AAE37678	Aae37678 Protein #	187	267.5	21.6	260	8	AD79842	Adf9842 Streptoco
115	293.5	23.7	266	9	ADY93175	Ady93175 Bacterial	188	266.5	21.5	266	6	ABU79070	Abu79070 S. aureus
116	292.5	23.6	221	4	AA67344	Aab67344 Streptoco	189	266.5	21.5	266	7	AD73292	Adf43292 Staphyloc
117	292.5	23.6	239	2	AA13206	Aar13206 Staphyloc	190	266.5	21.5	266	9	AEA02986	Aea02986 Staphyloc
118	292.5	23.6	239	2	AA13206	Aar13206 Staphyloc	191	265.5	21.4	239	2	AA106251	Aay06251 Staphyloc
119	292.5	23.6	239	8	ADY92319	Aay92319 Plant-opt	192	265.5	21.4	240	6	ABG71367	Aab67342 Staphyloc
120	292.5	23.6	266	3	AA13206	Aar13206 Staphyloc	193	265.5	21.4	240	6	ABG71367	Aab67342 Staphyloc
121	291.5	23.5	266	7	ABU62453	Abu62453 S. aureus	194	265.5	21.4	240	6	ABG71367	Aab67342 Staphyloc
122	290.5	23.5	239	5	AB76237	Abb76237 Staphyloc	195	265.5	21.4	231	9	AB70861	Aeb70861 Staphyloc
123	290.5	23.5	239	8	ADS87892	Ads87892 Staphyloc	196	258.5	20.9	266	3	AA170108	Aay70108 Staphyloc
124	290.5	23.5	251	7	ABU62460	Abu62460 Streptoco	197	258.5	20.9	266	6	ABU10087	Abu10087 Streptoco
125	289.5	23.4	251	2	AAW59798	Aaw59798 Amino aci	198	258.5	20.9	266	6	ABU10087	Abu10087 Streptoco
126	289.5	23.4	251	3	AAW59781	Aaw59781 Amino aci	199	258.5	20.9	266	7	ABU62330	Abu62330 S. aureus
127	289.5	23.4	251	3	AAW70109	Aay70109 Streptoco	200	258.5	20.9	266	7	AAE37682	Aae37682 Staphyloc
128	289.5	23.4	251	5	AB79508	Abb79508 Streptoco	201	258.5	20.9	266	9	ADY93183	Ady93183 Staphyloc
129	289.5	23.4	251	6	ABU10088	Abu10088 Streptoco	202	256.5	20.7	220	7	ABU62334	Abu62334 Streptoco
130	289.5	23.4	251	7	ABU62331	Abu62331 Streptoco	203	256.5	20.7	220	7	AAE37687	Aae37687 Streptoco
131	289.5	23.4	251	7	AAE37683	Aae37683 Streptoco	204	256.5	20.7	468	7	ABU62335	Abu62335 SFEA L42R
132	289.5	23.4	251	9	ADY93185	Ady93185 Streptoco	205	256.5	20.7	468	7	AAE37684	Aae37684 Streptoco
133	289.5	23.4	266	3	AA54464	Aay54464 Amino aci	206	256	20.7	209	8	ADG69997	Adg69997 Streptoco
134	288.5	23.3	239	2	AAW59781	Aaw59781 Amino aci	207	256	20.7	233	3	AA170109	Aay70109 Amino aci
135	288.5	23.3	239	5	AB79505	Abb79505 Staphyloc	208	254.5	20.6	220	7	AAE37689	Aae37689 S. pyogen
136	288.5	23.3	239	6	ABU10085	Abu10085 Staphyloc	209	253.5	20.5	220	7	AAE37688	Aae37688 S. pyogen
137	288.5	23.3	239	7	ABU62328	Abu62328 S. aureus	210	253.5	20.5	468	7	AAE37691	Aae37691 S. pyogen
138	288.5	23.3	239	7	AAE37680	Aae37680 Protein #	211	250	20.2	209	8	ADG69998	Adg69998 Mutant St
139	288.5	23.3	239	9	ADY93179	Ady93179 Bacterial	212	250	20.2	209	8	ADG70011	Adg70011 Mutant St
140	288.5	23.3	240	3	AA54465	Aay54465 Mutant St	213	247.5	20.0	209	8	ADG69999	Adg69999 Mutant St
141	288.5	23.3	240	6	ABG71369	Abg71369 Staphyloc	214	247.5	20.0	209	8	ADG70010	Adg70010 Mutant St
142	288.5	23.3	240	9	AB70854	Aeb70854 Staphyloc	215	245.5	19.8	231	7	ADG64940	Adg64940 SSB pepti
143	287.5	23.2	239	2	AAW06256	Aay06256 Staphyloc	216	245	19.8	250	6	ABU79074	Abu79074 S. pyogen
144	287.5	23.2	239	3	AAW70106	Aay70106 Mutant St	217	245	19.8	250	7	AD73300	Adf43300 Pyrogenic
145	287.5	23.2	240	6	ABG71372	Abg71372 Staphyloc	218	245	19.8	250	9	AEA02994	Aea02994 Streptoco
146	287.5	23.2	240	9	AB70857	Aeb70857 Staphyloc	219	239	19.3	209	8	AD79845	Adf89845 Streptoco
147	287.5	23.2	266	7	ABU62454	Abu62454 S. aureus	220	232	18.7	258	5	AB29565	Abp29565 Streptoco
148	286.5	23.1	239	8	ADS87885	Ads87885 Staphyloc	221	220.5	17.8	240	8	AD79826	Adf89826 Staphyloc
149	285.5	23.1	239	2	AAW06255	Aay06255 Staphyloc	222	217	17.5	234	3	AA170109	Aay70109 Amino aci
150	285.5	23.1	239	8	ADL14256	Adl14256 Modified	223	217	17.5	234	5	ABE29092	Abp29092 Streptoco
151	285.5	23.1	239	8	ADS87888	Ads87888 Staphyloc	224	216	17.4	210	8	AD79843	Adf89843 Streptoco
152	285.5	23.1	240	6	ABG71371	Abg71371 Staphyloc	225	215	17.4	82	6	ABU10090	Abu10090 Bacterial
153	285.5	23.1	240	9	AB70856	Aeb70856 Staphyloc	226	215	17.4	82	7	ABU62337	Abu62337 S. aureus
154	285.5	23.1	266	8	ADP89828	Adp89828 Staphyloc	227	215	17.4	82	9	ADY93187	Ady93187 Staphyloc
155	284.5	23.0	251	2	AAW12149	Aaw12149 Streptoco	228	197	15.9	236	3	AA170109	Aay70109 Amino aci
156	284.5	23.0	251	2	AAW12152	Aaw12152 Streptoco	229	197	15.9	236	5	ABE29358	Abp29358 Streptoco
157	284.5	23.0	266	7	ABU62452	Abu62452 S. aureus	230	197	15.9	236	8	AD79844	Adf89844 Streptoco
158	284.5	23.0	266	7	ABU62451	Abu62451 S. aureus	231	197	15.9	236	8	AD79844	Adf89844 Streptoco
159	283.5	22.9	239	2	AAW06252	Aay06252 Staphyloc	232	193	15.6	232	5	ABP29143	Abp29143 Streptoco
160	283.5	22.9	240	6	ABG71368	Abg71368 Staphyloc	233	191	15.4	45	2	AAW04488	Aaw04488 Staphyloc
161	283.5	22.9	240	9	AB70853	Aeb70853 Staphyloc	234	191	15.4	45	2	AAW73917	Aaw73917 Staphyloc
162	283.5	22.9	251	2	AAW12149	Aaw12149 Streptoco	235	185	14.9	234	8	AD79841	Adf89841 Streptoco
163	282.5	22.8	250	2	AAW12145	Aaw12145 Streptoco	236	183.5	14.8	235	2	AAW62788	Aaw62788 Mutant st
164	282.5	22.8	266	5	AB79504	Abb79504 Staphyloc	237	183.5	14.8	235	2	AAW62787	Aaw62787 Mutant st
165	282.5	22.8	266	6	ABU10084	Abu10084 Staphyloc	238	183.5	14.8	235	2	AAW62784	Aaw62784 Streptoco
166	282.5	22.8	266	7	ABU62327	Abu62327 S. aureus	239	182.5	14.7	207	5	AAE325373	Aae325373 S. pyogen
167	282.5	22.8	266	7	AAE37679	Aae37679 Protein #	240	181.5	14.7	207	5	AAE325364	Aae325364 Streptoco
168	281.5	22.7	238	9	ADY93177	Ady93177 Bacterial	241	181.5	14.7	208	2	AA13210	Aar13210 Streptoco
169	280.5	22.7	239	8	AD79827	Adf89827 Staphyloc	242	181.5	14.7	208	2	AA13210	Aar13210 Streptoco
170	280	22.6	265	3	AAW70104	Aay70104 Staphyloc	243	181.5	14.7	208	4	AA567345	Aab67345 Streptoco

244	181.5	14.7	208	5	ABB76241	Abb76241 Staphyloc
245	180.5	14.6	207	5	AAE25372	Rae25372 S. pyogen
246	180.5	14.6	207	5	AAE25374	Rae25374 S. pyogen
247	180.5	14.6	207	5	AAE25370	Rae25370 S. pyogen
248	180	14.5	235	5	ABP29257	Abp29257 Streptoco
249	180	14.5	235	8	ADR83915	Adr83915 S. pyogen
250	179.5	14.5	207	5	AAE25367	Rae25367 S. pyogen
251	179.5	14.5	207	5	AAE25371	Rae25371 S. pyogen
252	178.5	14.4	207	5	AAE25395	Rae25395 S. pyogen
253	178.5	14.4	207	5	AAE25368	Rae25368 S. pyogen
254	177.5	14.3	207	5	AAE25365	Rae25365 S. pyogen
255	176.5	14.3	207	5	AAE25369	Rae25369 S. pyogen
256	173.5	14.0	235	2	AAW62786	Aaw62786 Mutant st
257	173.5	14.0	235	2	AAW62785	Aaw62785 Mutant st
258	170	13.7	137	3	AAE25374	Rae25374 Amino aci
259	151	12.2	107	9	ADY93189	Ady93189 Ubiquitin
260	147.5	11.9	143	5	AAE25363	Rae25363 Streptoco
261	145	11.7	90	9	ADY93195	Ady93195 Staphyloc
262	137.5	11.1	89	6	ABU10092	Abu10092 Bacterial
263	137.5	11.1	89	6	ABU62339	Abu62339 S. aureus
264	137.5	11.1	89	9	ADY93189	Ady93189 Bacterial
265	134	10.8	227	8	ADE11158	Adel1158 S. pyogen
266	129	10.4	28	2	AAW04489	Raw04489 Staphyloc
267	129	10.4	28	2	AAW73916	Raw73916 Staphyloc
268	127	10.3	24	3	AAE25363	Rae25363 Staphyloc
269	127	10.3	24	3	AAE25363	Rae25363 Staphyloc
270	126	10.2	23	2	AAW04492	Raw04492 Staphyloc
271	126	10.2	23	2	AAW73919	Raw73919 Staphyloc
272	126	10.2	233	8	ADE11156	Adel1156 S. pyogen
273	124	10.0	29	2	AAW04493	Raw04493 Staphyloc
274	124	10.0	29	2	AAW73915	Raw73915 Staphyloc
275	121	9.8	79	6	ABU10096	Abu10096 Bacterial
276	121	9.8	79	7	ABU62343	Abu62343 Streptoco
277	121	9.8	79	9	ADY93193	Ady93193 Streptoco
278	120	9.7	22	2	AAW04491	Raw04491 Staphyloc
279	120	9.7	22	2	AAW73914	Raw73914 Staphyloc
280	116.5	9.4	231	6	ABM71652	Abm71652 Staphyloc
281	116	9.4	190	2	AAE25374	Rae25374 S. pyogen
282	115.5	9.3	190	2	AAE25370	Rae25370 S. pyogen
283	115	9.3	190	2	AAE25371	Rae25371 S. pyogen
284	115	9.3	190	2	AAE25395	Rae25395 S. pyogen
285	114	9.2	190	2	AAE25368	Rae25368 S. pyogen
286	114	9.2	190	2	AAE25365	Rae25365 S. pyogen
287	113	9.1	190	2	AAE25369	Rae25369 S. pyogen
288	113	9.1	190	2	AAE25374	Rae25374 Amino aci
289	113	9.1	232	6	ABU42318	Abu42318 Protein e
290	112.5	9.1	89	6	ABU10094	Abu10094 Bacterial
291	112.5	9.1	89	6	ABU10095	Abu10095 Bacterial
292	112.5	9.1	89	7	ABU62342	Abu62342 S. aureus
293	112.5	9.1	89	7	ABU62341	Abu62341 S. aureus
294	112.5	9.1	89	9	ADY93192	Ady93192 Staphyloc
295	112.5	9.1	89	9	ADY93191	Ady93191 Staphyloc
296	112	9.0	190	2	AAE25370	Rae25370 S. pyogen
297	112	9.0	190	2	AAE25395	Rae25395 S. pyogen
298	112	9.0	190	2	AAE25368	Rae25368 S. pyogen
299	112	9.0	190	2	AAE25365	Rae25365 S. pyogen
300	112	9.0	190	2	AAE25369	Rae25369 S. pyogen

ALIGNMENTS

RESULT 1
 ABP58456
 ID ABP58456 standard; protein; 233 AA.
 XX
 AC ABP58456;
 XX
 DT 14-APR-2003 (first entry)
 DE Staphylococcal enterotoxin E.
 XX
 KW Superantigen; staphylococcal enterotoxin E; antibody; cancer; tumour;

KW cytostatic; vaccine.
 XX
 OS Staphylococcus sp.
 XX
 PN WO2003002143-A1.
 XX
 PD 09-JAN-2003.
 XX
 XX 19-JUN-2002; 2002WO-SR001188.
 XX
 XX 28-JUN-2001; 2001SE-00002327.
 XX
 PA (ACTI-) ACTIVE BIOTECH AB.
 XX
 XX Forsberg G, Erlandsson E, Antonsson P, Walse B;
 PI WPI; 2003-201467/19.
 XX
 DR Conjugate for therapy, has bacterial superantigen with a region in T-cell
 XX receptor and four regions to determine binding to class II major
 PT histocompatibility complex, antibody to cancer associated cell surface
 PT structure.
 XX
 XX Example 3; Fig 4; 102pp; English.
 PS
 CC The present sequence is the protein sequence of staphylococcal
 CC enterotoxin SEE. The invention provides novel conjugates (see ABP58454)
 CC for human cancer therapy. These comprise an engineered bacterial
 CC superantigen, such as novel SEA/E-120 (see ABP58455), which is based on
 CC SEE, and an antibody moiety, such as tumour reactive antibody 574. The
 CC superantigen is engineered to reduce seroreactivity whilst maintaining
 CC biological activity and production levels. The conjugates are designed to
 CC target and destroy cancer cells, including cancer of the lung, breast,
 CC colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
 XX
 SQ Sequence 233 AA;
 Query Match 100.0%; Score 1238; DB 6; Length 233;
 Best Local Similarity 100.0%; Pred. No. 8.1e-116;
 Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKKSELQBNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGSPFTG 60
 DB 1 SEKSEINEKDLRKKSELQBNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGSPFTG 60
 QY 61 HPWNVDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLT 120
 DB 61 HPWNVDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLT 120
 QY 121 EEKVPINLWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKVKQ 180
 DB 121 EEKVPINLWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKVKQ 180
 QY 181 RGLIVFHSSEGSVSYVDLFDAGQYPTLLRIYRDNKTINSENLHIDLXYLT 233
 DB 181 RGLIVFHSSEGSVSYVDLFDAGQYPTLLRIYRDNKTINSENLHIDLXYLT 233
 RESULT 2
 AAU14103
 ID AAU14103 standard; peptide; 257 AA.
 XX
 AC AAU14103;
 XX
 DT 21-NOV-2001 (first entry)
 XX
 DE Peptide sequence from Staphylococcus aureus enterotoxin type E.
 XX
 XX Anti-retroviral; DP178-like; DP107-like; enterotoxin type E;
 KW antifusogenic; antiviral; HIV transmission.
 XX
 XX Staphylococcus aureus.
 OS

```
PN W0200151673-A2.
XX
XX 19-JUL-2001.
XX
XX 05-JUL-2000; 2000WO-US035727.
XX
XX 09-JUL-1999; 99US-00350841.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
XX WPI; 2001-442157/47.
XX
XX Identifying a compound that inhibits the formation of or disrupts a
PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral
PT or intracellular modulatory activity, by detecting the formation of a
PT DP107/DP178 complex.
XX
XX Disclosure; Fig 41; 259pp; English.
XX
XX The present invention relates to peptides which exhibit anti-retroviral
CC activity. The peptides of the invention (AAU12559-AAU14009) comprise
CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to
CC amino acids 639-673 of the transmembrane protein gp41 from human
CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide
CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention
CC also relates to a method of identifying compounds that inhibit the
CC formation of or disrupts a DP107/DP178 complex. The method comprises
CC detecting the formation of a DP107/DP178 complex, both in the presence or
CC absence of a test compound, in a reaction mixture containing DP107 and
CC DP178 peptides. The method is useful for identifying compounds, including
CC small molecule compounds, which may themselves exhibit antifusogenic,
CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like
CC peptides are useful to inhibit human and non-human retroviral,
CC particularly HIV, transmission to uninfected cells. The present sequence
CC represents a peptide sequence from Staphylococcus aureus enterotoxin type
CC E
XX
XX Sequence 257 AA;
SQ
Query Match 100.0%; Score 1238; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 9.3e-116;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVLDGSKDATNKYKGKKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVLDGSKDATNKYKGKKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTSVSYDLFDAQQYQPDTLRIYRDNKTINSENHLIDLVLTYTT 233
DB 205 RGLIVFHSSEGSTSVSYDLFDAQQYQPDTLRIYRDNKTINSENHLIDLVLTYTT 257
RESULT 3
ABO10268
ID ABO10268 standard; protein; 257 AA.
XX
XX ABO10268;
XX
XX 19-AUG-2003 (first entry)
XX
XX S. aureus enterotoxin E.
XX
XX HIV; DP107; DP178; glycoprotein 41; antiviral; virucide; EBV;
KW Epstein-Barr virus infection; heptad repeat motif.
XX
XX Staphylococcus aureus.
XX
XX US6518013-B1.
XX
XX 11-FEB-2003.
XX
XX 07-JUN-1995; 95US-00485546.
XX
XX 07-JUN-1993; 93US-00073028.
XX
XX 07-JUN-1994; 94US-00255208.
XX
XX 20-DEC-1994; 94US-00360107.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX Barney SO, Lambert DM, Petteway SR;
XX WPI; 2003-465599/44.
XX
XX Inhibiting transmission of Epstein-Barr virus to a cell, by contacting
PT the cell with a peptide consisting of a region of Epstein-Barr virus
PT protein.
XX
XX Example; Fig 41; 716pp; English.
XX
XX The invention relates to inhibiting (M) transmission of an Epstein-Barr
CC virus to a cell, comprising contacting the cell with an effective
CC concentration of a peptide consisting of a region of 16-39 consecutive
CC amino acids of an Epstein-Barr virus protein for an effective period of
CC time, where the region is recognised by one or more of ALLMOT15,
CC 107x178x4 or PLZIP sequence search motifs, the peptide further comprises
CC an amino terminal X, and a carboxy terminal Z in which X comprises an
CC amino group, acetyl group, 9-fluorenylmethoxy-carbonyl group, hydrophobic
CC group or macromolecular carrier group, and Z comprises a carboxyl group,
CC amido group, hydrophobic group, or macromolecular carrier group, and
CC fusion of the virus to the cell is inhibited. The peptides were
CC identified by analysing the structure/motifs present in the HIV-1
CC glycoprotein 41 anti-HIV peptides DP107 and DP178. These heptad repeat
CC motif containing peptides were used to design the motifs cited above,
CC which in turn were used to analyse proteins from other pathogenic
CC organisms and HIV isolates, looking for DP107/178 structural analogues.
CC The method is useful for inhibiting transmission of Epstein-Barr virus to
CC a cell and Epstein-Barr virus infection. The present sequence is a
CC protein from a pathogenic organism analysed for regions analogous to
CC DP107 or DP178
XX
XX Sequence 257 AA;
SQ
Query Match 100.0%; Score 1238; DB 6; Length 257;
Best Local Similarity 100.0%; Pred. No. 9.3e-116;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVLDGSKDATNKYKGKKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVLDGSKDATNKYKGKKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTSVSYDLFDAQQYQPDTLRIYRDNKTINSENHLIDLVLTYTT 233
DB 205 RGLIVFHSSEGSTSVSYDLFDAQQYQPDTLRIYRDNKTINSENHLIDLVLTYTT 257
RESULT 4
ADF89830
ID ADF89830 standard; protein; 257 AA.
```

```
XX ADF89830;
AC
XX
XX 26-FEB-2004 (first entry)
DT
XX
XX Staphylococcal enterotoxin E (SEE) superantigen.
DE
XX
XX Superantigen; SAg; Staphylococcal enterotoxin; SE; SEE; cytostatic;
KW gene therapy; cancer.
KW
XX
XX Staphylococcus sp.
OS
XX
XX WO2003094846-A2.
PN
XX
XX 20-NOV-2003.
PD
XX
XX 08-MAY-2003; 2003WO-US014381.
XX
XX 08-MAY-2002; 2002US-0378988P.
PR 15-JUN-2002; 2002US-0389366P.
PR 28-AUG-2002; 2002US-0406697P.
PR 29-AUG-2002; 2002US-0406750P.
PR 01-OCT-2002; 2002US-0415310P.
PR 02-OCT-2002; 2002US-0415400P.
PR 09-JAN-2003; 2003US-0438686P.
XX
XX (TERM/) Terman D S.
PA
XX
XX Terman DS;
XX
XX WPI; 2004-011997/01.
DR
XX
XX Treating a subject with cancer or malignant diseases comprises
PT intratumoral, intrathecal or intracavitary administration of an amount of
PT a superantigen composition to the subject.
XX
XX Disclosure; SEQ ID NO 7; 91pp; English.
PS
XX
XX The invention relates to treating a subject with cancer. The method
CC involves administering an amount of a superantigen (SAG) composition
CC comprising a molecule selected from: a native SAG protein; its
CC biologically active fragment or a biologically active homologue or a
CC biologically active fusion protein comprising the SAG or its fragment or
CC homologue fused to a fusion partner polypeptide or peptide. The SAG is
CC selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic
CC exotoxin, Y. pseudotuberculosis SAG, Mycoplasma arthritides SAG and
CC Clostridium perfringens exotoxin. The method is useful in treating cancer
CC or malignant diseases such as malignant pleural effusion, ascites,
CC pericardial effusion or meningeal carcinomatosis. The present sequence
CC represents a Staphylococcal enterotoxin E (SEE) superantigen.
XX
XX Sequence 257 AA;
SQ
Query Match 100.0%; Score 1238; DB 8; Length 257;
Best Local Similarity 100.0%; Pred. No. 9.3e-116;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOARNLSNLRQIYYNEKAITENKESDDQFLENTLLPKGFFTG 60
DB 25 SEKSEINEKDLRKSELOARNLSNLRQIYYNEKAITENKESDDQFLENTLLPKGFFTG 84
QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
DB 85 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDFGKVQ 180
DB 145 EEKVPINLWIDGKQTTPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDFGKVQ 204
QY 181 RGLIVFHSSEGSTSVSYDLFDAQOQYPTLLRIYRDNKTINSENHLIDLTYTT 233
DB 205 RGLIVFHSSEGSTSVSYDLFDAQOQYPTLLRIYRDNKTINSENHLIDLTYTT 257

RESULT 5
AAB67339
ID AAB67339 standard; peptide; 230 AA.
XX
XX AAB67339;
AC
XX
XX 23-APR-2001 (first entry)
DT
XX
XX Staphylococcus aureus enterotoxin E protein.
DE
XX
XX Tumour; cancer; immune; enterotoxin.
KW
XX
XX Staphylococcus aureus.
OS
XX
XX US6180097-B1.
PN
XX
XX 30-JAN-2001.
PD
XX
XX 30-OCT-1998; 98US-00183437.
XX
XX 03-OCT-1989; 89US-00416530.
PR 17-JAN-1990; 90US-0046577.
PR 17-JAN-1991; 91WO-US000342.
PR 01-JUN-1992; 92US-00891718.
PR 02-MAR-1993; 93US-00025144.
PR 31-JAN-1994; 94US-00189424.
PR 19-JUN-1995; 95US-00491746.
XX
XX (TERM/) Terman D S.
PA
XX
XX Terman DS;
XX
XX WPI; 2001-158657/16.
DR
XX
XX Tumor cell capable of stimulating antitumor immune reactivity in vitro or
PT in vivo comprises exogenous nucleic acids encoding a superantigen and a
PT costimulatory molecule.
XX
XX Disclosure; Fig 2; 16pp; English.
PS
XX
XX The present invention relates to a tumour cell capable of stimulating
CC antitumor immune reactivity in vitro or in vivo contains and expresses an
CC exogenous nucleic acid molecule encoding a superantigen or its active
CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
CC molecule that activates T cells in conjunction with an antigenic
CC stimulus. The invention may be used for cancer therapy by stimulating an
CC anticancer immune response in vivo or ex vivo
XX
XX Sequence 230 AA;
SQ
Query Match 98.9%; Score 1224; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 2e-114;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 SESEINEKDLRKSELOARNLSNLRQIYYNEKAITENKESDDQFLENTLLPKGFFTGHPW 63
DB 1 SESEINEKDLRKSELOARNLSNLRQIYYNEKAITENKESDDQFLENTLLPKGFFTGHPW 60
QY 64 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLTEK 123
DB 61 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLTEK 120
QY 124 KVPINLWIDGKQTTPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDFGKVQ 183
DB 121 KVPINLWIDGKQTTPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDFGKVQ 180
QY 184 IVFHSSEGSTSVSYDLFDAQOQYPTLLRIYRDNKTINSENHLIDLTYTT 233
DB 181 IVFHSSEGSTSVSYDLFDAQOQYPTLLRIYRDNKTINSENHLIDLTYTT 230

RESULT 6
```


Query Match	97.7%;	Score 1210;	DB 6;	Length 233;	
Best Local Similarity	97.9%;	Pred. No. 5.3e-113;			
Matches 228;	Conservative	1;	Mismatches 4;	Indels 0;	Gaps 0;
QY	1	SEKSEINEKDLRKKSQELQNALSNLROIYYNEKAITENKESDDQFLENTLLFKGFFTG	60		
DB	1	SEKSEINEKDLRKKSQELQNALSNLROIYYNEKAITENKESDDQFLENTLLFKGFFTG	60		
QY	61	HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT	120		
DB	61	HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT	120		
QY	121	EKKVPINLWIDGKQTTPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ	180		
DB	121	EKKVPINLWIDGKQTTPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ	180		
QY	181	RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDKNKTINSENHLIDLYLYTT	233		
DB	181	RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDKNKTINSENHLIDLYLYTT	233		
RESULT 8					
AAW35375					
ID	AAW35375	standard; peptide; 245 AA.			
XX					
AC	AAW35375;				
XX					
DT	20-APR-1998	(first entry)			
XX					
DE	Staphylococcus enterotoxin	SEE modified superantigen.			
XX					
KW	SEE; SEA; Staphylococcus enterotoxin;	superantigen; conjugate; treatment;			
KW	cancer; infection; autoimmune disease;	antibody; modified.			
XX					
OS	Staphylococcus sp.				
XX					
FH	Key	Location/Qualifiers			
FT	Misc-difference 20	/label= R20G			
FT		/note= "wild-type Arg is replaced by Gly"			
FT	Misc-difference 21	/label= N21T			
FT		/note= "wild-type Asn is replaced by Thr"			
FT	Misc-difference 24	/label= S24G			
FT		/note= "wild-type Ser is replaced by Gly"			
FT	Misc-difference 27	/label= R27K			
FT		/note= "wild-type Arg is replaced by Lys"			
XX					
PN	WO9736932-A1.				
XX					
PD	09-OCT-1997.				
XX					
PF	26-MAR-1997;	97WO-SR000537.			
XX					
PR	29-MAR-1996;	96SE-00001245.			
PR	12-AUG-1996;	96US-00695692.			
XX					
PA	(PHAA) PHARMACIA & UPJOHN AB.				
XX					
PI	Antonsson P, Hansson J, Bjoerk P, Dohlsten M, Kalland T;				
PI	Abrahmsen L, Forsberg G;				
XX					
DR	WPI; 1997-503052/46.				
XX					
PT	Conjugate of target seeking moiety and modified superantigen - useful for				
PT	activating the immune system to treat cancer, viral infections, parasitic				
PT	infestations and autoimmune diseases.				
XX					
PS	Claim 5; Page; 58pp; English.				
XX					
This is a modified Staphylococcus enterotoxin SEE superantigen. The wild type SEE superantigen is modified to be used in a novel conjugate. The novel conjugate comprises a target seeking moiety and a modified wild type superantigen. This modified superantigen retains its ability to activate a subset of T cells, even though 1 or more wild-type amino acid residues in at least 1 region which functions in determining binding to T cell receptor (TCR) and activation of a subset of T cells has/have been replaced. Such a modified superantigen can optionally be used as part of a conjugate with a target seeking moiety, for activating the immune system to treat a mammalian disease. A pharmaceutical composition can be prepared comprising a modified antibody (preferably a Fab fragment fused to a peptide moiety providing activation of T cells in Vbeta specific manner) in which cysteines providing for interchain cysteine linkages in the native antibody have been replaced (preferably by serine residues) to prohibit cysteine formation. The modified wild-type superantigen is used for treating cancer, viral infections, parasitic infestations and autoimmune disease. The modified wild type superantigen has a lower immunogenicity and reactivity with neutralising antibodies and has fewer side-effects when used as a drug, compared to wild type superantigen. Note: This sequence is not provided in the specification. It has been created by modifying the wild-type SEE superantigen sequence in Pages 38-39 of the specification					
XX					
SQ	Sequence 245 AA;				
Query Match		97.1%;	Score 1202;	DB 2;	Length 245;
Best Local Similarity		93.5%;	Pred. No. 3.6e-112;		
Matches 229;		Conservative	1;	Mismatches 3;	Indels 12;
					Gaps 1;
QY	1	SEKSEINEKDLRKKSQELQNALSNLROIYYNEKAITENKESDDQFLENTLLFKGFFTG	60		
DB	1	SEKSEINEKDLRKKSQELQNALSNLROIYYNEKAITENKESDDQFLENTLLFKGFFTG	60		
QY	61	HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT	120		
DB	61	HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT	120		
QY	121	EKKVPINLWIDGKQTTPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ	180		
DB	121	EKKVPINLWIDGKQTTPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ	180		
QY	181	RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDKNKTINSENHLIDLYLYTT	228		
DB	181	RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDKNKTINSENHLIDLYLYTT	228		
QY	229	YLYTT 233			
DB	241	YLYTT 245			
RESULT 9					
ABU79072					
ID	ABU79072	standard; protein; 248 AA.			
XX					
AC	ABU79072;				
XX					
DT	18-JUN-2003	(first entry)			
XX					
DE	S. aureus SEE (staphylococcus enterotoxin E) protein.				
XX					
KW	Superantigen; SAG; staphylococcal enterotoxin; tumour; cancer; apoptosis;				
KW	gene therapy; mammalian cell receptor; tumour associated lipid; anergy;				
KW	T cell; antigen presenting cell; tumouricidal immunocyte; cytostatic;				
XX	APC; antitumour.				
OS	Staphylococcus aureus.				
XX					
PN	US2002177551-A1.				
XX					
PD	28-NOV-2002.				
XX					
PF	30-MAY-2001; 2001US-00870759.				
XX					

PR 31-MAY-2000; 2000US-0208128P.
XX (TERM/) Terman D S.
PA Terman DS;
XX WPI; 2003-361759/34.
DR N-PSDB; AC364698.
XX A mammalian cell receptor, useful in the treatment of cancer by binding
PT to tumor associated lipids where the binding induces anergy or apoptosis
PT in T cells and antigen presenting cells.
XX Disclosure; Page; 167pp; English.
XX The invention relates to a mammalian cell receptor, useful in the
XX treatment of cancer, which binds to tumour associated lipids and induces
CC anergy or apoptosis in the T cells and antigen presenting cells (APCs).
CC Also included are a mammalian cell useful in the treatment of cancer
CC where the receptor which binds tumour associated lipids and induces
CC cellular inactivation or death is deleted or functionally deactivated,
CC producing (M1) a tumouricidal immunocyte population in vivo in a mammal
CC (by allowing tumour associated lipids to contact immunocytes in which
CC receptors for immunosuppressive fatty acids, ceramides, glycolipids,
CC sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
CC sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
CC deleted), a construct useful in the treatment of cancer comprising a
CC superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell
CC useful in the treatment of cancer (where an adaptor protein which
CC inhibits T cell activation by tumour associated antigens is deleted or
CC functionally deactivated), a composition useful in the treatment of
CC cancer (comprising a lipid raft conjugated to a superantigen), producing
CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
CC allowing tumour associated lipids to contact immunocytes, in which
CC receptors for the lipids are inactivated or deleted to produce a
CC tumouricidal immunocyte population, and administering the tumouricidally
CC activated immunocytes to the host), producing (M3) a tumouricidal APC
CC population ex vivo in a mammal (by allowing a tumour associated lipid to
CC contact APCs, in which receptors for the tumour associated lipids are
CC inactivated or deleted to produce a tumouricidally activated population,
CC and administering APCs to the host), producing a tumouricidal T cell
CC population ex vivo in a mammal (by allowing a tumour associated lipids to
CC contact T cells, in which adaptor proteins, which inhibit T cell
CC activation by tumour associated antigens, are deleted or functionally
CC deactivated to produce a tumouricidal population of T cells, and
CC administering the tumouricidally activated T cells to the host, or
CC allowing a superantigen-lipid raft to contact T cells ex vivo, and
CC administering the tumouricidally activated T cells to the host), treating
CC (M5) cancer in a mammal (by administering a lipid binding molecule which
CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)
CC a tumouricidal T cell population in vivo in a mammal (by allowing a
CC tumour associated antigen to contact immunocytes in which adaptor
CC proteins which inhibit T cell activation by tumour associated antigens
CC are deleted or functionally deactivated) and producing (M7) a
CC tumouricidal T cell population ex vivo in a mammal comprising allowing a
CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The
CC receptors, methods and compositions are useful for treating cancers and
CC tumours. Bacterial superantigens are co-administered or administered as
CC fusion constructs with anti-tumour proteins or motifs. The present
CC sequence represents a bacterial superantigen protein (e.g. a
CC staphylococcal enterotoxin). Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format from the US patent office website at
CC "seqdata.uspto.gov/sequence.html?DocID=20020177551"
XX Sequence 248 AA;
XX Query Match 96.0%; Score 1188; DB 6; Length 248;
XX Best Local Similarity 100.0%; Pred. No. 9.5e-111; Indels 0; Gaps 0;
XX Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1 SEKSEINEKDLRKSELOLQNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
|||||

DB 25 SEKSEINEKDLRKSELOLQNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTCMYGGVTLHDNRLLT 120
DB 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTCMYGGVTLHDNRLLT 144
QY 121 BEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKQV 180
DB 145 BEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKQV 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQVDPDTLLRIYRDNKNTINSEN 224
DB 205 RGLIVFHSSEGSTVSVDLFDAGQVDPDTLLRIYRDNKNTINSEN 248
RESULT 10
ADP43296
ID ADP43296 standard; protein; 248 AA.
XX AC ADP43296;
XX 12-FEB-2004 (first entry)
XX Staphylococcal enterotoxin E polypeptide seq id 16.
XX receptor; lipid-based tumour associated antigen; cytostatic;
KW antimicrobial; gene therapy; neoplastic disease; tumour; cancer;
KW infectious disease; Staphylococcal enterotoxin E; SEE; enterotoxin E.
XX OS Staphylococcus.
XX US2003157113-A1.
XX 21-AUG-2003.
XX 28-DEC-2000; 2000US-00751708.
XX 28-DEC-1999; 99US-01737371P.
XX (TERM/) Terman D S.
XX Terman DS;
XX WPI; 2003-787326/74.
XX New receptor in a mammalian cell that inhibits regular activation by
PT receptors specific for lipid-based tumour associated antigens, useful for
PT treating a neoplastic disease or tumor, and infectious diseases.
XX Example 3; SEQ ID NO 16; 151pp; English.
XX The invention describes a receptor in a mammalian cell that inhibits
CC regular activation by receptors specific for lipid-based tumour
CC associated antigen. The receptor has cytostatic and antimicrobial
CC properties and is suitable for use in gene therapy. The receptors,
CC methods and compositions are useful for treating a neoplastic disease or
CC tumour (cancer), and infectious diseases. This is the amino acid sequence
CC of an enterotoxin superantigen polypeptide the DNA encoding which can be
CC transfected in to a cell alone or with DNA encoding a cell surface moiety
CC to generate antitumour immunity.
XX Sequence 248 AA;
XX Query Match 96.0%; Score 1188; DB 7; Length 248;
XX Best Local Similarity 100.0%; Pred. No. 9.5e-111; Indels 0; Gaps 0;
XX Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOLQNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOLQNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTCMYGGVTLHDNRLLT 120
|||||

85	HPWYNDLILVDLGSKDATNKYKKGKVDLIGAYYGVCAGGTENKTACHMYGGVTLHDNNRLT	144
Db		
Qy	121 EEKKVPINIWIDGKQTTPVIDKVTSKSKEVTVQELDLQARHYLHGKGLYNSDSFGSKVQ	180
Db	145 EEKKVPINIWIDGKQTTPVIDKVTSKSKEVTVQELDLQARHYLHGKGLYNSDSFGSKVQ	204
Qy	181 RGLIVFHSSEGSTVSVDLFDAGQCPDPTLLRIYRDNKTINSEN	224
Db	205 RGLIVFHSSEGSTVSVDLFDAGQCPDPTLLRIYRDNKTINSEN	248

RESULT 11	
AEA02990	
ID	AEA02990 standard; protein; 248 AA.
XX	
XX	AEA02990;
XX	
XX	28-JUL-2005 (first entry)
XX	
XX	Staphylococcal enterotoxin E (SEE) amino acid sequence SEQ ID NO:16.
XX	
KW	tumor; neoplasm; gene therapy; immunotherapy; cytostatic;
KW	Staphylococcal enterotoxin E.
XX	
XX	Staphylococcus sp.
XX	
PN	US2005112141-A1.
XX	
XX	26-MAY-2005.
XX	
XX	08-SEP-2004; 2004US-00937758.
XX	
PR	30-AUG-2000; 2000US-00650884.
XX	
XX	(TERM/) Terman D S.
XX	
XX	Terman DS;
XX	
XX	WPI; 2005-394926/40.
XX	
XX	N-PSDB; AEA02989.
XX	
PT	New composition for treating a tumor or neoplastic disease in a subject
PT	comprises conjugates comprising superantigen polypeptides or nucleic
PT	acids with other molecules that produce a tumoricidal response.
XX	
PS	Example 3; SEQ ID NO 16; 125pp; English.

CC which may be used in the methods of the invention for treating cancer in
CC a patient. These SEs, and homologues of them, can be used as tumouricidal
CC agents for treating cancers and autoimmune disease. They exhibit
CC tumouricidal activity and toxicity identical to that observed for the
CC Protein A perfusion system. They may be administered by i.v. injection.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 230 AA;

Query Match 95.2%; Score 1179; DB 2; Length 230;
Best Local Similarity 96.1%; Pred. No. 6.9e-110;
Matches 221; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 4 SEEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPW 63
DB 1 SEEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPW 60
QY 64 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEK 123
DB 61 YNDLLVDKSGKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEK 120
QY 124 KVPINLWIDGKQTTPIDVKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRL 183
DB 121 XVXXBKWIDGKQTTPIDVKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRL 180
QY 184 IVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHIDLILYTT 233
DB 181 IVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHIDLILYTT 230

RESULT 13
ABB76235
ID ABB76235 standard; protein; 230 AA.
XX
AC ABB76235;
DT 09-AUG-2002 (first entry)
XX
DE Staphylococcus aureus enterotoxin E.
XX
KW Enterotoxin E; SEE; superantigen; antigen; tumour; cancer; antitumour;
KW therapy.
XX
OS Staphylococcus aureus.
XX
PH Key Location/Qualifiers
FT Misc-difference 120
FT Misc-difference 121 /note= "given as 'J' in the specification"
FT Misc-difference 123 /note= "given as 'J' in the specification"
FT Misc-difference 123 /note= "given as 'O' in the specification"
FT Misc-difference 124 /note= "given as 'O' in the specification"
FT Misc-difference 125 /note= "given as 'U' in the specification"
FT Misc-difference 125 /note= "given as 'V' in the specification"
XX

US2002051765-A1.
XX
XX 02-MAY-2002.
XX
XX 19-DEC-2000; 2000US-00741503.
XX
XX 03-OCT-1989; 89US-00416530.
XX
XX 17-JAN-1990; 90US-00466577.
XX
XX 17-JAN-1991; 91WO-US000342.
XX
XX 01-JUN-1992; 92US-00891718.
XX
XX 02-MAR-1993; 93US-00025144.
XX
XX 31-JAN-1994; 94US-00189424.
XX
XX 19-JUN-1995; 95US-00491746.
XX
XX (TERM/) TERMAN D S.

PI Terman DS;
XX
DR WPI; 2002-415198/44.
XX
PT Reagent for treating cancer without the need for e.g. radiotherapy,
PT comprises a specific V beta subset of T cells sensitized to a growing
PT tumor and stimulated with superantigens.
XX
PS Disclosure; Fig 2; 17pp; English.
XX
CC The present sequence is the protein sequence of enterotoxin E (SEE) of
CC Staphylococcus aureus. Similarity is shown, in several stretches of
CC sequence, between staphylococcal enterotoxins, streptococcal pyrogenic
CC exotoxins and staphylococcal exfoliative toxins (see ABB76234-44). In the
CC present invention, synthetic polypeptides useful in tumour therapy and in
CC blocking or destroying autoreactive T and B lymphocyte populations are
CC characterised by substantial structural homology to staphylococcal
CC enterotoxin A and enterotoxin B, and to streptococcal pyrogenic
CC exotoxins, with statistically significant sequence homology and
CC similarity (Z value of Lipman and Pearson algorithm in Monte Carlo
CC analysis exceeding 6) to include alignment of cysteine residues and
CC similar hydrophathy profiles. These superantigens are used to treat solid
CC tumours, including their metastases, without radiation, surgery or
CC standard chemotherapeutic agents. A claimed method of human cancer
CC treatment involves contacting haematopoietic cells from a patient with
CC one or more superantigens ex vivo to generate stimulated cells, selecting
CC a specific V beta subset of cells, and reintroducing these cells into the
CC patient to induce an in vivo therapeutic, tumouricidal reaction
XX
SQ Sequence 230 AA;

Query Match 94.9%; Score 1175; DB 5; Length 230;
Best Local Similarity 96.1%; Pred. No. 1.7e-109;
Matches 221; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
QY 4 SEEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPW 63
DB 1 SEEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPW 60
QY 64 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEK 123
DB 61 YNDLLVDKSGKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEK 120
QY 124 KVPINLWIDGKQTTPIDVKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRL 183
DB 121 XVXXBKWIDGKQTTPIDVKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRL 180
QY 184 IVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHIDLILYTT 233
DB 181 IVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHIDLILYTT 230

RESULT 14
AAR13204
ID AAR13204 standard; protein; 230 AA.
XX
XX AAR13204;
XX
XX 15-OCT-1991 (first entry)
XX
DE Staphylococcal enterotoxin E.
XX
KW SEE; cancer treatment; pyrogen; tumouricide.
XX
OS Staphylococcus aureus.
XX
XX WO9110680-A.
XX
XX 25-JUL-1991.
XX
XX 17-JAN-1990; 90US-00466577.
XX
XX 17-JAN-1990; 90US-00466577.

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XX (TERM/) Terman D S.
XX Terman DS;
XX WPI; 1991-237984/32.
XX Treating cancer with enterotoxin from Staphylococcus aureus -
XX PT administered by IV injection, having same tumoricidal activity as
XX STaphylococcal protein A without potential toxic reactions.
XX PS Disclosure; Fig 1; 74pp; English.
XX SEE was isolated and purified from S.aureus. It can be used for treating
XX cancer, activating cytokine mediators and procoagulant systems,
XX augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be
XX administered intravenously, optionally with ibuprofen to attenuate toxic
XX reaction to SEE. Synthetic polypeptides having structural homology to
XX Staphylococcal exotoxins are claimed, provided the homology includes
XX statistically significant sequence homology, alignment of Cysteine
XX residues and similar hydropathy profiles. See AAR13203-R13211
XX SQ Sequence 230 AA;
XX
XX Query Match 93.4%; Score 1156; DB 2; Length 230;
XX Best Local Similarity 93.9%; Pred. No. 1.4e-107;
XX Matches 216; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
XX
QY 4 SEEINERKDLRKSELOLNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTGHPW 63
DB 1 SEEINERKDLRKSELOLNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTGHPW 60
QY 64 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEK 123
DB 61 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEX 120
QY 124 KVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQGL 183
DB 121 XVQXBRWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQGL 180
QY 184 IVPHSSEGSTVSYDLFDAQGYQPDTLRLIYRDNKTINSENHLHDLYLYTT 233
DB 181 IVPHSSEGSTVSYDLFDAQGYQPDTLRLIYRDNKTINSENHNHDIYLYTT 230
XX
RESULT 15
ID ABP58455
AC ABP58455 standard; protein; 233 AA.
XX
XX ABP58455;
XX
XX 14-APR-2003 (first entry)
XX Engineered superantigen SEA/E-120 for human cancer therapy.
XX
XX Superantigen; staphylococcal enterotoxin; antibody; cancer; tumour;
XX cytostatic; vaccine; SEA/E-120; mutant; mutein.
XX
XX Staphylococcus sp.
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 20
FT Misc-difference 21 /note= "wild-type Arg substituted by Gly"
FT Misc-difference 24 /note= "wild-type Asn substituted by Thr"
FT Misc-difference 27 /note= "wild-type Ser substituted by Gly"
FT Misc-difference 27 /note= "wild-type Arg substituted by Lys"
FT Misc-difference 79 /note= "wild-type Lys substituted by Glu"
FT Misc-difference 81

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FT Misc-difference 83 /note= "wild-type Lys substituted by Glu"
FT FT Misc-difference 84 /note= "wild-type Lys substituted by Ser"
FT FT Misc-difference 227 /note= "wild-type Lys substituted by Ser"
FT FT Misc-difference 227 /note= "wild-type Asp substituted by Ser"
XX WO2003002143-A1.
XX 09-JAN-2003.
XX 19-JUN-2002; 2002WO-SE001188.
XX 28-JUN-2001; 2001SE-00002327.
XX (ACTI-) ACTIVE BIOTECH AB.
XX Forsberg G, Erlandsson E, Antonsson P, Walse B;
XX WPI; 2003-201467/19.
XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
XX receptor and four regions to determine binding to class II major
XX histocompatibility complex, antibody to cancer associated cell surface
XX structure.
XX Claim 8; Fig 2; 102pp; English.
XX
XX The present sequence is the protein sequence of engineered staphylococcal
XX superantigen SEA/E-120. The superantigen is derived from staphylococcal
XX enterotoxin E (SEE) by the incorporation of the following amino acid
XX substitutions to reduce seroreactivity whilst maintaining production
XX levels and biological activity: R20G, N21T, S24G, R27K, K79E, K81E, K83S
XX and D227S. SEA/E-120 has been genetically fused to the Fab moiety of the
XX tumour reactive antibody 5T4 to form a claimed conjugate (see ABP58454)
XX designed to target and destroy cancer cells, including cancer of the
XX lung, breast, colon, kidney, pancreas, ovary, stomach, cervix and
XX prostate (claimed)
XX SQ Sequence 233 AA;
XX
XX Query Match 89.4%; Score 1107; DB 6; Length 233;
XX Best Local Similarity 89.7%; Pred. No. 1.2e-102;
XX Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
XX
QY 1 SEKSEINEKDLRKSELOLNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKSELOLNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 181 RGLIVPHSSEGSTVSYDLFDAQGYQPDTLRLIYRDNKTINSENHLHDLYLYTT 233
DB 181 RGLIVPHSSEGSTVSYDLFDAQGYQPDTLRLIYRDNKTINSENHLHDLYLYTT 233
XX
RESULT 16
ID ABP58454
XX ABP58454 standard; protein; 672 AA.
XX AC ABP58454;
XX 14-APR-2003 (first entry)
XX Engineered superantigen for human cancer therapy.
XX

```


XX The present invention relates to peptides which exhibit anti-retroviral
CC activity. The peptides of the invention (AAU12559-AAU14009) comprise
CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to
CC amino acids 639-673 of the transmembrane protein gp41 from human
CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide
CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention
CC also relates to a method of identifying compounds that inhibit the
CC formation of or disrupts a DP107/DP178 complex. The method comprises
CC detecting the formation of a DP107/DP178 complex, both in the presence or
CC absence of a test compound, in a reaction mixture containing DP107 and
CC DP178 peptides. The method is useful for identifying compounds, including
CC small molecule compounds which may themselves exhibit antifuogenic,
CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like
CC peptides are useful to inhibit human and non-human retroviral,
CC particularly HIV, transmission to uninfected cells. The present sequence
CC represents a peptide sequence from Staphylococcus aureus enterotoxin A
XX Sequence 257 AA;
SQ
Query Match 82.6%; Score 1023; DB 4; Length 257;
Best Local Similarity 82.0%; Pred. No. 4e-94;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINEKDKRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDKRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTD 84
QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
DB 85 HSWYNLLVDLGSKDIDVYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGYNSDSFGGKVQ 180
DB 145 EEKVPINLWIDGKQNTVPLETKNKNVTQVELDLQARRYLQEKYLYNSDSVDFGKVQ 204
QY 181 RGLIVPHSSEGSTSVSYDLFDAGQGYPTLLRIYRDNKTINSENHLDLYLTT 233
DB 205 RGLIVPHSTEPSVNYDLFGAQGYNTLLRIYRDNKTINSENHLDLYLTS 257
RESULT 20
ABO10269
ID ABO10269 standard; protein; 257 AA.
XX
AC ABO10269;
XX
DT 19-AUG-2003 (first entry)
XX
DE S. aureus enterotoxin A.
XX
KW HIV; DP107; DP178; glycoprotein 41; antiviral; virucide; EBV;
KW Epstein-Barr virus infection; heptad repeat motif.
XX
OS Staphylococcus aureus.
XX
XX US6518013-B1.
PN 11-FEB-2003.
XX
XX 07-JUN-1995; 95US-00485546.
XX
PR 07-JUN-1993; 93US-00073028.
PR 07-JUN-1994; 94US-00255208.
PR 20-DEC-1994; 94US-00360107.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX Barney SO, Lambert DM, Petteway SR;
PI WPI; 2003-465599/44.
DR
XX Inhibiting transmission of Epstein-Barr virus to a cell, by contacting

PT the cell with a peptide consisting of a region of Epstein-Barr virus
PT protein.
XX
PS Example; Fig 42; 716pp; English.
XX
CC The invention relates to inhibiting (M) transmission of an Epstein-Barr
CC virus to a cell, comprising contacting the cell with an effective
CC concentration of a peptide consisting of a region of 16-39 consecutive
CC amino acids of an Epstein-Barr virus protein for an effective period of
CC time, where the region is recognised by one or more of AILMOR15,
CC 107x178x4 or PLZIP sequence search motifs, the peptide further comprises
CC an amino terminal X, and a carboxy terminal Z in which X comprises an
CC amino group, acetyl group, 9-fluorenylmethoxy-carbonyl group, hydrophobic
CC group or macromolecular carrier group, and Z comprises a carboxyl group,
CC amido group, hydrophobic group, or macromolecular carrier group, and
CC fusion of the virus to the cell is inhibited. The peptides were
CC identified by analysing the structure/motifs present in the HIV-1
CC glycoprotein 41 anti-HIV peptides DP107 and DP178. These heptad repeat
CC motif containing peptides were used to design the motifs cited above,
CC which in turn were used to analyse proteins from other pathogenic
CC organisms and HIV isolates, looking for DP107/178 structural analogues.
CC The method is useful for inhibiting transmission of Epstein-Barr virus to
CC a cell and Epstein-Barr virus infection. The present sequence is a
CC protein from a pathogenic organism analysed for regions analogous to
CC DP107 or DP178
XX Sequence 257 AA;
SQ
Query Match 82.6%; Score 1023; DB 6; Length 257;
Best Local Similarity 82.0%; Pred. No. 4e-94;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINEKDKRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDKRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTD 84
QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
DB 85 HSWYNLLVDLGSKDIDVYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGYNSDSFGGKVQ 180
DB 145 EEKVPINLWIDGKQNTVPLETKNKNVTQVELDLQARRYLQEKYLYNSDSVDFGKVQ 204
QY 181 RGLIVPHSSEGSTSVSYDLFDAGQGYPTLLRIYRDNKTINSENHLDLYLTT 233
DB 205 RGLIVPHSTEPSVNYDLFGAQGYNTLLRIYRDNKTINSENHLDLYLTS 257
RESULT 21
ADD44368
ID ADD44368 standard; protein; 257 AA.
XX
AC ADD44368;
XX
DT 15-JAN-2004 (first entry)
XX
DE Staphylococcus aureus enterotoxin A protein.
XX
KW enterotoxin A; ent A; food poisoning; bacterium; food; milk; fruit juice;
KW ice cream.
XX
OS Staphylococcus aureus.
XX
XX WO2003080865-A1.
PN 02-OCT-2003.
XX
XX 26-MAR-2002; 2002WO-IB001150.
XX
XX 26-MAR-2002; 2002WO-IB001150.
XX
XX (COUL) COUNCIL SCI & IND RES.
PA


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XX Padmapriya BP, Ramesh A, Chandrashekar A, Varadaraj MC;
XX WPI: 2003-779273/73.
XX N-PSDB; ADD44369.
XX Novel oligonucleotide primers directed against enterotoxin A gene of
PT Staphylococcus aureus and heat stable enterotoxin gene of Yersinia
PT enterocolitica, useful for detecting food poisoning causing bacteria.
XX Example 2; Page 14-15; 34pp; English.
XX The invention relates to novel oligonucleotide primers directed against
CC enterotoxin A gene (ent A) of Staphylococcus aureus and heat stable
CC enterotoxin gene (yst) of bacteria Yersinia enterocolitica. The novel
CC oligonucleotide primers are useful for simultaneously detecting food
CC poisoning bacterial species Staphylococcus aureus and/or Yersinia
CC enterocolitica in food systems e.g., milk, fruit juices and ice creams,
CC without prior enrichment for preventing food poisoning outbreak. The PCR
CC detection method is useful for detecting the bacteria strains in quantity
CC as low as one cell. The method can be directly used for detecting
CC bacterial strains. The oligonucleotide primers allow quick and highly
CC sensitive detection of the food poisoning bacterial species. This
CC sequence represents the protein derived from the enterotoxin A gene from
CC Staphylococcus aureus of the invention.
XX Sequence 257 AA;
XX
XX Query Match 82.6%; Score 1023; DB 7; Length 257;
XX Best Local Similarity 82.0%; Pred. No. 4e-94;
XX Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
XX
XX QY 1 SEKSEINEKDLRKKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
XX DB 25 SEKSEINEKDLRKKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTD 84
XX
XX QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNKTACWYGGVTLHDNNRLT 120
XX DB 85 HSWYNLLVDLGSKDIDVYKGGKVDLYGAYYGYQCAGGTPNKTACWYGGVTLHDNNRLT 144
XX
XX QY 121 EEKVPINLWIDGKQTPIDKVTTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
XX DB 145 EEKVPINLWIDGKQTPVLETVTKNKGNVTVOELDLQARRYLQEKYLNLYNSDVFQKQV 204
XX
XX QY 181 RGLIVFHSSEGSTVSYDLFDAQOQYPTLLRIYRDNKTINSENHLDLYLYTT 233
XX DB 205 RGLIVFHTSTEPSVNYDLFQAQOQYNTLLRIYRDNKTINSENHLDIYLYTS 257
XX
XX RESULT 22
XX ADH10956
XX ID ADH10956 standard; protein; 257 AA.
XX AC ADH10956;
XX
XX DT 11-MAR-2004 (first entry)
XX DE Enterotoxin A protein.
XX
XX KW Enterotoxin A; Computational design; protein binding peptide;
XX hydrophobic potential; solvent contact surface;
XX protein three-dimensional structure; two-dimensional characteristic map;
XX Fourier transformation.
XX
XX OS Staphylococcus aureus.
XX
XX JF2003263465-A.
XX
XX PD 19-SEP-2003.
XX
XX PF 07-MAR-2002; 2002JP-00062348.
XX
XX PR 07-MAR-2002; 2002JP-00062348.
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XX (ENKA-) ENKAKU IRYO KENKYUSHO KK.
XX WPI: 2004-075279/08.
XX Designing and selecting protein binding peptide by identifying peptide
PT binding region of protein, and designing peptides that bind to the region
PT using structure-biological activity relationship program of computer.
XX Example; SEQ ID NO 1; 11pp; Japanese.
XX The invention relates to a method for computational design and selection
CC of protein binding peptides, comprising computing the hydrophobic
CC potential of all surface points arranged on the solvent contact surface
CC of a protein three-dimensional structure, developing a two-dimensional
CC characteristic map by a self-assembly method, identifying a region of
CC hydrophobic amino acids by Fourier transformation and designing a protein
CC binding peptide corresponding to the hydrophobic region. The method is
CC useful for designing and selecting protein binding peptides. This
CC sequence represents an Enterotoxin A protein used in the scope of the
XX invention.
XX Sequence 257 AA;
XX
XX Query Match 82.6%; Score 1023; DB 8; Length 257;
XX Best Local Similarity 82.0%; Pred. No. 4e-94;
XX Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
XX
XX QY 1 SEKSEINEKDLRKKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
XX DB 25 SEKSEINEKDLRKKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTD 84
XX
XX QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNKTACWYGGVTLHDNNRLT 120
XX DB 85 HSWYNLLVDLGSKDIDVYKGGKVDLYGAYYGYQCAGGTPNKTACWYGGVTLHDNNRLT 144
XX
XX QY 121 EEKVPINLWIDGKQTPIDKVTTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
XX DB 145 EEKVPINLWIDGKQTPVLETVTKNKGNVTVOELDLQARRYLQEKYLNLYNSDVFQKQV 204
XX
XX QY 181 RGLIVFHSSEGSTVSYDLFDAQOQYPTLLRIYRDNKTINSENHLDLYLYTT 233
XX DB 205 RGLIVFHTSTEPSVNYDLFQAQOQYNTLLRIYRDNKTINSENHLDIYLYTS 257
XX
XX RESULT 23
XX ADV11662
XX ID ADV11662 standard; protein; 257 AA.
XX AC ADV11662;
XX
XX DT 24-FEB-2005 (first entry)
XX DE Staphylococcus aureus enterotoxin A.
XX
XX KW DNA amplification; DNA detection; food poisoning; food; toxin;
XX enterotoxin; enterotoxin A; entA.
XX
XX OS Staphylococcus aureus.
XX
XX US2004248089-A.
XX
XX PD 09-DEC-2004.
XX
XX PF 27-MAR-2002; 2002US-00107879.
XX
XX PR 27-MAR-2002; 2002US-00107879.
XX
XX (BANA/) BANADA P P.
XX (NAME/) RAMESH A.
XX (CHAN/) CHANDRASHEKAR A.
XX (VARA/) VARADARAJ M C.
XX
```

PI Banada PP, Ramesh A, Chandrashekar A, Varadaraj MC;
 XX WPI; 2005-046727/05.
 DR N-PSDB; ADV11663.
 XX
 PT New oligonucleotide primers useful for detecting poisoning in food
 PT systems and particles, in particular food poisoning from Staphylococcus
 PT aureus and/or Yersinia enterocolitica.
 XX
 PS Disclosure; Page 6; 13pp; English.
 XX
 CC The invention relates to PCR primers specific for the Staphylococcus
 CC aureus enterotoxin A (entA) gene (ADV1658-ADV11659) and the Yersinia
 CC enterocolitica heat stable enterotoxin (yvt) gene (ADV11660-ADV11661),
 CC and to their use in a highly sensitive and quick PCR-based method for the
 CC detection of these food poisoning-associated bacteria in food systems
 CC such as milk, fruit juice or ice cream. The invention also relates to a
 CC method of preparing the primers of the invention by identifying conserved
 CC sequences of the entA and yvt genes and using software programs to
 CC generate the primers. The primers and detection method are used to detect
 CC enterotoxigenic/pathogenic strains of Staphylococcus aureus and Yersinia
 CC enterocolitica in food samples, and therefore help to prevent food
 CC poisoning outbreaks. The detection method is highly sensitive, being able
 CC to detect the presence of a single target organism in a food sample. The
 CC present sequence represents Staphylococcus aureus enterotoxin A.
 XX
 SQ Sequence 257 AA;
 Query Match 82.6%; Score 1023; DB 9; Length 257;
 Best Local Similarity 82.0%; Pred. No. 4e-94;
 Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
 DB 25 SEKSEINEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 84
 QY 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNKTCMYGGVTLHNNRLT 120
 DB 85 HSWYNDLLVDFDSKDIYDKYKGGKVDLYGAYYGYQCAGGTPNKTCMYGGVTLHNNRLT 144
 QY 121 EEKVPINLWIDGKQTTPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVK 180
 DB 145 EEKVPINLWIDGKQNTVPLETVTKNKNVTQELDLQARRYLQEKYLYNSDVFQKVK 204
 QY 181 RGLIVPHSSEGSTVSVDLFDAGQYPTDILLRIYRDNKTINSENHLIDLYTT 233
 DB 205 RGLIVPHSTSTEPSVNYDLFQAQGYNTLLRIYRDNKTINSENHMDIYLYTS 257
 RESULT 24
 AEB13483
 ID AEB13483 standard; protein; 301 AA.
 XX
 AC AEB13483;
 XX
 DT 08-SEP-2005 (first entry)
 XX
 DE EGF-SEA fusion construct protein SEQ ID NO 2.
 XX
 KW fusion protein; cell proliferation; antigen; cancer;
 KW endothelial growth factor; EGF; vascular endothelial growth factor; VEGF;
 KW SEA; enterotoxin family; enterotoxin A; cytostatic; immunomodulator.
 XX
 OS Synthetic.
 XX
 PN WO2005061531-A1.
 XX
 PD 07-JUL-2005.
 XX
 PF 31-MAY-2004; 2004WO-CN000569.
 XX
 PR 21-DEC-2003; 2003CN-01109829.
 XX

PA (SUNJ/) SUN J.
 XX Sun J;
 PI
 XX WPI; 2005-488638/49.
 DR N-PSDB; AEB13482.
 XX
 PT Preparation of superantigen fusion proteins containing specific proteins
 PT and superantigens based on recombinant expression vectors and host cells,
 PT for producing medicines in e.g. antitumor therapy.
 XX
 PS Example 6; SEQ ID NO 2; 33pp; Chinese.
 XX
 CC This invention describes a novel fusion protein comprising a ligand which
 CC can promote the growth of cancer cells and also corresponds to the
 CC receptor of cancer-cell overexpression, as well as a specific polypeptide
 CC which has avidity to and antagonism against the cancer cell receptor or
 CC may interact directly with the cancer-cell surface, and a superantigen
 CC which can induce an antitumor immunological reaction. The invention also
 CC describes 1) a recombinant vector containing the nucleotide sequence for
 CC the fusion protein; 2) host cells containing the recombinant vector and
 CC 3) a method of producing the fusion protein by culturing the host cells
 CC before collecting the expressed fusion protein. The ligand is selected
 CC from endothelial growth factor (EGF) family, vascular endothelial growth
 CC factor (VEGF) family, basic fibroblast growth factor (bFGF) and GGF
 CC families, transforming growth factor (TGF-alpha), interleukin-4,
 CC interleukin-2, heregulin, interleukin-6, interleukin-13, interleukin-8,
 CC heparin-binding EGF-like growth factor, insulin-like growth factor, nerve
 CC growth factor, placenta growth factor, stem-cell growth factor,
 CC thrombopoietin, ephrin family, erbB ligand, desialic-acid glycoprotein,
 CC angiotensin, clotting factor VII, urokinase-type plasminogen activator,
 CC growth- hormone receptor hormone, growth inhibitor, chemotactic factor,
 CC low- density lipoprotein, transferrin and other ligands associated with
 CC cancer immunological diseases. The superantigen is chosen from SEA, SEB,
 CC SEC, SED and SEE of Staphylococcus aureus enterotoxin family, SPE-A, SPE-
 CC B and SPE-C of streptococci, especially SEA of Staphylococcus aureus
 CC enterotoxin family. The fusion protein preferably contains staphylococcal
 CC -enterotoxin A (SEA) as the superantigen and a ligand selected from EGF
 CC and VEG. The prepared proteins are useful in producing medicines for
 CC antitumor therapy or immunological reaction. Such drugs are more specific
 CC with enhanced activity and less toxic. This sequence represents a fusion
 CC construct composed of EGF and SEA.
 XX
 SQ Sequence 301 AA;
 Query Match 82.6%; Score 1023; DB 9; Length 301;
 Best Local Similarity 82.0%; Pred. No. 5.1e-94;
 Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
 DB 69 SEKSEINEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 128
 QY 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNKTCMYGGVTLHNNRLT 120
 DB 129 HSWYNDLLVDFDSKDIYDKYKGGKVDLYGAYYGYQCAGGTPNKTCMYGGVTLHNNRLT 188
 QY 121 EEKVPINLWIDGKQTTPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVK 180
 DB 189 EEKVPINLWIDGKQNTVPLETVTKNKNVTQELDLQARRYLQEKYLYNSDVFQKVK 248
 QY 181 RGLIVPHSSEGSTVSVDLFDAGQYPTDILLRIYRDNKTINSENHLIDLYTT 233
 DB 249 RGLIVPHSTSTEPSVNYDLFQAQGYNTLLRIYRDNKTINSENHMDIYLYTS 301
 RESULT 25
 AEB13485
 ID AEB13485 standard; protein; 369 AA.
 XX
 AC AEB13485;
 XX

08-SEP-2005 (first entry)
VEGF-SEA fusion construct protein SEQ ID NO 4.
fusion protein; cell proliferation; antigen; cancer;
endothelial growth factor; EGF; vascular endothelial growth factor; VEGF;
SEA; enterotoxin family; enterotoxin A; cytostatic; immunomodulator.
Synthetic.
WO2005061531-A1.
07-JUL-2005.
31-MAY-2004; 2004WO-CN000569.
21-DEC-2003; 2003CN-01109829.
(SUNJ/) SUN J.
Sun J;
WPI; 2005-488638/49.
N-PSDB; AEB13484.
Preparation of superantigen fusion proteins containing specific proteins
and superantigens based on recombinant expression vectors and host cells,
for producing medicines in e.g. antitumor therapy.
Example 6; SEQ ID NO 4; 33pp; Chinese.
This invention describes a novel fusion protein comprising a ligand which
can promote the growth of cancer cells and also corresponds to the
receptor of cancer-cell overexpression, as well as a specific polypeptide
which has avidity to and antagonism against the cancer cell receptor or
may interact directly with the cancer-cell surface, and a superantigen
which can induce an antitumor immunological reaction. The invention also
describes 1) a recombinant vector containing the nucleotide sequence for
the fusion protein; 2) host cells containing the recombinant vector and
3) a method of producing the fusion protein by culturing the host cells
before collecting the expressed fusion protein. The ligand is selected
from endothelial growth factor (EGF) family, vascular endothelial growth
factor (VEGF) family, basic fibroblast growth factor (bFGF) and FGF
families, transforming growth factor (TGF-alpha), interleukin-4,
interleukin-2, heregulin, interleukin-6, interleukin-13, interleukin-8,
heparin-binding EGF-like growth factor, insulin-like growth factor,
hepatocyte growth factor, platelet-derivatizing growth factor, nerve
growth factor, placenta growth factor, stem-cell growth factor,
thrombopoietin, ephrin family, erbB ligand, desialic-acid glycoprotein,
angiopoietin, clotting factor VII, urokinase-type plasminogen activator,
growth- hormone receptor hormone, growth inhibitor, chemotactic factor,
low- density lipoprotein, transferrin and other ligands associated with
cancer immunological diseases. The superantigen is chosen from SEA, SEB,
SEC, SED and SEE of *Staphylococcus aureus* enterotoxin family, SPE-A, SPE-
B and SPE-C of streptococci, especially SEA of *Staphylococcus aureus*
enterotoxin family. The fusion protein preferably contains staphylococcal
-enterotoxin A (SEA) as the superantigen and a ligand selected from EGF
and VEGF. The prepared proteins are useful in producing medicines for
anticancer therapy or immunological reaction. Such drugs are more specific
with enhanced activity and less toxic. This sequence represents a fusion
construct composed of VEGF and SEA.

Query Match 82.6%; Score 1023; DB 9; Length 369;
Best Local Similarity 82.0%; Pred. No. 6.8e-94;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
SQ Sequence 369 AA;
1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLPKGFPTG 60
137 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLPKGFPTD 196
61 HPWYNDLLVGLSKDATNKYGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120

08-SEP-2005 (first entry)
VEGF-SEA fusion construct protein SEQ ID NO 4.
fusion protein; cell proliferation; antigen; cancer;
endothelial growth factor; EGF; vascular endothelial growth factor; VEGF;
SEA; enterotoxin family; enterotoxin A; cytostatic; immunomodulator.
Synthetic.
WO2005061531-A1.
07-JUL-2005.
31-MAY-2004; 2004WO-CN000569.
21-DEC-2003; 2003CN-01109829.
(SUNJ/) SUN J.
Sun J;
WPI; 2005-488638/49.
N-PSDB; AEB13484.
Preparation of superantigen fusion proteins containing specific proteins
and superantigens based on recombinant expression vectors and host cells,
for producing medicines in e.g. antitumor therapy.
Example 6; SEQ ID NO 4; 33pp; Chinese.
This invention describes a novel fusion protein comprising a ligand which
can promote the growth of cancer cells and also corresponds to the
receptor of cancer-cell overexpression, as well as a specific polypeptide
which has avidity to and antagonism against the cancer cell receptor or
may interact directly with the cancer-cell surface, and a superantigen
which can induce an antitumor immunological reaction. The invention also
describes 1) a recombinant vector containing the nucleotide sequence for
the fusion protein; 2) host cells containing the recombinant vector and
3) a method of producing the fusion protein by culturing the host cells
before collecting the expressed fusion protein. The ligand is selected
from endothelial growth factor (EGF) family, vascular endothelial growth
factor (VEGF) family, basic fibroblast growth factor (bFGF) and FGF
families, transforming growth factor (TGF-alpha), interleukin-4,
interleukin-2, heregulin, interleukin-6, interleukin-13, interleukin-8,
heparin-binding EGF-like growth factor, insulin-like growth factor,
hepatocyte growth factor, platelet-derivatizing growth factor, nerve
growth factor, placenta growth factor, stem-cell growth factor,
thrombopoietin, ephrin family, erbB ligand, desialic-acid glycoprotein,
angiopoietin, clotting factor VII, urokinase-type plasminogen activator,
growth- hormone receptor hormone, growth inhibitor, chemotactic factor,
low- density lipoprotein, transferrin and other ligands associated with
cancer immunological diseases. The superantigen is chosen from SEA, SEB,
SEC, SED and SEE of *Staphylococcus aureus* enterotoxin family, SPE-A, SPE-
B and SPE-C of streptococci, especially SEA of *Staphylococcus aureus*
enterotoxin family. The fusion protein preferably contains staphylococcal
-enterotoxin A (SEA) as the superantigen and a ligand selected from EGF
and VEGF. The prepared proteins are useful in producing medicines for
anticancer therapy or immunological reaction. Such drugs are more specific
with enhanced activity and less toxic. This sequence represents a fusion
construct composed of VEGF and SEA.

Query Match 82.3%; Score 1019; DB 2; Length 233;
Best Local Similarity 81.9%; Pred. No. 8.9e-94;
Matches 190; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
SQ Sequence 233 AA;
2 EKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLPKGFPTG 61
2 EKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLPKGFPTD 61
62 PWYNDLLVGLSKDATNKYGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 121

197 HSWYNDLLVDFDSKDIYDKYGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 256
121 BEKKVPINLWIDGQKQTTVPIDKVKTSKVEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
257 BEKKVPINLWIDGQKQTTVPIDKVKTSKVEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 316
181 RGLIVFHSSEGSTSVSYDLFDAQQYPTDLLRIYRDNKTINSENHLDLYLYTT 233
317 RGLIVFHTSTEPSVNYDLFGAQQYNTLLRIYRDNKTINSENHLDLYLYTS 369

RESULT 26
AAW06738
ID AAW06738 standard; protein; 233 AA.
XX
AC AAW06738;
XX
DT 08-MAR-1997 (first entry)
XX
DE Staphylococcus enterotoxin A.
XX
KW Enterotoxin A; superantigen; antigen; cytokine; chemokine; T cell;
KW lymphocyte; monocyte; natural killer cell; gene therapy; cancer; vaccine;
KW adjuvant.
XX
OS Staphylococcus sp.
XX
PN WO9636366-A1.
XX
PD 21-NOV-1996.
XX
PF 20-MAY-1996; 96WO-US007432.
XX
PR 18-MAY-1995; 95US-00446918.
PR 23-DEC-1995; 95US-00580806.
XX
PA (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
XX
PI Dow SW, Elmslie RE, Potter TA;
XX
DR WPI; 1997-011857/01.
DR N-PSDB; AAT45699.
XX
PT Recombinant molecule encoding superantigen and opt. cytokine or
PT chemokine - controls activity of effector cells (T cells, monocytes,
PT natural killer cells), used for gene therapy of cancer.
XX
PS Example 1; Page 98-99; 131pp; English.
XX
CC A cDNA clone (AAT45699) codes for staphylococcal enterotoxin A (AAW06738)
CC superantigen. Nucleic acids encoding superantigens (see also AAW06737,
CC AAW06739), esp. truncated forms of the superantigen lacking the leader
CC peptide, can be used in the gene therapy of cancer, infectious diseases
CC and immunological disorders. The nucleic acid, optionally in combination
CC with cytokine or chemokine nucleic acids, is delivered to an animal using
CC e.g. liposomes. It acts by controlling the activity of effector cells,
CC such as T-cells, macrophages, monocytes and/or natural killer cells.
CC Localised prodn. of an effective but non-toxic amount of encoded proteins
CC allows safe treatment of the animal
XX
SQ Sequence 233 AA;

Db 62 SNWYDNLVDFDSKDIDYKYGKKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLTE 121

QY 122 EKKVPINLWIDGKQTTPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKQVOR 181

Db 122 EKKVPINLWIDGKQNTVPLETVTNKKNVTVOELDLQARRYLQEKYNLYNSDVDFGKQVOR 181

QY 182 GLIVFHSSEGSTVSVDLFDAGQGYPDTLRIYRDNKTINSENHLHDLYLTT 233

Db 182 GLIVFHTSTEPSVNYDLFGAQQGYNTLLRIYRDNKTINSENHDIYLYTS 233

RESULT 28

ADI95318

ID ADI95318 standard; protein; 233 AA.

AC ADI95318;

DT 04-NOV-2004 (first entry)

XX OSPP-related Staphylococcus aureus enterotoxin A protein.

DE immune response; overlapping synthetic peptide formulation; OSPP;

XX immunostimulant; viricide; antibacterial; antiparasitic; cytostatic;

KW vaccine; viral; bacterial; parasitic infection; prion disease;

KW neoplastic; toxin; enterotoxin A.

XX Staphylococcus aureus.

OS WO2004002415-A2.

PN 08-JAN-2004.

PD 27-JUN-2003; 2003WO-US020322.

XX 27-JUN-2002; 2002US-0392718P.

PR (DAND) DANA FARBER CANCER INST INC.

XX Ruprecht RM, Jiang S;

PI WPI; 2004-082868/08.

DR Modulating an immune response, useful for treating immune disorders, e.g.

XX viral, bacterial and parasitic infections, prion diseases, or neoplastic

PT diseases, administering to a subject an overlapping synthetic peptide

PT formulation.

XX Claim 13; SEQ ID NO 226; 175pp; English.

PS The invention relates to a novel method for modulating an immune response

XX comprising administering to a subject an overlapping synthetic peptide

CC formulation (OSPP) which comprises a combination of single chain peptides

CC corresponding to the amino acid sequence of a protein of interest. The

CC method of the invention has immunostimulant, viricide, antibacterial,

CC antiparasitic and cytostatic applications and may be useful during

CC vaccine production and for treating immune disorders including viral,

CC bacterial and parasitic infections, prion diseases, neoplastic diseases,

CC as well as providing protection against toxins. The current sequence is

CC that of the OSPP-related Staphylococcus aureus enterotoxin A protein of

CC the invention.

XX Sequence 233 AA;

SQ

Query Match 82.3%; Score 1019; DB 8; Length 233;

Best Local Similarity 81.5%; Pred. No. 8.9e-94;

Matches 190; Conservative 18; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSSELORNLSNRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60

Db 1 SEKSEINEKDLRKKSSELQGTAGNLRQIYYNEKAKTENKESHDFLOHTLLFKGFFTD 60

QY 61 HPWYDNLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120

Db 61 HSWYDNLVDFDSKDIDYKYGKKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120

QY 121 EKKVPINLWIDGKQTTPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180

Db 121 EKKVPINLWIDGKQNTVPLETVTNKKNVTVOELDLQARRYLQEKYNLYNSDVDFGKQV 180

QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPDTLRIYRDNKTINSENHLHDLYLTT 233

Db 181 RGLIVFHTSTEPSVNYDLFGAQQGYNTLLRIYRDNKTINSENHDIYLYTS 233

RESULT 28

AAW35373

ID AAW35373 standard; peptide; 233 AA.

XX AAW35373;

DT 20-APR-1998 (first entry)

XX Staphylococcus enterotoxin SEA wild-type superantigen.

DE SEE; SEA; Staphylococcus enterotoxin; superantigen; conjugate; treatment;

XX cancer; infection; autoimmune disease; antibody.

KW Staphylococcus sp.

OS WO9736932-A1.

PN 09-OCT-1997.

PD 26-MAR-1997; 97WO-SE000537.

XX 29-MAR-1996; 96SE-00001245.

PR 12-AUG-1996; 96US-00695692.

XX (PHAA) PHARMACIA & UPJOHN AB.

PA Antonsen P, Hansson J, Bjoerk P, Dohlaten M, Kalland T;

PI Abrahamson L, Forsberg G;

XX WPI; 1997-503052/46.

DR Conjugate of target seeking moiety and modified superantigen - useful for

XX activating the immune system to treat cancer, viral infections, parasitic

PT infestations and autoimmune diseases.

PT Claim 8; Page 36-37; 58pp; English.

PS This is the wild-type Staphylococcus enterotoxin SEA superantigen. This

XX SEA superantigen can be modified to be used in a novel conjugate. The

CC novel conjugate comprises a target seeking moiety and a modified wild

CC type superantigen. The modified superantigen retains its ability to

CC activate a subset of T cells, even though 1 or more wild-type amino acid

CC residues in at least 1 region which functions in determining binding to T

CC cell receptor (TCR) and activation of a subset of T cells has/have been

CC replaced. Such a modified superantigen can optionally be used as part of

CC a conjugate with a target seeking moiety, for activating the immune

CC system to treat a mammalian disease. A pharmaceutical composition can be

CC prepared comprising a modified antibody (preferably a Fab fragment fused

CC to a peptide moiety providing activation of T cells in Vbeta specific

CC manner) in which cysteines providing for interchain cysteine linkages in

CC the native antibody have been replaced (preferably by serine residues) to

CC prohibit cysteine formation. The modified wild-type superantigen is used

CC for treating cancer, viral infections, parasitic infestations and

CC autoimmune disease. The modified wild type superantigen has a lower

CC immunogenicity and reactivity with neutralising antibodies and has fewer

CC side-effects when used as a drug, compared to wild type superantigen

XX Sequence 233 AA;

SQ

Query Match 82.1%; Score 1016; DB 2; Length 233;

Best Local Similarity 81.5%; Pred. No. 1.8e-93;

Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

```
QY 1 SEKSEINEKDLRKKSSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 1 SEKSEINEKDLRKKSSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
QY 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 120
Db 61 HSWYNDLLVDFDSKDIYDKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 120
QY 121 EEKVPINLWIDGQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180
Db 121 EEKVPINLWIDGQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180
QY 121 RGLIVFHTSTEPSVNYDLFGAQOQSYNTLLRIYRDNKTINSENHIDILYLYTS 233
Db 181 RGLIVFHTSTEPSVNYDLFGAQOQSYNTLLRIYRDNKTINSENHIDILYLYTS 233

RESULT 29
AAB67338
ID AAB67338 standard; peptide; 233 AA.
XX
AC AAB67338;
XX
DT 23-APR-2001 (first entry)
XX
DE Staphylococcus aureus enterotoxin A protein.
XX
KW Tumour; cancer; immune; enterotoxin.
XX
OS Staphylococcus aureus.
XX
PN US6180097-B1.
XX
PD 30-JAN-2001.
XX
PF 30-OCT-1998; 98US-00183437.
XX
PR 03-OCT-1989; 89US-00416530.
XX
PR 17-JAN-1990; 90US-00466577.
XX
PR 17-JAN-1991; 91WO-US000342.
XX
PR 01-JUN-1992; 92US-00891718.
XX
PR 02-MAR-1993; 93US-00025144.
XX
PR 31-JAN-1994; 94US-00189424.
XX
PR 19-JUN-1995; 95US-00491746.
XX
PA (TERM/) Terman D S.
XX
PI Terman DS;
XX
DR WPI; 2001-158657/16.
XX
PT Tumor cell capable of stimulating antitumor immune reactivity in vitro or
PT in vivo comprises exogenous nucleic acids encoding a superantigen and a
PT costimulatory molecule.
XX
PS Disclosure; Fig 2; 16pp; English.
XX
CC The present invention relates to a tumour cell capable of stimulating
CC antitumor immune reactivity in vitro or in vivo contains and expresses an
CC exogenous nucleic acid molecule encoding a superantigen or its active
CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
CC molecule that activates T cells in conjunction with an antigenic
CC stimulus. The invention may be used for cancer therapy by stimulating an
CC anticancer immune response in vivo or ex vivo
XX
SQ Sequence 233 AA;
Query Match 82.1%; Score 1016; DB 4; Length 233;
Best Local Similarity 81.5%; Pred. No. 1.8e-93;
Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKSSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
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Db 1 SEKSEINEKDLRKKSSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
QY 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 120
Db 61 HSWYNDLLVDFDSKDIYDKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 120
QY 121 EEKVPINLWIDGQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180
Db 121 EEKVPINLWIDGQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180
QY 181 RGLIVFHTSTEPSVNYDLFGAQOQSYNTLLRIYRDNKTINSENHIDILYLYTT 233
Db 181 RGLIVFHTSTEPSVNYDLFGAQOQSYNTLLRIYRDNKTINSENHIDILYLYTS 233

RESULT 30
AAR45011
ID AAR45011 standard; protein; 233 AA.
XX
AC AAR45011;
XX
DT 25-MAR-2003 (revised)
DT 08-JUN-1994 (first entry)
XX
DE Staphylococcus enterotoxin SEA.
XX
KW Staphylococcus enterotoxin; SE; cancer; tumouricidal agent;
KW autoimmune disease; toxicity; Protein A; perfusion system.
XX
OS Staphylococcus aureus.
XX
FH Key Location/Qualifiers
FT Misc-difference 49
FT /note= "Given in the specification as O, no further
FT details given"
XX
PN WO9324136-A1.
XX
PD 09-DEC-1993.
XX
PF 01-JUN-1993; 93WO-US005213.
XX
PR 01-JUN-1992; 92US-00891718.
XX
PA (TERM/) Terman D S.
PA (STON/) STONE J L.
XX
PI Terman DS, Stone JL;
XX
DR WPI; 1993-405418/50.
XX
PT Use of staphylococcal enterotoxin(s) and homologues - for treating cancer
PT in a patient or for the treatment of auto-immune diseases.
XX
PS Disclosure; Fig 1; 90pp; English.
XX
CC The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
CC which may be used in the methods of the invention for treating cancer in
CC a patient. These SEs, and homologues of them, can be used as tumouricidal
CC agents for treating cancers and autoimmune disease. They exhibit
CC tumouricidal activity and toxicity identical to that observed for the
CC Protein A perfusion system. They may be administered by i.v. injection.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 233 AA;
Query Match 81.8%; Score 1013; DB 2; Length 233;
Best Local Similarity 81.5%; Pred. No. 3.6e-93;
Matches 190; Conservative 16; Mismatches 27; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKSSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
```

1 SEKSEINEKDLRKSELQCTALGNLKQIYYVNEKAKTENKESHQDLXHTILFKGFFTD 60
61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNRLLT 120
61 HSWYNDLLVDFDSKDVIYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNRLLT 120
121 BEKKVPINLWIDGKQTTPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
121 BEKKVPINLWIDGKQNTVPLETVTKNKNVTVOELDQARRYLQEKYKLYNSDVFEGKVQ 180
181 RGLIVFHSSEGSTVSYDLFDAQGYQPTDLLRIYRDNKTINSENHLIDLYLTT 233
181 RGLIVFHTSTEPSVNYDLFGAQGYQNTLLRIYRDNKTINSENHMHIDIVLYTS 233

RESULT 31
ABU79068
ID ABU79068 standard; protein; 257 AA.
XX
AC ABU79068;
XX
DT 18-JUN-2003 (first entry)
XX
DE S. aureus SEA (staphylococcus enterotoxin A) protein.
XX
KW Superantigen; SAG; staphylococcal enterotoxin; tumour; cancer; apoptosis;
KW Gene therapy; mammalian cell receptor; tumour associated lipid; anergy;
KW T cell; antigen presenting cell; tumouricidal immunocyte; cytostatic;
KW APC; antitumour.
XX
OS Staphylococcus aureus.
XX
XX
XX US2002177551-A1.
XX
XX 28-NOV-2002.
XX
XX 30-MAY-2001; 2001US-00870759.
XX
XX 31-MAY-2000; 2000US-0208128P.
XX
XX (TERM/) TERMAN D S.
XX
XX Terman DS;
XX
XX WPI; 2003-361759/34.
XX
XX N-PSDB; ACA64694.
XX
XX
XX A mammalian cell receptor, useful in the treatment of cancer by binding
XX to tumor associated lipids where the binding induces anergy or apoptosis
XX in T cells and antigen presenting cells.
XX
XX Disclosure; Page; 167pp; English.

The invention relates to a mammalian cell receptor, useful in the
treatment of cancer, which binds to tumour associated lipids and induces
anergy or apoptosis in the T cells and antigen presenting cells (APCs).
Also included are a mammalian cell useful in the treatment of cancer
where the receptor which binds tumour associated lipids and induces
cellular inactivation or death is deleted or functionally deactivated,
producing (M1) a tumouricidal immunocyte population in vivo in a mammal
(by allowing tumour associated lipids to contact immunocytes in which
receptors for immunosuppressive fatty acids, ceramides, glycolipids,
sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
deleted), a construct useful in the treatment of cancer comprising a
superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell
useful in the treatment of cancer (where an adaptor protein which
inhibits T cell activation by tumour associated antigens is deleted or
functionally deactivated), a composition useful in the treatment of
cancer (comprising a lipid raft conjugated to a superantigen), producing
(M2) a tumouricidal immunocyte population ex vivo in a mammal (by
allowing tumour associated lipids to contact immunocytes, in which
receptors for the lipids are inactivated or deleted to produce a

tumouricidal immunocyte population, and administering the tumouricidally
activated immunocytes to the host), producing (M3) a tumouricidal APC
population ex vivo in a mammal (by allowing a tumour associated lipid to
contact APCs, in which receptors for the tumour associated lipids are
inactivated or deleted to produce a tumouricidally activated population,
and administering APCs to the host), producing a tumouricidal T cell
population ex vivo in a mammal) by allowing a tumour associated lipids to
contact T cells, in which adaptor proteins, which inhibit T cell
activation by tumour associated antigens, are deleted or functionally
deactivated to produce a tumouricidal population of T cells, and
administering the tumouricidally activated T cells to the host, or
allowing a superantigen-lipid raft to contact T cells ex vivo, and
administering the tumouricidally activated T cells to the host), treating
(M5) cancer in a mammal (by administering a lipid binding molecule which
binds immunosuppressive tumour associated lipids in vivo), producing (M6)
a tumouricidal T cell population in vivo in a mammal (by allowing a
tumour associated antigen to contact immunocytes in which adaptor
proteins which inhibit T cell activation by tumour associated antigens
are deleted or functionally deactivated) and producing (M7) a
tumouricidal T cell population ex vivo in a mammal comprising allowing a
superantigen-lipid raft conjugate to contact immunocytes in vivo. The
receptors, methods and compositions are useful for treating cancers and
tumours. Bacterial superantigens are co-administered or administered as
fusion constructs with anti-tumour proteins or motifs. The present
sequence represents a bacterial superantigen protein (e.g. a
staphylococcal enterotoxin). Note: The sequence data for this patent did
not form part of the printed specification, but was obtained in
electronic format from the US patent office website at
"seqdata.uspto.gov/sequence.html?docID=20020177551"

Query Match 81.8%; Score 1013; DB 6; Length 257;
Best Local Similarity 81.5%; Pred. No. 4.1e-93;
Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

1 SEKSEINEKDLRKSELQARNALSNLRQIYYVNEKAITENKESDDQFLENTLLFKGFFTG 60
25 SEKSEINEKDLRKSELQALGNLKQIYYVNEKAKTENKESHQDLQHTILFKGFFTN 84
61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNRLLT 120
85 HSWYNDLLVDFDSKDVIYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNRLLT 144
121 BEKKVPINLWIDGKQTTPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
145 BEKKVPINLWIDGKQNTVPLETVTKNKNVTVOELDQARRYLQEKYKLYNSDVFEGKVQ 204
181 RGLIVFHSSEGSTVSYDLFDAQGYQPTDLLRIYRDNKTINSENHLIDLYLTT 233
205 RGLIVFHTSTEPSVNYDLFGAQGYQNTLLRIYRDNKTINSENHMHIDIVLYTS 257

RESULT 32
ADP43288
ID ADP43288 standard; protein; 257 AA.
XX
XX ADP43288;
XX
XX 12-FEB-2004 (first entry)
XX
XX Staphylococcal enterotoxin A polypeptide seq id 8.
XX
KW receptor; lipid-based tumour associated antigen; cytostatic;
KW antimicrobial; gene therapy; neoplastic disease; tumour; cancer;
KW infectious disease; Staphylococcal enterotoxin A; SEA; enterotoxin A.
XX
OS Staphylococcus.
XX
XX US2003157113-A1.
XX
XX 21-AUG-2003.
XX

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PF 28-DEC-2000; 2000US-00751708.
XX
XX 28-DEC-1999; 99US-0173371P.
XX
XX (TERM/) Terman D S.
XX
XX Terman DS;
XX
XX WPI; 2003-787326/74.
XX
XX New receptor in a mammalian cell that inhibits regular activation by
XX receptors specific for lipid-based tumor associated antigens, useful for
XX treating a neoplastic disease or tumor, and infectious diseases.
XX
XX Example 3; SEQ ID NO 8; 151pp; English.
XX
XX The invention describes a receptor in a mammalian cell that inhibits
XX regular activation by receptors specific for lipid-based tumor
XX associated antigen. The receptor has cytostatic and antimicrobial
XX properties and is suitable for use in gene therapy. The receptors,
XX methods and compositions are useful for treating a neoplastic disease or
XX tumor (cancer), and infectious diseases. This is the amino acid sequence
XX of an enterotoxin superantigen polypeptide the DNA encoding which can be
XX transfected in to a cell alone or with DNA encoding a cell surface moiety
XX to generate antitumor immunity.
XX
XX Sequence 257 AA;
XX
Query Match 81.8%; Score 1013; DB 7; Length 257;
Best Local Similarity 81.5%; Pred. No. 4.1e-93;
Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFPTG 60
Db 25 SEKSEINEKDLRKKSSELQNALGNLQIYYNEKAKTENKESHDLQHTILFKGFPTN 84
QY 61 HPWYNLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNLLVDFDSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKKVPINLWIDGKQTPVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKKVPINLWIDGKQNTVPLETVKTNKKNVTVOELDLQARRYLOEKYNLNSDVFQKVQ 204
QY 181 RGLIVFHSSSGSTVSYDLFDAQGYPTDLLRIYRDNKTINSENHLIDLYLYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQGQNSNTLLRIYRDNKTINSENHNHIDLYLYTS 257
RESULT 33
AEA02982
ID AEA02982 standard; protein; 257 AA.
XX
XX AC AEA02982;
XX
XX 28-JUL-2005 (first entry)
XX
XX Staphylococcal enterotoxin A (SEA) amino acid sequence SEQ ID NO:8.
XX
XX tumor; neoplasm; gene therapy; immunotherapy; cytostatic;
XX Staphylococcal enterotoxin A.
XX
XX Staphylococcus sp.
XX
XX US2005112141-A1.
XX
XX 26-MAY-2005.
XX
XX 08-SEP-2004; 2004US-00937758.
XX
XX 30-AUG-2000; 2000US-00650884.
XX
XX (TERM/) Terman D S.
XX
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XX
XX Terman DS;
XX
XX WPI; 2005-394926/40.
XX
XX N-PSDB; AEA02981.
XX
XX New composition for treating a tumor or neoplastic disease in a subject
XX comprises conjugates comprising superantigen polypeptides or nucleic
XX acids with other molecules that produce a tumoricidal response.
XX
XX Example 3; SEQ ID NO 8; 125pp; English.
XX
XX The invention relates to a composition for treating a tumor or neoplastic
XX disease in a subject. Also described: (1) a mammalian cell comprising an
XX exogenous nucleic acid encoding a superantigen expressed in the cell,
XX which cell also produces or expresses all alpha-anomers of the
XX monoglycosylceramide or diglycosylceramide, where expression of the
XX superantigen and the mono- or diglycosylceramide is capable of eliciting
XX an antitumor immune response in a mammal into which the cell is
XX introduced; (2) treating a tumor or neoplastic disease in a subject; (3)
XX preparing a population of immunotherapeutic T or natural killer T (NKT)
XX cells useful to treat a tumor or neoplastic disease in a subject; (4) an
XX apoptotic cell preparation or lysate useful for treating a tumor or
XX neoplastic disease in a subject, comprising a cell population that has
XX been transfected with naked DNA encoding a superantigen, and treated to
XX undergo apoptosis or lysis; and (5) a cell that has ingested or been
XX transfected with the above apoptotic preparation or lysate, thus,
XX rendering the cell effective in presenting material expressed from
XX transfecting nucleic acid or material ingested to the immune system of a
XX mammal to elicit an anti-tumor immune response. The composition and
XX methods are useful for treating tumors or neoplastic diseases. The
XX present sequence represents a Staphylococcal enterotoxin A (SEA) protein
XX sequence, which is used in an example from the present invention. Note -
XX The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from the
XX USPTO web site.
XX
XX Sequence 257 AA;
XX
Query Match 81.8%; Score 1013; DB 9; Length 257;
Best Local Similarity 81.5%; Pred. No. 4.1e-93;
Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFPTG 60
Db 25 SEKSEINEKDLRKKSSELQNALGNLQIYYNEKAKTENKESHDLQHTILFKGFPTN 84
QY 61 HPWYNLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNLLVDFDSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKKVPINLWIDGKQTPVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKKVPINLWIDGKQNTVPLETVKTNKKNVTVOELDLQARRYLOEKYNLNSDVFQKVQ 204
QY 181 RGLIVFHSSSGSTVSYDLFDAQGYPTDLLRIYRDNKTINSENHLIDLYLYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQGQNSNTLLRIYRDNKTINSENHNHIDLYLYTS 257
RESULT 34
ABB76234
ID ABB76234 standard; protein; 233 AA.
XX
XX AC ABB76234;
XX
XX 09-AUG-2002 (first entry)
XX
XX Staphylococcus aureus enterotoxin A.
XX
XX Enterotoxin A; SEA; superantigen; antigen; tumour; cancer; antitumour;
XX therapy.
XX
```

OS Staphylococcus aureus.

XX Key Location/Qualifiers

FT Misc-difference 49 /note= "amino acid residue given as 'O' in the

FT specification"

XX

PN US2002051765-A1.

XX

PD 02-MAY-2002.

XX

XX 19-DEC-2000; 2000US-00741503.

XX

PR 03-OCT-1989; 89US-00418530.

PR 17-JAN-1990; 90US-00466577.

PR 17-JAN-1991; 91WO-US000342.

PR 01-JUN-1992; 92US-00891718.

PR 02-MAR-1993; 93US-00025144.

PR 31-JAN-1994; 94US-00189424.

PR 19-JUN-1995; 95US-00491746.

XX

PA (TERM/) Terman D S.

XX

XX Terman DS;

XX

XX WPI; 2002-415198/44.

DR

XX Reagent for treating cancer without the need for e.g. radiotherapy,

FT comprises a specific V beta subset of T cells sensitized to a growing

PT tumor and stimulated with superantigens.

PT

XX Disclosure; Fig 2; 17pp; English.

XX

XX The present sequence is the protein sequence of enterotoxin A (SEA) of

CC Staphylococcus aureus. Similarity is shown, in several stretches of

CC sequence, between staphylococcal enterotoxins, streptococcal pyrogenic

CC exotoxins and staphylococcal exfoliative toxins (see ABB76234-44). In the

CC present invention, synthetic polypeptides useful in tumour therapy and in

CC blocking or destroying autoreactive T and B lymphocyte populations are

CC characterised by substantial structural homology to staphylococcal

CC enterotoxin A and enterotoxin B, and to streptococcal pyrogenic

CC exotoxins, with statistically significant sequence homology and

CC similarity (Z value of Lipman and Pearson algorithm in Monte Carlo

CC analysis exceeding 6) to include alignment of cysteine residues and

CC similar hydropathy profiles. These superantigens are used to treat solid

CC tumours, including their metastases, without radiation, surgery or

CC standard chemotherapeutic agents. A claimed method of human cancer

CC treatment involves contacting haematopoietic cells from a patient with

CC one or more superantigens ex vivo to generate stimulated cells, selecting

CC a specific V beta subset of cells, and reintroducing these cells into the

CC patient to induce an in vivo therapeutic, tumouricidal reaction

XX

SQ Sequence 233 AA;

Query Match 81.1%; Score 1004; DB 5; Length 233;

Best Local Similarity 81.1%; Pred.No. 2.9e-92; Indels 0; Gaps 0;

Matches 169; Conservative 16; Mismatches 28; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLFLKGFFTG 60

DB 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLFLKGFFTD 60

QY 61 HPYNDLLVDSKDATNKKYKGVLDLYGAYGYCQAGGTPNKTCMYGGVTLHDNRRLT 120

DB 61 HSWYNDLLVDFDSKDIYDKYKGVLDLYGAYGYCQAGGTPNKTCMYGGVTLHDNRRLT 120

QY 121 EEKKVPINLWIDGQKTVPTIDKVKTSKEVTVQELDQARHYLHGKFLYNSDSFGKVKQ 180

DB 121 EEKKVPINLWIDGQKTVPTIDKVKTSKEVTVQELDQARHYLHGKFLYNSDSFGKVKQ 180

QY 181 RGLIVFHSSEGSTVSYDLFDAQQOYPTDLLRIYRDNKNTINSENLHIDLXYTT 233

DB 181 RGLIVFHTSTEPSVNYDLFQAQOYSNTLLRIYRDNKNTINSENLHIDLXYTS 233

RESULT 35

ABB79501

ID ABB79501 standard; protein; 257 AA.

XX

AC ABB79501;

XX

DT 23-SEP-2002 (first entry)

XX

DE Staphylococcal enterotoxin A vaccine, periplasmic (A489270P).

KW Enterotoxin A; superantigen; antigen; toxin; vaccine; A489270P;

KW attenuation; mutant; mutein.

XX

OS Staphylococcus sp.

XX Synthetic.

FH Key Location/Qualifiers

FT Peptide 1..25

FT Protein /label= Signal_peptide

FT /label= Mature_protein

FT Misc-difference 72 /note= "wild-type Leu substituted by Arg"

FT Misc-difference 94 /note= "wild-type Asp substituted by Arg"

FT Misc-difference 116 /note= "wild-type Tyr substituted by Ala"

XX

PN US6399332-B1.

XX

PD 04-JUN-2002.

XX

PF 01-SEP-1998; 98US-00144776.

XX

PR 25-JUN-1997; 97US-00882431.

XX

PA (USSA) US SEC OF ARMY.

PI Ulrich RG, Olson MA, Bavari S;

DR WPI; 2002-546281/58.

DR N-PSDB; ABB84222.

XX

XX Novel isolated and purified superantigen toxin DNA fragment which has

PT been genetically altered, useful for producing vaccine for treatment of

PT superantigen toxin-associated bacterial diseases.

XX

PS Claim 4; Col 33-35; 46pp; English.

XX

CC The present sequence is the protein sequence of staphylococcal

CC enterotoxin A (SEA) vaccine, periplasmic (A489270P). The vaccine

CC comprises 3 amino acid substitutions introduced into the SEA sequence:

CC L48R, Y89A and D70R. These mutations reduce the binding of the toxin to

CC major histocompatibility complex (MHC) Class II and/or T cell receptors.

CC The full-length expressed product is secreted into the periplasmic space

CC of Escherichia coli host cells, and the leader peptide is recognised and

CC cleaved by a native mechanism. The vaccine is used to protect against

CC superantigen toxin infections. Superantigen attributes are absent, but

CC the superantigen is effectively recognised by the immune system and an

CC appropriate antibody response is produced. In examples from the

CC invention, attenuated superantigen toxins were shown to protect animals

CC against challenge with wild-type toxin. Methods of producing and using

CC the altered superantigen toxins as vaccines, and in diagnosis and

CC therapy, are provided. A multivalent vaccine consisting of altered

CC superantigen toxins from SEA, SEB, SEC-1, TSST-1 and streptococcal SPEA

CC is predicted to provide protective immunity against the majority of

CC bacterial superantigen toxins

XX

SQ Sequence 257 AA;

Query Match 80.8%; Score 1000; DB 5; Length 257;

Best Local Similarity 80.7%; Pred. No. 8.3e-92;
Matches 188; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSSELQNALSNLROIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKSSELQNALSNLROIYYNEKAITENKESDDOFLNTLLFKGFFTG 84
QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNLLVRFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTPIDKVKTSKKEVTVQELDLQARHYLHGKGLYNSDSFGKVKQ 180
DB 145 EEKVPINLWIDGKQTPIDKVKTSKKEVTVQELDLQARHYLHGKGLYNSDSFGKVKQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQOQYPTLLRIYRDNKTINSENHLIDLYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFQAQOQSYNTLLRIYRDNKTINSENHIDLYLYTS 257

RESULT 36
ABU10081
ID ABU10081 standard; protein; 257 AA.
AC ABU10081;
XX
DT 11-AUG-2003 (first entry)
XX
DE Staphylococcal enterotoxin A #1.
KW Enterotoxin A; superantigen-associated bacterial infection; vaccine;
KW superantigen toxin.
XX
OS Staphylococcus sp.
XX
PN US2003009015-A1.
XX
PD 09-JAN-2003.
XX
PF 25-JUN-1997; 97US-00882431.
XX
PR 25-JUN-1997; 97US-00882431.
XX
PA (ULRI/) ULRICH R G.
PA (OLSO/) OLSON M A.
PA (BAVA/) BAVARI S.
XX
PI Ulrich RG, Olson MA, Bavari S;
XX
DR WPI; 2003-401542/38.
DR N-PSDB; ACA61177.
XX
PT New superantigen toxin and/or DNA fragment with an altered binding of the
PT encoded altered toxin to either MHC class II or T cell antigen receptor,
PT useful for treating or ameliorating superantigen-associated bacterial
PT infection.
XX
PS Claim 10; Page 18-19; 50pp; English.
XX
CC The invention relates to an isolated and purified superantigen toxin
CC and/or DNA fragment, which has been altered so that the binding of the
CC encoded toxin to either major histocompatibility complex (MHC) class II
CC or T cell antigen receptor is altered. The superantigen toxins, DNA
CC fragments, and vaccines are useful for treating or ameliorating
CC superantigen-associated bacterial infection. The DNA fragments are
CC particularly useful for producing vaccine against superantigen toxin
CC infections. The transformed host cells are useful for analysing the
CC effectiveness of drugs and agents that affect the binding of
CC superantigens to MHC class II or T-cell antigen receptors. The present
CC sequence represents the amino acid sequence of staphylococcal enterotoxin
CC A #1
XX
SQ Sequence 257 AA;

Query Match 80.8%; Score 1000; DB 6; Length 257;
Best Local Similarity 80.7%; Pred. No. 8.3e-92;
Matches 188; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSSELQNALSNLROIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKSSELQNALSNLROIYYNEKAITENKESDDOFLNTLLFKGFFTG 84
QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNLLVRFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTPIDKVKTSKKEVTVQELDLQARHYLHGKGLYNSDSFGKVKQ 180
DB 145 EEKVPINLWIDGKQTPIDKVKTSKKEVTVQELDLQARHYLHGKGLYNSDSFGKVKQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQOQYPTLLRIYRDNKTINSENHLIDLYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFQAQOQSYNTLLRIYRDNKTINSENHIDLYLYTS 257

RESULT 37
ABU62324
ID ABU62324 standard; protein; 257 AA.
AC ABU62324;
XX
DT 27-AUG-2003 (first entry)
XX
DE S. aureus periplasmic enterotoxin A mutant #1.
XX
KW SEA; staphylococcal enterotoxin A; mutein; mutant; vaccine;
KW superantigen toxin; MHC; superantigen-associated bacterial infection;
KW bacterial infection; antibacterial.
XX
OS Staphylococcus aureus.
OS Synthetic.
XX
PH Location/Qualifiers
FT Peptide 1..24
FT /label= Signal_peptide
FT Protein 25..257
FT /label= Mature_SEA_mutant #1
FT Misc-difference 66
FT /note= "Wild-type Leu substituted by Glu"
FT Misc-difference 72
FT /note= "Wild-type Leu substituted by Arg"
FT Misc-difference 94
FT /note= "Wild-type Asp substituted by Arg"
FT Misc-difference 113
FT /note= "Wild-type Tyr substituted by Gly"
FT Misc-difference 116
FT /note= "Wild-type Tyr substituted by Ala"
XX
PN US2003036644-A1.
XX
PD 20-FEB-2003.
XX
PF 26-NOV-2001; 2001US-00002784.
XX
PR 25-JUN-1997; 97US-00882431.
PR 01-SEP-1998; 98US-00144776.
XX
PA (ULRI/) ULRICH R G.
XX
PI Ulrich RG;
XX
DR WPI; 2003-492125/46.
DR N-PSDB; ACD28894.
XX
PT New superantigen toxin DNA fragment, useful for preparing a composition
PT for treating or preventing bacterial infection.

XX PS Disclosure; Page 22-23; 68pp; English.

XX CC The invention relates to an isolated and purified superantigen toxin DNA fragment is altered so that binding of the encoded altered toxin to either the MHC class II or T cell antigen receptor is altered. Also included are a recombinant DNA construct (comprising a vector and an isolated and purified altered superantigen toxin DNA fragment), a host cell transformed with the recombinant DNA construct, producing altered superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin) superantigen toxin peptide, diagnosing superantigen-associated bacterial infection, a vaccine (comprising an altered superantigen toxin for producing antigenic and immunogenic response resulting in the protection of a mammal against superantigen-associated bacterial infection), CC treating/ameliorating a superantigen-associated bacterial infection, an antiserum isolated from individuals immunised with one or more altered TSST-1 superantigen toxin and an antibody which recognises altered TSST-1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA, SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and SPEb). The superantigen toxin DNA fragment is useful for preparing a composition for treating or preventing bacterial infection. The present CC sequence represents the L42E/L48R/D70R/Y89G/Y92A (with reference to the mature protein sequence) mutant of periplasmic SEA

XX SQ Sequence 257 AA;

Query Match 80.8%; Score 1000; DB 7; Length 257;
Best Local Similarity 80.7%; Pred. No. 8.3e-92;
Matches 188; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSSELQNALSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKSSELQNTALGNLQIYYNEKAKTENKESHDFRQHTILFKGFPTD 84

QY 61 HPWYNDLLVDLGSKDNTNKKYKGVLDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVRFDSKDIDVKKYKGVLDLYGAYAGYQCAGGTPNKTCMYGGVTLHDNNRLT 144

QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKVKQ 180
DB 145 EEKKVPINLWLDGKQNTVPLETKNKQNTVQELDLQARRYLQEKYKLYNSDVDFGKVKQ 204

QY 181 RGLIVFHSSEGSTVSYDLFDAQQYPTDLLRIYRDNKTINSENHLIDLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFQAQGYNTLLRIYRDNKTINSENHMDIYLYTS 257

RESULT 38
AAE37676
ID AAE37676 standard; protein; 257 AA.

XX AC AAE37676;

XX DT 06-OCT-2003 (first entry)

XX DE Protein #1 related to the invention.

XX KW Superantigen toxin; vaccine; infection; gene therapy.

XX OS Unidentified.

XX PN WO2003056015-A1.

XX PD 10-JUL-2003.

XX PF 26-NOV-2001; 2001WO-US046540.

XX PR 26-NOV-2001; 2001US-00002784.

XX PA (USMB-) US MEDICAL RES INST INFECTIOUS DISEASES.

XX PI Ulrich RG;

DR WPI: 2003-492125/46.
DR N-PSDB; AAD56764.

XX PT New superantigen toxin DNA fragment, useful for preparing a composition for treating or preventing bacterial infection.

XX PS Disclosure; Page 108-109; 141pp; English.

XX CC The invention provides a superantigen toxin DNA fragment which has been genetically altered such that binding of the encoded altered toxin to either the MHC class II or T cell antigen receptor is disrupted or altered. DNA fragments of the invention are useful in the production of CC vaccines against bacterial superantigen toxin infections. They are also CC useful in gene therapy. The present sequence is a protein related to the CC invention

XX SQ Sequence 257 AA;

Query Match 80.8%; Score 1000; DB 7; Length 257;
Best Local Similarity 80.7%; Pred. No. 8.3e-92;
Matches 188; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSSELQNALSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKSSELQNTALGNLQIYYNEKAKTENKESHDFRQHTILFKGFPTD 84

QY 61 HPWYNDLLVDLGSKDNTNKKYKGVLDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVRFDSKDIDVKKYKGVLDLYGAYAGYQCAGGTPNKTCMYGGVTLHDNNRLT 144

QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKVKQ 180
DB 145 EEKKVPINLWLDGKQNTVPLETKNKQNTVQELDLQARRYLQEKYKLYNSDVDFGKVKQ 204

QY 181 RGLIVFHSSEGSTVSYDLFDAQQYPTDLLRIYRDNKTINSENHLIDLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFQAQGYNTLLRIYRDNKTINSENHMDIYLYTS 257

RESULT 39
ADY93171
ID ADY93171 standard; protein; 257 AA.

XX AC ADY93171;

XX DT 02-JUN-2005 (first entry)

XX DE Bacterial superantigen toxin related protein, SEQ ID NO: 2.

XX KW Vaccine; toxin; diagnosis; bacterial infection; antibacterial; infection; antigen.

XX OS Unidentified.

XX PN US2005064526-A1.

XX PD 24-MAR-2005.

XX PF 29-JAN-2004; 2004US-00767687.

XX PR 25-JUN-1997; 97US-00882431.

XX PA (ULRI/) ULRICH R G.
PA (OLSO/) OLSON M A.
PA (BAVA/) BAVARI S.

XX PI Ulrich RG, Olson MA, Bavari S;

XX WPI: 2005-252679/26.
DR N-PSDB; ADY93170.

XX PT Novel altered superantigen toxin that alters binding of encoded altered toxin to major histocompatibility complex class II or T cell antigen

PT receptor, useful for preparing vaccine for treating superantigen-
PT associated bacterial infection.
PS Disclosure; SEQ ID NO 2; 51pp; English.
XX
XX
CC The present invention relates to a altered superantigen toxin that alters
CC binding of encoded altered toxin to major histocompatibility complex
CC class II or T cell antigen receptor. The invention is useful for
CC preparing vaccine for treating superantigen-associated bacterial
CC infection. The present sequence is the bacterial superantigen toxin
CC related protein.
XX
SQ Sequence 257 AA;

Query Match 80.8%; Score 1000; DB 9; Length 257;
Best Local Similarity 80.7%; Pred. No. 8.3e-92;
Matches 188; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOLNALSNLQIYYINEKAITENKESDDQPLENTLLFKGFTTG 60
DB 25 SEKSEINEKDLRKSELOLNALSNLQIYYINEKAITENKESDDQPLENTLLFKGFTTG 84
QY 61 HPWYNDLLVLDGSKDATNKYKGVLDYGYAGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVLDGSKDIIVDKYKGVLDYGYAGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHLYLHGKFGLYNSDSFGKQV 180
DB 145 EEKVPINLWIDGKQNTVPLETVKTNKNTVQELDLQARYLQEKYLNLYNSDVFQKQV 204
QY 181 RGLIVFHSSEGSTVSVDLFDQAQGYPTDRLRIYRDNKTINSENHLIDLYLTT 233
DB 205 RGLIVFHTSTEPSVNYDLFQAQGYSNLTLRIYRDNKTINSENHIDILYLYTS 257

RESULT 40
AAY54463
ID AAY54463 standard; protein; 233 AA.
XX
AC AAY54463;
XX
XX
DT 25-APR-2000 (first entry)
DE Amino acid sequence of a mutant Staphylococcal enterotoxin A.
XX
KW Mutant; SEA gene; enterotoxin A; SEB gene; nucleic acid vaccine;
KW Venezuelan equine encephalitis virus; vaccine vector; vaccine;
KW Staphylococcal intoxication; Staphylococcus exotoxin.
XX
OS Staphylococcus aureus.
XX
XX
PH Key Location/Qualifiers
FT Misc-difference 2 /note= "Glu encoded by AGAA"
FT FT Misc-difference 4
FT FT Misc-difference 4 /note= "Ser encoded by C"
XX
XX
PN W0200002523-A2.
XX
XX
PD 20-JAN-2000.
XX
XX
XX 09-JUL-1999; 99WO-US015569.
XX
XX
XX 10-JUL-1998; 98US-0092416P.
XX
XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
XX
XX Lee JS, Pushko P, Smith JF, Ulrich RG;
XX
XX WPI; 2000-160826/14.
DR N-PSDB; AAZ45833.
XX
XX New DNA construct useful as vaccines against enterotoxins of

PT Staphylococcus aureus which causes gastrointestinal distress, or toxic
PT shock syndrome.
PS Disclosure; Page 28; 30pp; English.
XX
XX
CC The present sequence is represents a mutant Staphylococcal enterotoxin A.
CC It is encoded by a mutant SEA gene. The mutant gene product is unable to
CC bind to the MHC on T-cells, and so is non-toxic. Mutant SEA and SEB genes
CC were inserted into a Venezuelan equine encephalitis (VEE) replicon
CC vector, to produce vaccine vectors. The mutant gene product is unable to
CC bind to the MHC on T-cells, and so is non-toxic. Self-replicating RNA
CC derived from the recombinant VEE vectors can be used as a nucleic acid
CC vaccine, or to transfect cells along with RNA from helper plasmids. The
CC recombinant proteins produced are used as vaccines for providing immunity
CC against Staphylococcal intoxication or as a diagnostic tool for detection
CC of Staphylococcus exotoxin. The transformed host cells are used to
CC analyse the effectiveness of drugs and agents which inhibit S. aureus
CC exotoxins or release of exotoxins. Infectious alpha-virus particles
CC comprising the mutant SEA or SEB genes are used for providing immunity
CC against Staphylococcal exotoxins by generating a protective immune
CC reaction in humans or animals. The vaccines are used to reduce disease
CC symptoms or reduce severity of disease caused by enterotoxins of S.
CC aureus
XX
SQ Sequence 233 AA;

Query Match 80.5%; Score 996; DB 3; Length 233;
Best Local Similarity 80.6%; Pred. No. 1.8e-91;
Matches 187; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKSELOLNALSNLQIYYINEKAITENKESDDQPLENTLLFKGFTTG 61
DB 2 EKSEINEKDLRKSELOLNALSNLQIYYINEKAITENKESDDQPLENTLLFKGFTTG 61
QY 62 PWYNDLLVLDGSKDATNKYKGVLDYGYAGYQCAGGTPNKTCMYGGVTLHDNNRLTE 121
DB 62 SWYNDLLVLDGSKDIIVDKYKGVLDYGYAGYQCAGGTPNKTCMYGGVTLHDNNRLTE 121
QY 122 EKVVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHLYLHGKFGLYNSDSFGKQV 181
DB 122 EKVVPINLWIDGKQNTVPLETVKTNKNTVQELDLQARYLQEKYLNLYNSDVFQKQV 181
QY 182 GLIVFHSSEGSTVSVDLFDQAQGYPTDRLRIYRDNKTINSENHLIDLYLTT 233
DB 182 GLIVFHTSTEPSVNYDLFQAQGYSNLTLRIYRDNKTINSENHIDILYLYTS 233

RESULT 41
ABB79502
ID ABB79502 standard; protein; 233 AA.
XX
AC ABB79502;
XX
DT 23-SEP-2002 (first entry)
DE Staphylococcal enterotoxin A vaccine, cytoplasmic (A489270C).
XX
XX Enterotoxin A; superantigen; antigen; toxin; vaccine; A489270C;
KW attenuation; mutant; mutein.
XX
OS Staphylococcus sp.
OS Synthetic.
XX
XX
PH Key Location/Qualifiers
FT Misc-difference 1 /note= "encoded by AT, apparent frameshift"
FT FT Misc-difference 48
FT FT Misc-difference 48 /note= "wild-type Leu substituted by Arg"
FT FT Misc-difference 70 /note= "wild-type Asp substituted by Arg"
FT FT Misc-difference 92 /note= "wild-type Tyr substituted by Ala"
FT FT


```

QY 62 PNYNDLLVDLGSKDATNKYKGVKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
Db 62 SWYNDLLVRFDSKDIYDKYKGVKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
QY 122 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQR 181
Db 122 EKKVPINLWLDGKQNTVPLETVKTNKQNTVQELDLQARRYLQEKYKLYNSDVDFGKVQR 181
QY 182 GLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHLDLYLYTT 233
Db 182 GLIVFHTSTEPSVNYDLFQAQGYSNLTLLRIYRDNKTINSENHLDIYLYTS 233

RESULT 45
ADY93173
ID ADY93173 standard; protein; 233 AA.
XX
AC ADY93173;
XX
DT 02-JUN-2005 (first entry)
XX
DE Bacterial superantigen toxin related protein, SEQ ID NO: 4.
XX
KW Vaccine; toxin; diagnosis; bacterial infection; antibacterial; infection;
KW antigen.
XX
OS Unidentified.
XX
Key Location/Qualifiers
FH Misc-difference 1..2
FT Misc-difference 1..2 /note= "Encoded by AT"
FT
XX
PN US2005064526-A1.
XX
XX 24-MAR-2005.
XX
XX 29-JAN-2004; 2004US-00767687.
XX
XX 25-JUN-1997; 97US-00882431.
XX
XX {ULRI//} ULRICH R G.
PA {OLSO//} OLSON M A.
PA {BAVA//} BAVARI S.
XX
PI Ulrich RG, Olson MA, Bavari S;
XX
XX WPI; 2005-252679/26.
DR N-PSDB; ADY93172.
XX
XX Novel altered superantigen toxin that alters binding of encoded altered
PT toxin to major histocompatibility complex class II or T cell antigen
PT receptor, useful for preparing vaccine for treating superantigen-
PT associated bacterial infection.
XX
XX Disclosure; SEQ ID NO 4; 51pp; English.
XX
XX The present invention relates to a altered superantigen toxin that alters
CC binding of encoded altered toxin to major histocompatibility complex
CC class II or T cell antigen receptor. The invention is useful for
CC preparing vaccine for treating superantigen-associated bacterial
CC infection. The present sequence is the bacterial superantigen toxin
CC related protein.
XX
XX Sequence 233 AA;
SQ
Query Match 80.5%; Score 996; DB 9; Length 233;
Best Local Similarity 80.6%; Pred. No. 1.8e-91;
Matches 187; Conservative 17; Mismatches 28; Indels 0; Gaps 0;
QY 2 EKSEINEKDLRKKSELQRNALNLRQIYYNNEKAITENKESDDQFLENTLLPKGFPTH 61
Db 2 EKSEINEKDLRKKSELQGTALNLRQIYYNNEKAKTENKESHDQPRQHTILPKGFPTH 61

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RESULT 46

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ABU10099
ID ABU10099 standard; protein; 233 AA.
XX
AC ABU10099;
XX
DT 11-AUG-2003 (first entry)
XX
DE Staphylococcus enterotoxin A K14E substitution mutant.
XX
KW Enterotoxin A; superantigen-associated bacterial infection; mutant;
KW superantigen toxin; vaccine; mutein.
XX
XX Staphylococcus sp.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 14
FT Misc-difference 14 /note= "Wild-type Lys substituted by Glu"
FT
XX
XX US2003009015-A1.
PN
XX
XX 09-JAN-2003.
XX
XX 25-JUN-1997; 97US-00882431.
XX
XX 25-JUN-1997; 97US-00882431.
XX
XX {ULRI//} ULRICH R G.
PA {OLSO//} OLSON M A.
PA {BAVA//} BAVARI S.
XX
XX Ulrich RG, Olson MA, Bavari S;
PI
XX
XX WPI; 2003-401542/38.
DR
XX
XX New superantigen toxin and/or DNA fragment with an altered binding of the
PT encoded altered toxin to either MHC class II or T cell antigen receptor,
PT useful for treating or ameliorating superantigen-associated bacterial
PT infection.
XX
XX Example 7; Page: 50pp; English.
XX
XX The invention relates to an isolated and purified superantigen toxin
CC and/or DNA fragment, which has been altered so that the binding of the
CC encoded toxin to either major histocompatibility complex (MHC) class II
CC or T cell antigen receptor is altered. The superantigen toxins, DNA
CC fragments, and vaccines are useful for treating or ameliorating
CC superantigen-associated bacterial infection. The DNA fragments are
CC particularly useful for producing vaccine against superantigen toxin
CC infections. The transformed host cells are useful for analysing the
CC effectiveness of drugs and agents that affect the binding of
CC superantigens to MHC class II or T-cell antigen receptors. The present
CC sequence represents the amino acid sequence of the staphylococcus
CC enterotoxin A K14E mutant. Note: The present sequence is not present in
CC the specification but was created by the indexer from the wild-type
CC staphylococcus enterotoxin A sequence (see ACA61178)
XX
XX Sequence 233 AA;
SQ

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superantigen-associated bacterial infection. The DNA fragments are particularly useful for producing vaccine against superantigen toxin infections. The transformed host cells are useful for analysing the effectiveness of drugs and agents that affect the binding of superantigens to MHC class II or T-cell antigen receptors. The present sequence represents the amino acid sequence of the staphylococcus enterotoxin A Y64A mutant. Note: The present sequence is not present in the specification but was created by the indexer from the wild-type staphylococcus enterotoxin A sequence (see ACA61178)

DR	WFI; 2000-224177/19.
XX	N-PSDB; AAZ51105.
PT	Nucleic acid encoding superantigen toxin useful as a vaccine and for diagnosis of superantigen-associated bacterial infections.
PP	
XS	Claim 7; Page 72-73; 118pp; English.
XX	The present amino acid sequence is the Staphylococcal enterotoxin A (SEA), a bacterial superantigen toxin (SAG). The coding region of the SAG toxin when altered by site directed mutagenesis, results in disruption of binding of the toxin to both the MHC class II or T-cell antigen receptor. SEA has antibacterial and cytostatic activity. This sequence is useful for the production of SEA vaccines and specific antibodies. This vaccine overcomes the disadvantages of the chemically inactivated toxoids and is designed to protect individuals against one or several related CC staphylococcal and streptococcal toxins. It is used for the diagnosis and treatment or amelioration of superantigen- associated bacterial infections
XX	
SQ	Sequence 257 AA;
	Query Match 79.4%; Score 983; DB 3; Length 257;
	Best Local Similarity 79.8%; Pred. No. 4.3e-90;
	Matches 186; Conservative 17; Mismatches 30; Indels 0; Gaps 0
QY	1 SEKSEETNEKDRLRKSELQRNALSNLRQIYYINEKATENKESDDOFLNTLLPKGFFTG 60
Db	25 SEKSEETNEKDRLRKSEKGQTALGNLKRQIYYINEKATENKESHDOFQHRTILFKGFSTD 84
QY	61 HPWYNDDLVLGSKDATNKYKGKKVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 120
Db	85 HSWNDLLVRFDSDKIYDKYKGKKVDLYGAYGAYQCAGGTENKTACMYGGVTLHDNNRLT 144
QY	121 BEKKVPINLMIDGHQTTVPDIDKVTSKKEVTVQELDLQARHYLGKFGLYNSDSFGGKVQ 180
Db	145 EEKKVPINLMIDGQNTPVLETVTNKNKVVTVQELDLQARRYLQEKYNLYNSDVDFGKVQ 204
QY	181 RGLIVFHSSSEGTSYSLDFAQGQYPTDLLRIYRDNKNTINSNLHIDLPLYTT 233
Db	205 RGLIVFHTSTEPSVNYDLFGNQGYNTLLRIYRDNKNTINSNMHIDIPLYTS 257
RESULT 50	
AAV70103	
ID	AAV70103 standard; protein; 233 AA.
XX	
AC	AAV70103;
XX	
DT	05-JUN-2000 (first entry)
XX	
DE	Mutant Staphylococcal enterotoxin A for vaccine A489270P.
XX	
KW	Superantigen toxin; SAG; Staphylococcal enterotoxin A; SEA; cytostatic;
KW	antibacterial; vaccine; MHC class II receptor; T-cell antigen receptor;
KW	antibody; toxoid; staphylococcal/streptococcal toxin; diagnosis; mutant;
KW	treatment; superantigen-associated bacterial infection; A489270P.
XX	
OS	Staphylococcus sp.
XX	
PH	Key Location/Qualifiers
FT	Protein 1. .233
FT	/label= Mature_Staphylococcal_enterotoxin_A
FT	/note= Mutant sequence without the leader peptide"
FT	Misc-difference 2
FT	/note= "Encoded by AG"
FT	Misc-difference 18
FT	/note= "Encoded by TTG"
FT	Misc-difference 48
FT	/note= "Wild type Leu substituted with Arg"
FT	Misc-difference 70
FT	/note= "Wild type Asp substituted with Arg"
FT	Misc-difference 92

FT /note= "Wild type Tyr substituted with Ala"
 FT Misc-difference 157
 FT /note= "Encoded by CTT"
 FT Misc-difference 180
 FT /note= "Encoded by CAG"
 XX
 FN WO200009154-A1.
 XX
 XX 24-FEB-2000.
 XX
 XX 13-AUG-1998; 98WO-US016766.
 XX
 XX 13-AUG-1998; 98WO-US016766.
 PR (REED-) REED ARMY INST RES WALTER.
 XX
 XX Ulrich RG, Olson MA, Bavari S;
 XX WPI; 2000-224177/19.
 DR N-PSDB; AA251106.
 XX
 XX Nucleic acid encoding superantigen toxin useful as a vaccine and for
 PT diagnosis of superantigen-associated bacterial infections.
 XX
 XX Claim 8; Page 74-76; 118pp; English.

XX The present amino acid sequence is the mutant Staphylococcal enterotoxin
 CC A (SEA), a bacterial superantigen toxin (SAG), used for the formulation
 CC of SEA vaccine A489270P. The coding region of this SAG toxin is altered
 CC by site directed mutagenesis, that results in disruption of binding of
 CC the toxin to both the MHC class II or T-cell antigen receptor. This
 CC altered SAG toxin has the leader peptide cleaved by native bacterial
 CC enzymatic mechanism and the first residue of the mature protein is
 CC encoded by the transcriptional start site (ATG). SEA has antibacterial
 CC and cytostatic activity. This sequence is useful for the production of
 CC SEA vaccines and specific antibodies. This vaccine overcomes the
 CC disadvantages of the chemically inactivated toxins and is designed to
 CC protect individuals against one or several related staphylococcal and
 CC streptococcal toxins. It is used for the diagnosis and treatment or
 CC amelioration of superantigen-associated bacterial infections
 XX
 XX Sequence 233 AA;
 SQ
 Query Match 79.0%; Score 978; DB 3; Length 233;
 Best Local Similarity 79.3%; Pred. No. 1.2e-89;
 Matches 184; Conservative 17; Mismatches 31; Indels 0; Gaps 0;
 QY 2 EKSEINEKDLRKSEKQGTALGNLQIYYNEKAKTENKESDQFLENLTLFKGFTGH 61
 DB 2 EKSEINEKDLRKSEKQGTALGNLQIYYNEKAKTENKESDQFLENLTLFKGFTGH 61
 QY 62 PWNDLLVGLSKDATNKYKGVLDYGYAGYQCAGGTENKTKACMYGGVTLHDNNRLTE 121
 DB 62 SWNDLLVGLSKDATNKYKGVLDYGYAGYQCAGGTENKTKACMYGGVTLHDNNRLTE 121
 QY 122 EKKVPINLWDGKQTTVPIDKVTSKKEVTQVQLDQARHYLHGKFLYNSDSFGGKVQR 181
 DB 122 EKKVPINLWDGKQTTVPIDKVTSKKEVTQVQLDQARHYLHGKFLYNSDSFGGKVQR 181
 QY 182 GLIVFHSSEGSTVSVDLFDAGQGVPTLLRIYRDNKTINSENHLIDLYLTT 233
 DB 182 GLIVFHSSEGSTVSVDLFDAGQGVPTLLRIYRDNKTINSENHLIDLYLTT 233

RESULT 51
 ADF89835
 ID ADF89835 standard; protein; 268 AA.
 XX ADF89835;
 XX AC
 XX ADF89835;
 DT 26-FEB-2004 (first entry)
 XX
 XX Staphylococcal enterotoxin J (SEJ) superantigen.

XX Superantigen; SAG; Staphylococcal enterotoxin; SE; SEJ; cytostatic;
 KW gene therapy; cancer.
 XX Staphylococcus sp.
 XX WO2003094846-A2.
 XX 20-NOV-2003.
 PD
 XX 08-MAY-2003; 2003WO-US014381.
 XX
 XX 08-MAY-2002; 2002US-0378988P.
 PR 15-JUN-2002; 2002US-0389366P.
 PR 28-AUG-2002; 2002US-0406697P.
 PR 29-AUG-2002; 2002US-0406750P.
 PR 01-OCT-2002; 2002US-0415310P.
 PR 02-OCT-2002; 2002US-0415400P.
 PR 09-JAN-2003; 2003US-0438686P.
 XX
 XX (TERM/) TERMAN D S.
 PA
 XX Terman DS;
 PI
 XX WPI; 2004-011997/01.
 DR
 XX Treating a subject with cancer or malignant diseases comprises
 PT intratumoral, intrathecal or intracavitary administration of an amount of
 PT a superantigen composition to the subject.
 XX
 XX Disclosure; SEQ ID NO 12; 91pp; English.
 XX
 XX The invention relates to treating a subject with cancer. The method
 CC involves administering an amount of a superantigen (SAG) composition
 CC comprising a molecule selected from: a native SAG protein; its
 CC biologically active fragment or a biologically active homologue or a
 CC biologically active fusion protein comprising the SAG or its fragment or a
 CC homologue fused to a fusion partner polypeptide or peptide. The SAG is
 CC selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic
 CC exotoxin, Y. pseudotuberculosis SAG, Mycoplasma arthritides SAG and
 CC Clostridium perfringens exotoxin. The method is useful in treating cancer
 CC or malignant diseases such as malignant pleural effusion, ascites,
 CC pericardial effusion or meningeal carcinomatosis. The present sequence
 CC represents a Staphylococcal enterotoxin J (SEJ) superantigen.
 XX
 XX Sequence 268 AA;
 SQ
 Query Match 67.0%; Score 830; DB 8; Length 268;
 Best Local Similarity 64.9%; Pred. No. 1.1e-74;
 Matches 150; Conservative 38; Mismatches 43; Indels 0; Gaps 0;
 QY 3 KSEINEKDLRKSEKQGTALGNLQIYYNEKAKTENKESDQFLENLTLFKGFTGH 62
 DB 27 KSEINEKDLRKSEKQGTALGNLQIYYNEKAKTENKESDQFLENLTLFKGFTGH 62
 QY 63 WYNDLLVGLSKDATNKYKGVLDYGYAGYQCAGGTENKTKACMYGGVTLHDNNRLTE 122
 DB 63 WYNDLLVGLSKDATNKYKGVLDYGYAGYQCAGGTENKTKACMYGGVTLHDNNRLTE 122
 QY 87 QYNDLLVGLSKDATNKYKGVLDYGYAGYQCAGGTENKTKACMYGGVTLHDNNRLTE 146
 DB 87 QYNDLLVGLSKDATNKYKGVLDYGYAGYQCAGGTENKTKACMYGGVTLHDNNRLTE 146
 QY 123 KKVPIINLWDGKQTTVPIDKVTSKKEVTQVQLDQARHYLHGKFLYNSDSFGGKVQR 182
 DB 123 KKVPIINLWDGKQTTVPIDKVTSKKEVTQVQLDQARHYLHGKFLYNSDSFGGKVQR 182
 QY 147 KKVPIINLWDGKQTTVPIDKVTSKKEVTQVQLDQARHYLHGKFLYNSDSFGGKVQR 206
 DB 147 KKVPIINLWDGKQTTVPIDKVTSKKEVTQVQLDQARHYLHGKFLYNSDSFGGKVQR 206
 QY 183 LIVFHSSEGSTVSVDLFDAGQGVPTLLRIYRDNKTINSENHLIDLYLTT 233
 DB 183 LIVFHSSEGSTVSVDLFDAGQGVPTLLRIYRDNKTINSENHLIDLYLTT 233
 QY 207 LIVFHSSEGSTVSVDLFDAGQGVPTLLRIYRDNKTINSENHLIDLYLTT 257
 DB 207 LIVFHSSEGSTVSVDLFDAGQGVPTLLRIYRDNKTINSENHLIDLYLTT 257

RESULT 52
 ABU79071
 ID ABU79071 standard; protein; 258 AA.
 XX ABU79071;
 AC ABU79071;

PT in vivo comprises exogenous nucleic acids encoding a superantigen and a
 PT costimulatory molecule.

PS Disclosure; Fig 2; 16pp; English.

XX The present invention relates to a tumour cell capable of stimulating
 CC antitumor immune reactivity in vitro or in vivo contains and expresses an
 CC exogenous nucleic acid molecule encoding a superantigen or its active
 CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
 CC molecule that activates T cells in conjunction with an antigenic
 CC stimulus. The invention may be used for cancer therapy by stimulating an
 CC anticancer immune response in vivo or ex vivo

XX Sequence 228 AA;

Query Match 53.1%; Score 657; DB 4; Length 228;
 Best Local Similarity 55.6%; Pred. No. 2.3e-57;
 Matches 125; Conservative 33; Mismatches 67; Indels 0; Gaps 0;

QY 7 INEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTHGHPWYND 66

Db 2 VKEKELHKSELSSTALNNMKHSYADKNPIIGENKSTGDOFLENTLLYKKFFTDLINFD 61

QY 67 LLVDLGSKDATNKYKGGKVDLYGAYGYOCAGTGNKTAACMGVTLHDNNRLTEKKVP 126

Db 62 LLINFNSKEMAHQHFKSKNVDVPIRYSINCYGGEIDRTACTYGGVTPHEGNKLERKKIP 121

QY 127 INLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGVLYNSDSFGKVGQGLIVF 186

Db 122 INLWINGVQKEVSLDKVQTDKNVTVOELDAQARYVQLKDLKLYNNDTLGGKIQRGKIEF 181

QY 187 HSSEGSTSVSYDLFDAQGYQPTLLRIYRDNKTINSENHLHIDLYI 231

Db 182 DSSDGSKVSYDLFDVKGDFPEKQLRIYSDNKTLSLHIDLYI 226

RESULT 58

ABB76236

ID ABB76236 standard; protein; 228 AA.

XX ABB76236;

DT 09-AUG-2002 (first entry)

XX Staphylococcus aureus enterotoxin D.

XX Enterotoxin D; SED; superantigen; antigen; tumour; cancer; antitumour;
 KW therapy.

XX Staphylococcus aureus.

XX US2002051765-A1.

XX 02-MAY-2002.

XX 19-DEC-2000; 2000US-00741503.

XX 03-OCT-1989; 89US-00416530.

XX 17-JAN-1990; 90US-00466577.

XX 17-JAN-1991; 91WO-US0000342.

XX 01-JUN-1992; 92US-00891718.

XX 02-MAR-1993; 93US-00025144.

XX 31-JAN-1994; 94US-00189424.

XX 19-JUN-1995; 95US-00491746.

XX (TERM/) TERMAN D S.

XX Terman DS;

XX WPI; 2002-415198/44.

XX Reagent for treating cancer without the need for e.g. radiotherapy,
 PT comprises a specific V beta subset of T cells sensitized to a growing

PT tumor and stimulated with superantigens.

XX Disclosure; Fig 2; 17pp; English.

XX The present sequence is the protein sequence of enterotoxin D (SED) of
 CC Staphylococcus aureus. Similarity is shown, in several stretches of
 CC sequence, between staphylococcal enterotoxins, streptococcal pyrogenic
 CC exotoxins and staphylococcal exfoliative toxins (see ABB76234-44). In the
 CC present invention, synthetic polypeptides useful in tumour therapy and in
 CC blocking or destroying autoreactive T and B lymphocyte populations are
 CC characterised by substantial structural homology to staphylococcal
 CC enterotoxin A and enterotoxin B, and to streptococcal pyrogenic
 CC exotoxins, with statistically significant sequence homology and
 CC similarity (Z value of Lipman and Pearson algorithm in Monte Carlo
 CC analysis exceeding 6) to include alignment of cysteine residues and
 CC similar hydrophathy profiles. These superantigens are used to treat solid
 CC tumours, including their metastases, without radiation, surgery or
 CC standard chemotherapeutic agents. A claimed method of human cancer
 CC treatment involves contacting haematopoietic cells from a patient with
 CC one or more superantigens ex vivo to generate stimulated cells, selecting
 CC a specific V beta subset of cells, and reintroducing these cells into the
 CC patient to induce an in vivo therapeutic, tumouricidal reaction

XX Sequence 228 AA;

Query Match 53.1%; Score 657; DB 5; Length 228;
 Best Local Similarity 55.6%; Pred. No. 2.3e-57;
 Matches 125; Conservative 33; Mismatches 67; Indels 0; Gaps 0;

QY 7 INEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTHGHPWYND 66

Db 2 VKEKELHKSELSSTALNNMKHSYADKNPIIGENKSTGDOFLENTLLYKKFFTDLINFD 61

QY 67 LLVDLGSKDATNKYKGGKVDLYGAYGYOCAGTGNKTAACMGVTLHDNNRLTEKKVP 126

Db 62 LLINFNSKEMAHQHFKSKNVDVPIRYSINCYGGEIDRTACTYGGVTPHEGNKLERKKIP 121

QY 127 INLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGVLYNSDSFGKVGQGLIVF 186

Db 122 INLWINGVQKEVSLDKVQTDKNVTVOELDAQARYVQLKDLKLYNNDTLGGKIQRGKIEF 181

QY 187 HSSEGSTSVSYDLFDAQGYQPTLLRIYRDNKTINSENHLHIDLYI 231

Db 182 DSSDGSKVSYDLFDVKGDFPEKQLRIYSDNKTLSLHIDLYI 226

RESULT 59

AAR13205

ID AAR13205 standard; protein; 228 AA.

XX AAR13205;

DT 15-OCT-1991 (first entry)

XX Staphylococcal enterotoxin D.

XX SED; cancer treatment; pyrogen; tumouricide.

XX Staphylococcus aureus.

XX WO9110680-A.

XX 25-JUL-1991.

XX 17-JAN-1990; 90US-00466577.

XX 17-JAN-1990; 90US-00466577.

XX (TERM/) TERMAN D S.

XX Terman DS;

XX WPI; 1991-237984/32.

XX
PT Treating cancer with enterotoxin from *Staphylococcus aureus* -
PT administered by IV injection, having same tumoricidal activity as
PT Staphylococcal protein A without potential toxic reactions.
XX
PS Disclosure; Fig 1; 74pp; English.
XX
CC SED was isolated and purified from *S. aureus*. It can be used for treating
CC cancer, activating cytokine mediators and procoagulant systems,
CC augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be
CC administered intravenously, optionally with ibuprofen to attenuate toxic
CC reaction to SED. Synthetic polypeptides having structural homology to
CC Staphylococcal exotoxins are claimed, provided the homology includes
CC statistically significant sequence homology, alignment of Cysteine
CC residues and similar hydropathy profiles. See AAR13203-K13211
XX
SQ Sequence 228 AA;
Query Match 52.4%; Score 649; DB 2; Length 228;
Best Local Similarity 55.1%; Pred. No. 1.5e-56;
Matches 124; Conservative 33; Mismatches 68; Indels 0; Gaps 0;
QY 7 INEKDLRKSEQLQNALSLNRQIYYNKEAITENKESDDQFLENTLLFKGFTGHPWYND 66
DB 2 VKEKELHKKSELSTALNNMKHSYADKNPIIGENKSTGQFLENTLLYKKFTDLINPED 61
QY 67 LLVDLGSKDATNKYKGGKVDLYGAYYGYQCAGTGNKTCMYGGVTLHDNNRLTEKKVP 126
DB 62 LLINFNSEKEMACHFKSKNDVYPIRYSINCYGGEIDRTACTYGGVTPHEGNLKERKIP 121
QY 127 INLWIDGKOTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQGLIVF 186
DB 122 IMLWINGQKVELSDKQTDKGNVTVOELDAQARRYLQKDLKLYNNDTLGGKIQRKIEF 181
QY 187 HSSEGSTVSYDLFDAQOQYPTLLRIYRDNKTINSENHLIDLYLY 231
DB 182 DSSDGSKVSVDLFDVKGDFPEKQLRIYSDNKTLSLSTLHLDIYLY 226
RESULT 60
ABP58459
ID ABP58459 standard; protein; 203 AA.
XX
AC ABP58459;
XX
DT 14-APR-2003 (first entry)
XX
DE Staphylococcal enterotoxin D.
XX
KW Superantigen; staphylococcal enterotoxin D; antibody; cancer; tumour;
KW cytostatic; vaccine.
XX
OS Staphylococcus sp.
XX
PN WO2003002143-A1.
XX
PD 09-JAN-2003.
XX
PF 19-JUN-2002; 2002WO-SE001188.
XX
PR 28-JUN-2001; 2001SE-00002327.
XX
PA (ACT-) ACTIVE BIOTECH AB.
XX
PI Forsberg G, Erlandsson E, Antonsson P, Walse B;
XX
DR WPI; 2003-201467/19.
XX
PT Conjugate for therapy, has bacterial superantigen with a region in T-cell
PT receptor and four regions to determine binding to class II major
PT histocompatibility complex, antibody to cancer associated cell surface
PT structure.
XX

PS
XX Example 3; Fig 3; 102pp; English.
CC The present sequence is the protein sequence of staphylococcal
CC enterotoxin D (SED). The invention provides novel conjugates (see
CC ABP58454) for human cancer therapy. These comprise an engineered
CC bacterial superantigen, such as novel SEA/E-120 (see ABP58455), and an
CC antibody moiety, such as tumour reactive antibody ST4. Bacterial
CC enterotoxins such as SEA, SEE, SED and SEH were used in the molecular
CC modelling of the engineered superantigens. The superantigens were
CC engineered to reduce seroreactivity whilst maintaining biological
CC activity and production levels. The novel conjugates were designed to
CC target and destroy cancer cells, including cancer of the lung, breast,
CC colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
XX
SQ Sequence 203 AA;
Query Match 42.2%; Score 523; DB 6; Length 203;
Best Local Similarity 49.5%; Pred. No. 6e-44;
Matches 109; Conservative 25; Mismatches 66; Indels 20; Gaps 3;
QY 12 LRKKSLEQNALSLNRQIYYNKEAITENKESDDQFLENTLLFKGFTGHPWYNDLVDL 71
DB 2 LHKSELSTALNNMKHSYADANPIIGANKSTGQFLENTLLYKAF-----LLINF 53
QY 72 GSKDATNKYKGGKVDLYGAYYGYQCAGTGNKTCMYGGVTLHDNNRLTEKKVPINLWI 131
DB 54 NSAEWAQHFKSKNDVYAIRYAAAC-----RTACTYGGVTPHAGNALKARKKIPINLWI 107
QY 132 DGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQGLIVFHSSEG 191
DB 108 IGQKSEVSLDKVQTDKGNVTVOELDAQARRYLQKDLKLYNA-----IQRGKLEFDSAAA 161
QY 192 STVSVDLFDPAQOQYPTLLRIYRDNKTINSENHLIDLYLY 231
DB 162 SKVSVDLFDVAGDFPEKQLRIYSDNKTLSLSTLHLDIYLY 201
RESULT 61
ABM70958
ID ABM70958 standard; protein; 250 AA.
XX
AC ABM70958;
XX
DT 20-NOV-2003 (first entry)
XX
DE Staphylococcus aureus protein #198.
XX
KW Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
KW enzymatic assay; antibiotic target.
XX
OS Staphylococcus aureus.
XX
PN WO200294868-A2.
XX
PD 28-NOV-2002.
XX
PF 27-MAR-2002; 2002WO-IB002637.
XX
PR 27-MAR-2001; 2001GB-00007661.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Masignani V, Mora M, Scarselli M;
XX
DR WPI; 2003-120786/11.
DR N-PSDB; ACF72518.
XX
PT New Staphylococcus aureus protein, useful as a vaccine for treating or
PT preventing Staphylococcal infection, specifically an infection caused by
XX *S. aureus*, e.g. sepsis.
XX Claim 1; SEQ ID NO 396; 49pp; English.
XX

CC of a mammal against superantigen-associated bacterial infection),
 CC treating/ameliorating a superantigen-associated bacterial infection,
 CC antisera isolated from individuals immunised with one or more altered
 CC TSST-1 superantigen toxin and an antibody which recognises altered TSST-
 CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
 CC SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and
 CC SPEb). The superantigen toxin DNA fragment is useful for preparing a
 CC composition for treating or preventing bacterial infection. The present
 CC sequence represents the *S. aureus* enterotoxin E, SEE, MHC binding region
 XX
 XX Sequence 82 AA;

Query Match 36.9%; Score 457; DB 7; Length 82;
 Best Local Similarity 100.0%; Pred. No. 7.2e-38;
 Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 43 SDDQFLENTLLPKGFTHPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPN 102
 DB 1 SDDQFLENTLLPKGFTHPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPN 60
 QY 103 KTACMYGGVTLHDNNRLTEKK 124
 DB 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 64
 ADY93188
 ID ADY93188 standard; protein; 82 AA.
 XX
 AC ADY93188;
 XX
 DT 02-JUN-2005 (first entry)
 XX
 DE Staphylococcal enterotoxin E (SEE) protein, SEQ ID NO: 19.
 XX
 KW Vaccine; toxin; diagnosis; bacterial infection; antibacterial; infection;
 KW enterotoxin.
 XX
 OS Staphylococcus aureus.
 XX
 PN US2005064526-A1.
 XX
 PD 24-MAR-2005.
 XX
 PF 29-JAN-2004; 2004US-00767687.
 XX
 PR 25-JUN-1997; 97US-00882431.
 XX
 XX {ULRI/} ULRICH R G.
 PA {OLSO/} OLSON M A.
 PA {BAVA/} BAVARI S.
 XX
 PI Ulrich RG, Olson MA, Bavari S;
 XX
 DR WPI; 2005-252679/26.
 XX
 XX Novel altered superantigen toxin that alters binding of encoded altered
 PT toxin to major histocompatibility complex class II or T cell antigen
 PT receptor, useful for preparing vaccine for treating superantigen-
 PT associated bacterial infection.
 XX
 PS Disclosure; SEQ ID NO 19; 51pp; English.
 XX
 CC The present invention relates to a altered superantigen toxin that alters
 CC binding of encoded altered toxin to major histocompatibility complex
 CC class II or T cell antigen receptor. The invention is useful for
 CC preparing vaccine for treating superantigen-associated bacterial
 CC infection. The present sequence is the Staphylococcal enterotoxin E (SEE)
 CC protein.
 XX
 SQ Sequence 82 AA;
 XX
 Query Match 36.9%; Score 457; DB 9; Length 82;

Best Local Similarity 100.0%; Pred. No. 7.2e-38;
 Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 43 SDDQFLENTLLPKGFTHPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPN 102
 DB 1 SDDQFLENTLLPKGFTHPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPN 60
 QY 103 KTACMYGGVTLHDNNRLTEKK 124
 DB 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 65
 ABU10089
 ID ABU10089 standard; protein; 82 AA.
 XX
 AC ABU10089;
 XX
 DT 11-AUG-2003 (first entry)
 XX
 DE Bacterial superantigen toxin SEA.
 XX
 KW Superantigen-associated bacterial infection; superantigen toxin; vaccine;
 KW SEA.
 XX
 OS Unidentified.
 XX
 PN US2003009015-A1.
 XX
 PD 09-JAN-2003.
 XX
 PF 25-JUN-1997; 97US-00882431.
 XX
 PR 25-JUN-1997; 97US-00882431.
 XX
 XX {ULRI/} ULRICH R G.
 PA {OLSO/} OLSON M A.
 PA {BAVA/} BAVARI S.
 XX
 PI Ulrich RG, Olson MA, Bavari S;
 XX
 DR WPI; 2003-401542/38.
 XX
 XX New superantigen toxin and/or DNA fragment with an altered binding of the
 PT encoded altered toxin to either MHC class II or T cell antigen receptor,
 PT useful for treating or ameliorating superantigen-associated bacterial
 PT infection.

Example 1; Page 35; 50pp; English.
 XX
 PS The invention relates to an isolated and purified superantigen toxin
 CC and/or DNA fragment, which has been altered so that the binding of the
 CC encoded toxin to either major histocompatibility complex (MHC) class II
 CC or T cell antigen receptor is altered. The superantigen toxins, DNA
 CC fragments, and vaccines are useful for treating or ameliorating
 CC superantigen-associated bacterial infection. The DNA fragments are
 CC particularly useful for producing vaccine against superantigen toxin
 CC infections. The transformed host cells are useful for analysing the
 CC effectiveness of drugs and agents that affect the binding of
 CC superantigens to MHC class II or T-cell antigen receptors. The present
 CC sequence represents the amino acid sequence of the bacterial superantigen
 CC toxin SEA
 XX
 SQ Sequence 82 AA;

Query Match 32.2%; Score 399; DB 6; Length 82;
 Best Local Similarity 86.6%; Pred. No. 5e-32;
 Matches 71; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 QY 43 SDDQFLENTLLPKGFTHPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPN 102
 DB 1 SHDQFLQHTILPKGFTHSWYNDLLVDFDSKDIDVKYKGVLDLYGAYGYQCAGGTPN 60


```

QY 103 KTACMYGGVTLHDNNRLTEKK 124
Db 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 66
ABU62336
ID ABU62336 standard; protein; 82 AA.
XX
AC ABU62336;
XX
DT 27-AUG-2003 (first entry)
XX
DE S. aureus enterotoxin A, SEA, MHC binding region.
XX
KW SEA; staphylococcal enterotoxin A; vaccine; superantigen toxin; MHC;
KW superantigen-associated bacterial infection; bacterial infection;
KW antibacterial.
XX
OS Staphylococcus aureus.
XX
PN US2003036644-A1.
XX
PD 20-FEB-2003.
XX
PF 26-NOV-2001; 2001US-00002784.
XX
PR 25-JUN-1997; 97US-00882431.
PR 01-SEP-1998; 98US-0014776.
XX
PA (ULRI/) ULRICH R G.
XX
PI Ulrich RG;
XX
DR WPI; 2003-492125/46.
XX
PT New superantigen toxin DNA fragment, useful for preparing a composition
PT for treating or preventing bacterial infection.
XX
PS Disclosure; Fig 3; 68pp; English.
XX
CC The invention relates to an isolated and purified superantigen toxin DNA
CC fragment is altered so that binding of the encoded altered toxin to
CC either the MHC class II or T cell antigen receptor is altered. Also
CC included are a recombinant DNA construct (comprising a vector and an
CC isolated and purified altered superantigen toxin DNA fragment), a host
CC cell transformed with the recombinant DNA construct, producing altered
CC superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
CC superantigen toxin peptide, diagnosing superantigen-associated bacterial
CC infection, a vaccine (comprising an altered superantigen toxin for
CC producing antigenic and immunogenic response resulting in the protection
CC of a mammal against superantigen-associated bacterial infection),
CC treating/ameliorating a superantigen-associated bacterial infection, an
CC antiserum isolated from individuals immunised with one or more altered
CC TSST-1 superantigen toxin and an antibody which recognises altered TSST-
CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
CC SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and
CC SPEb). The superantigen toxin DNA fragment is useful for preparing a
CC composition for treating or preventing bacterial infection. The present
CC sequence represents the S. aureus enterotoxin A, SEA, MHC binding region
XX
SQ Sequence 82 AA;

Query Match 32.2%; Score 399; DB 7; Length 82;
Best Local Similarity 86.6%; Pred. No. 5e-32;
Matches 71; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 43 SDDQFLNTLLFKGFFTHPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGTGN 102
Db 1 SHDQFLQHTILFKGFFTHSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGTGN 60

QY 103 KTACMYGGVTLHDNNRLTEKK 124
Db 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 68
AAW24299
ID AAW24299 standard; protein; 91 AA.
XX
AC AAW24299;
XX
DT 14-APR-1998 (first entry)
XX
DE Staphylococcus aureus Gene #5 polypeptide sequence 2.
XX

```


GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 15, 2006, 20:13:35 ; Search time 13.3878 Seconds
(without alignments)
1674.542 Million cell updates/sec

Title: US-09-900-766-7

Perfect score: 1238

Sequence: 1 SEKSEINEXDLKKSELQR.....RDNKTINSENHIDLYLYTT 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1238	100.0	257	2 A28179	enterotoxin E prec
2	1023	82.6	257	2 A28664	enterotoxin A prec
3	994	80.3	260	2 C89884	enterotoxin P imp
4	663	53.6	258	2 A33953	enterotoxin D prec
5	461.5	37.3	258	2 H89968	enterotoxin SeN [i
6	387.5	31.3	260	2 C89969	enterotoxin SeO [i
7	339.5	27.4	242	2 C89969	extracellular ente
8	337	27.2	240	2 G89951	extracellular ente
9	320	25.8	229	2 D89969	enterotoxin SEM [i
10	300.5	24.3	266	1 ENSAB6	enterotoxin B prec
11	295.5	23.9	251	1 S29659	enterotoxin type A pr
12	285.5	23.1	266	2 S11885	enterotoxin C3 - S
13	281.5	22.7	266	2 A60114	enterotoxin C-2 pr
14	279.5	22.6	236	2 S18783	exotoxin A precurs
15	277.5	22.4	236	2 S18783	exotoxin type A pr
16	272.5	22.0	236	2 S18786	exotoxin type A pr
17	266.5	21.5	266	1 ENSAC1	enterotoxin C-1 pr
18	255.5	20.6	258	2 G89969	extracellular ente
19	245	19.8	250	1 A26152	streptococcal pyro
20	201	16.2	157	2 A89942	hypothetical prote
21	197	15.9	136	2 A89969	enterotoxin YENT2
22	183.5	14.8	235	2 A30509	exotoxin C precurs
23	144	11.6	62	2 H89941	hypothetical prote
24	123	9.9	133	2 B89969	enterotoxin Yent1
25	113	9.1	232	2 F89807	exotoxin 13 [impor
26	107.5	8.7	234	1 XCSA51	toxic shock syndro
27	105.5	8.5	234	2 B89992	toxic shock syndro
28	101	8.2	232	2 B89807	exotoxin 12 [impor
29	99.5	8.0	231	2 D89807	exotoxin 11 [impor

exotoxin 14 [impor
cell shape determi
transferrin-binding
hypothetical prote
exotoxin 6 [impor
multidrug resistanc
trse-like protein
B. subtilis YjBk p
flagellar hook pro
hypothetical prote
phospholipase A2-1
DNA-directed DNA p
hypothetical prote
MG032 homolog B01
beta-fructofuranos
arginyl tRNA synth
protein with DnaJ
conserved hypothet
cell wall-associat
probable periplasm
major blood-stage
DNA endonuclease a
glycosidase homolo
hypothetical prote
arginyl tRNA synth
hypothetical prote
diphosphate-fructo
lactocepin [EC 3.4
MG288 homolog P02
ABC transporter, A
erythrocyte membra
exotoxin 15 [impor
transposase of IS1
glycerol kinase -
chitinase chi-A or
penicillin-binding
penicillin-binding
penicillin-binding
major surface glyc
hypothetical prote
GAG protein - yeast
Li protein - human
ABC transporter, A
outer membrane ush
transposase of IS1
hypothetical prote
hypothetical prote
probable transcrip
hypothetical prote
transferrin-bindin
hypothetical prote
hypothetical prote
uncharacterized pr
exotoxin 9 [impor
rare lipoprotein A
p-aminobenzoate sy
hypothetical secre
membrane conserved
putative autotransp
probable ferric si
hypothetical prote
upiquitin-like pro
hypothetical prote
DNA-directed RNA p
tyrocidine synthet
exotoxin 8 [impor
replication protei
hypothetical prote
protein F53H1.4 [i
hypothetical prote
hypothetical prote

103	81.5	6.6	1893	2	G82875	hypothetical prote	176	77.5	6.3	361	2	E86692	N-acetylmutamoyl-L
104	81.5	6.6	2870	2	H96974	cyclic beta 1-2 gl	177	77.5	6.3	372	2	C53312	HD-GYP hydrolase d
105	81	6.5	299	2	Af1193	hypothetical prote	178	77.5	6.3	419	1	G93312	thymidine phosphor
106	81	6.5	333	2	A99582	hypothetical prote	179	77.5	6.3	429	2	A25145	keratin, 47k type
107	81	6.5	402	2	S23240	probable carboxyl-	180	77.5	6.3	467	2	D69849	endo-1,4-beta-xyla
108	81	6.5	528	2	S23207	DNA-directed RNA p	181	77.5	6.3	522	2	D96913	GTPase, sulfate ad
109	81	6.5	562	2	S01312	alpha-amylase (EC	182	77.5	6.3	547	2	S49815	transferrin-bindin
110	81	6.5	580	2	S49308	beta-fructofuranos	183	77.5	6.3	554	2	S41526	hemolysin accesso
111	81	6.5	616	2	A36094	diphosphate-fructo	184	77.5	6.3	581	2	T51580	ovule development
112	81	6.5	626	2	B98115	hypothetical prote	185	77.5	6.3	590	2	H70130	oligoendopeptidase
113	81	6.5	1021	2	I40805	collagenase - Clos	186	77.5	6.3	609	2	T32302	hypothetical prote
114	81	6.5	1217	2	T21403	hypothetical prote	187	77.5	6.3	707	2	S78538	site-specific reco
115	81	6.5	1561	1	S06839	surface antigen ap	188	77.5	6.3	709	2	A41976	structure-specific
116	81	6.5	1997	2	F71607	DNA helicase II BR	189	77.5	6.3	817	2	F86742	ribonuclease limpo
117	81	6.5	2144	2	A97942	metalloproteinas	190	77.5	6.3	1269	2	A90267	proteinase related
118	81	6.5	2485	1	H71621	serine/threonine-s	191	77.5	6.3	1325	1	S73723	probable lipoprote
119	80.5	6.5	261	2	A84077	transposase (06) B	192	77.5	6.3	3206	1	GNVSPV	genome polypotein
120	80.5	6.5	344	2	C81920	hypothetical prote	193	77	6.2	421	2	A11112	hypothetical prote
121	80.5	6.5	413	2	S59650	hypothetical prote	194	77	6.2	425	2	T43772	hypothetical prote
122	80.5	6.5	933	2	A97334	type II restrictio	195	77	6.2	500	2	B43577	perfringolysin O p
123	80.5	6.5	1151	2	A45226	integrin alpha-1 c	196	77	6.2	620	2	E90575	lipoprotein [impor
124	80.5	6.5	1427	2	S22695	restin - human	197	77	6.2	646	2	H95155	prolyl oligopeptid
125	80.5	6.5	1520	2	T23620	hypothetical prote	198	77	6.2	797	2	D71621	hypothetical prote
126	80.5	6.5	1959	2	AG1085	hypothetical prote	199	77	6.2	876	2	A89944	alanyl-tRNA synthe
127	80	6.5	276	2	T12558	porin - common ice	200	77	6.2	893	2	S64926	probable membrane
128	80	6.5	1008	2	T18508	hypothetical prote	201	77	6.2	1118	2	H97298	subtilisin like pr
129	80	6.5	1231	2	S70553	chromosome-associa	202	77	6.2	1422	2	T18404	chromatin remodell
130	80	6.5	1388	2	T38720	chromodomain helic	203	77	6.2	1449	2	T30857	glucosyltransferas
131	80	6.5	1902	2	S06997	lactocepin (EC 3.4	204	77	6.2	1484	2	T42632	breast cancer tumo
132	79.5	6.4	156	2	AG0817	bacterioferritin c	205	77	6.2	1707	2	T18951	hypothetical prote
133	79.5	6.4	243	2	H71082	hypothetical prote	206	76.5	6.2	246	2	I40763	hypothetical prote
134	79.5	6.4	344	2	E81183	copper ABC transpo	207	76.5	6.2	272	2	C86642	transposase of IS1
135	79.5	6.4	358	2	G84550	hypothetical prote	208	76.5	6.2	331	2	D84413	cysteine proteinas
136	79.5	6.4	532	2	C97228	probable peptide A	209	76.5	6.2	350	2	T76651	hypothetical prote
137	79.5	6.4	556	2	C72204	alpha-amylase - Th	210	76.5	6.2	423	2	T15309	hypothetical prote
138	79.5	6.4	637	2	S35523	E1 protein - human	211	76.5	6.2	443	2	S23771	outer membrane por
139	79.5	6.4	677	2	B82870	DNA topoisomerase	212	76.5	6.2	455	2	S39663	aminopeptidase hom
140	79.5	6.4	1211	2	D64702	DNA polymerase III	213	76.5	6.2	480	2	T34294	hypothetical prote
141	79.5	6.4	1392	2	A43336	microtubule-vesicl	214	76.5	6.2	601	2	S74239	secretogranin II p
142	79.5	6.4	2269	2	T18472	hypothetical prote	215	76.5	6.2	669	2	S78050	high mobility grou
143	79.5	6.4	2894	2	C64474	hypothetical prote	216	76.5	6.2	729	2	QJ1898	probable RNA-direc
144	79	6.4	348	2	F69597	uncharacterized co	217	76.5	6.2	776	2	AH1506	preprotein translo
145	79	6.4	368	2	A82148	probable porin VCI	218	76.5	6.2	801	2	H90574	lipoprotein [impor
146	79	6.4	378	2	F64446	chromatase synthas	219	76.5	6.2	873	2	F71092	ATP-dependent RNA
147	79	6.4	419	2	H81667	transcription term	220	76.5	6.2	963	2	B83502	ribonucleoside red
148	79	6.4	426	2	B97126	cystathionine beta	221	76.5	6.2	1002	2	T09438	toxR-activated lip
149	79	6.4	628	2	AF2393	hypothetical prote	222	76.5	6.2	1013	2	B82276	toxR-activated gen
150	79	6.4	660	2	S70904	transferrin-bindin	223	76.5	6.2	1018	2	A32192	fibronectin-bindin
151	79	6.4	745	2	D82568	conserved hypotet	224	76.5	6.2	1047	2	S19508	MSH3 protein - yea
152	79	6.4	788	2	A71076	hypothetical prote	225	76.5	6.2	1086	2	T17628	endo-1,4-beta-xyla
153	79	6.4	1104	2	A60999	alpha-amylase (EC	226	76.5	6.2	1213	2	T19835	hypothetical prote
154	79	6.4	1131	2	T19442	hypothetical prote	227	76.5	6.2	1312	2	S68593	DNA-directed DNA p
155	79	6.4	1902	2	B45764	lactocepin (EC 3.4	228	76.5	6.2	1379	2	C71622	hypothetical prote
156	79	6.4	2183	2	T42764	coagulation factor	229	76.5	6.2	3890	2	C89921	hypothetical prote
157	79	6.4	4981	2	T18489	hypothetical prote	230	76	6.1	225	2	D86370	26.4k hypotethical
158	78.5	6.3	359	2	B82348	probable lipopolys	231	76	6.1	274	2	F81350	formyltetrahydrofo
159	78.5	6.3	318	2	T38919	conserved hypotet	232	76	6.1	370	2	A89782	conserved hypotet
160	78.5	6.3	627	2	G97975	hypothetical prote	233	76	6.1	396	2	A95038	glucuronyl hydrola
161	78.5	6.3	722	2	E71403	hypothetical prote	234	76	6.1	409	2	D97908	unsaturated glucur
162	78.5	6.3	781	2	T36143	probable secreted	235	76	6.1	432	2	E69886	processing protein
163	78.5	6.3	836	2	AB0540	outer-membrane fim	236	76	6.1	432	2	A64602	ribosomal protein
164	78.5	6.3	998	2	I41078	hemolysin - Escher	237	76	6.1	511	2	T11940	glycerol-3-phospha
165	78	6.3	416	2	A11760	B. subtilis YvIB p	238	76	6.1	527	2	C70130	hypothetical prote
166	78	6.3	476	2	G90512	p60-like (mycoplas	239	76	6.1	530	2	G64480	hypothetical prote
167	78	6.3	626	2	E95250	glycosyl hydrolase	240	76	6.1	630	1	1W1L35	E1 protein - human
168	78	6.3	669	2	T05212	hypothetical prote	241	76	6.1	636	2	F90094	hypothetical prote
169	78	6.3	681	2	F69295	acetyl-CoA synthet	242	76	6.1	650	2	T40830	nitrogen permease
170	78	6.3	692	2	B64381	hypothetical prote	243	76	6.1	680	2	D90575	lipoprotein [impor
171	78	6.3	933	2	AE1905	outer membrane sec	244	76	6.1	747	1	A27366	AMP deaminase (EC
172	78	6.3	1091	2	AF1380	glycosidase homolo	245	76	6.1	762	2	A34355	cell surface prote
173	78	6.3	2013	2	C71610	probable membrane	246	76	6.1	827	2	A90544	hypothetical prote
174	77.5	6.3	241	2	B89888	hypothetical prote	247	76	6.1	834	2	B82940	conserved hypotet
175	77.5	6.3	252	2	E95884	hypothetical prote	248	76	6.1	847	2	T19544	hypothetical prote

translation initia
isoleucyl-tRNA syn
feroxidase (EC 1.
hypothetical prote
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immunoglobulin Al
zinc metalloprotei
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bacterioferritin c
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conserved hypothet
hypothetical prote
lipoprotein [impor
RstA1/RstA2 protei
hypothetical prote
alpha-1-antitrypsi
ovule development
beta-fructofuranos
choline binding pr
hypothetical prote
hypothetical prote
protein ZK1127.7 l
DNA dependent ATPa
PK4 protein kinase
fusion of alpha-gl
hypothetical prote
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hypothetical prote
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hypothetical prote
hypothetical prote
type I site-specif
hypothetical prote
DNA-directed RNA p
hypothetical prote

249 76 6.1 882 2 H70199
250 76 6.1 960 2 AF1940
251 76 6.1 1069 1 KUHU
252 76 6.1 1132 2 H82887
253 76 6.1 1377 2 D90538
254 76 6.1 1449 2 T30552
255 76 6.1 1856 2 C95008
256 76 6.1 1876 2 E97944
257 76 6.1 1948 2 S00485
258 76 6.1 2233 2 B95075
259 75.5 6.1 156 2 B85891
260 75.5 6.1 156 2 F91046
261 75.5 6.1 156 2 B49749
262 75.5 6.1 244 2 H89942
263 75.5 6.1 246 2 E81373
264 75.5 6.1 266 2 C90520
265 75.5 6.1 359 2 G82197
266 75.5 6.1 419 2 S06784
267 75.5 6.1 420 2 A28882
268 75.5 6.1 550 2 S71365
269 75.5 6.1 592 2 S56681
270 75.5 6.1 627 2 E95107
271 75.5 6.1 655 2 S57119
272 75.5 6.1 808 2 A82877
273 75.5 6.1 816 2 C88196
274 75.5 6.1 1121 2 S30862
275 75.5 6.1 1123 2 T28139
276 75.5 6.1 1157 2 P97255
277 75.5 6.1 1712 2 T05113
278 75.5 6.1 3066 2 T28625
279 75.5 6.1 3649 1 S18268
280 75 6.1 194 2 AB1195
281 75 6.1 253 2 C97026
282 75 6.1 254 2 B64011
283 75 6.1 299 2 AB0440
284 75 6.1 313 2 C71428
285 75 6.1 345 2 E82469
286 75 6.1 351 2 D96958
287 75 6.1 364 2 AB1918
288 75 6.1 375 2 S73530
289 75 6.1 438 2 S42581
290 75 6.1 462 1 WTHUB
291 75 6.1 502 2 T13620
292 75 6.1 512 1 WMCVFM
293 75 6.1 717 2 S50852
294 75 6.1 730 2 A96988
295 75 6.1 849 2 G64342
296 75 6.1 1009 2 C89310
297 75 6.1 1025 2 T44802
298 75 6.1 1250 2 A96586
299 75 6.1 1434 2 C82923
300 75 6.1 1549 2 T21809

ALIGNMENTS

RESULT 1
A28179
enterotoxin E precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C:Accession: A28179
J:Couch, J.L.; Soltis, M.T.; Betley, M.J.
R: Bacteriol. 170, 2954-2960, 1988
A:Title: Cloning and nucleotide sequence of the type E staphylococcal enterotoxin gene.
A:Reference number: A28179; MUID:88257005; PMID:3384800
A:Accession: A28179
A:Molecule type: DNA
A:Residues: 1-257 <COU>
A:Cross-references: UNIPROT:P12993; UNIPARC:UPI000012A275; GB:M21319; NID:g153001; PIDN:
C:Superfamily: enterotoxin B

Query Match 100.0%; Score 1238; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 2.3e-93;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTC 60
DB 25 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTC 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 121 EEKKVPINLWIDGKQTTVPIDVKVTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
DB 145 EEKKVPINLWIDGKQTTVPIDVKVTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 204
QY 181 RGLIVPHSSEGSTVSYDLFDAOGQYPTLLRIYRDNKNTINSENHLHDLYTT 233
DB 205 RGLIVPHSSEGSTVSYDLFDAOGQYPTLLRIYRDNKNTINSENHLHDLYTT 257

RESULT 2
A28664
enterotoxin A precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C:Accession: A28664; A29566
J:Betley, M.J.; Mekalanos, J.J.
R: Bacteriol. 170, 34-41, 1988
A:Title: Nucleotide sequence of the type A staphylococcal enterotoxin gene.
A:Reference number: A28664; MUID:88086892; PMID:3335483
A:Accession: A28664
A:Molecule type: DNA
A:Residues: 1-257 <BET>
A:Cross-references: UNIPROT:P13163; UNIPARC:UPI000012A273; GB:M18970; NID:g153120; PIDN:
A:Experimental source: strain FR1337
R:Huang, I.Y.; Hughes, J.B.; Bergdoll, M.S.; Schantz, E.J.
J. Biol. Chem. 262, 7006-7013, 1987
A:Title: Complete amino acid sequence of staphylococcal enterotoxin A.
A:Reference number: A29566; MUID:87222293; PMID:3584106
A:Accession: A29566
A:Molecule type: protein
A:Residues: 25-241, S',243-257 <HUA>
A:Cross-references: UNIPARC:UPI00001766F5
C:Genetics:
A:Gene: entA
A:Map position: 6
C:Superfamily: enterotoxin B

Query Match 82.6%; Score 1023; DB 2; Length 257;
Best Local Similarity 82.0%; Pred. No. 7.1e-76;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTC 60
DB 25 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLOHTLLFKGFFTD 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 121 EEKKVPINLWIDGKQTTVPIDVKVTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
DB 145 EEKKVPINLWIDGKQNTVPLETVKTNKNVTVOELDLQARRYLQEKYLYNSDVFQKVKQ 204
QY 181 RGLIVPHSSEGSTVSYDLFDAOGQYPTLLRIYRDNKNTINSENHLHDLYTT 233
DB 205 RGLIVFHTSTPEPSVNYDLFGAOGQVSNLTLLRIYRDNKNTINSENMMHIDLYTS 257

RESULT 3
C89984
enterotoxin P [imported] - Staphylococcus aureus (strain N315)

QY	191	GSTVSYDLFAQOQYPTLLRIYRDNKTINSENHLIDL 228
Db	194	GSFSYDLFDGTGQAESFLKYNDRKNTVETEKFLDVLV 231
RESULT 10		
ENSAB6		
enterotoxin B precursor - Staphylococcus aureus		
C:Species: Staphylococcus aureus		
C:Date: 24-Apr-1984 #sequence revision 15-Oct-1996 #text_change 09-Jul-2004		
C:Accession: S27360; A92065; S27240; A01815		
R:Jones, C.L.; Khan, S.A.		
J. Bacteriol. 166, 29-33, 1986		
A:Title: Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.		
A:Reference number: S27360; MUID:86168029; PMID:3957869		
A:Accession: S27360		
A:Molecule type: DNA		
A:Residues: 1-266 <JON>		
A:Cross-references: UNIPROT:P01552; UNIPARC:UPI0000010DB; EMBL:M11118; NID:g152999; PID		
R:Huang, I.Y.; Bergdoll, M.S.		
J. Biol. Chem. 245, 3518-3525, 1970		
A:Title: The primary structure of staphylococcal enterotoxin B. III. The cyanogen bromide		
A:Reference number: A92065; MUID:71007902; PMID:5470821		
A:Accession: A92065		
A:Molecule type: protein		
A:Residues: 28-55, 'NND', 59-68, 'NE', 71, 'FDLIYL', 78-117, 119-127, 'N', 129, 'D', 131-132, 'ENT',		
A:Cross-references: UNIPARC:UPI000014FD39		
A:Experimental source: strain S-6		
R:Huang, I.Y.; Bergdoll, M.S.		
J. Biol. Chem. 245, 3511-3517, 1970		
A:Title: The primary structure of staphylococcal enterotoxin B. II. Isolation, compositi		
A:Reference number: A92064; MUID:71007901; PMID:5470820		
A:Contents: annotation; chymotryptic peptides		
R:Huang, I.Y.; Bergdoll, M.S.		
J. Biol. Chem. 245, 3493-3510, 1970		
A:Title: The primary structure of staphylococcal enterotoxin B. I. Isolation, compositi		
A:Reference number: A92063; MUID:71007900; PMID:5470819		
A:Contents: annotation; tryptic peptides		
R:Schantz, E.J.; Roessler, W.G.; Wagman, J.; Spero, L.; Dunnyer, D.A.; Bergdoll, M.S.		
Biochemistry 4, 1011-1016, 1965		
A:Title: Purification of staphylococcal enterotoxin B.		
A:Reference number: A90548; MUID:66035792; PMID:4953912		
A:Contents: annotation; biological source of protein		
R:Alakhov, V.Y.; Klinsky, E.Y.; Kolosov, M.I.; Maurer-Fogy, I.; Moskaleva, E.Y.; Sveshni		
Eur. J. Biochem. 209, 823-828, 1992		
A:Title: Identification of functionally active fragments of staphylococcal enterotoxin B		
A:Reference number: S27240; MUID:93049338; PMID:14255690		
A:Accession: S27240		
A:Molecule type: protein		
A:Residues: 28-42; 128-148 <ALA>		
A:Cross-references: UNIPARC:UPI0000173634; UNIPARC:UPI0000173635		
C:Superfamily: enterotoxin B		
C:Keywords: enterotoxin; extracellular protein; toxin		
F:1-27/Domain: signal sequence #status predicted <SIG>		
F:28-266/Product: enterotoxin B #status experimental <MAT>		
F:120-140/Disulfide bonds: #status experimental		
Query Match 24.3%; Score 300.5; DB 1; Length 266;		
Best Local Similarity 33.6%; Pred. No. 4.4e-17;		
Matches 82; Conservative 47; Mismatches 96; Indels 19; Gaps 8;		
QY	1	SEKSEBINEKDLRKSELORNALSRLQIYYNEKAITENKESDDOFLNTLLFGKFFTG 60
Db	27	AESQDPKPELDLHKSSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKOTK 84
QY	61	HPWYNDLLVLDGSKDATNKYKGKKVDLYGAYGYQC-----AGGTPNKTCMYGG 110
Db	85	LGNVDNVFVFNKKDLADKKYDVDFGANYYYQCYFSKKTNDINSHQTDKRTCMYGG 144
QY	111	VTLHDNNRLTEKKVPINLWIDGKQTTPIDPKVTSKKEVTQVELDQARHYLHGKFGLY 170
Db	145	VTEHNGQLDKYRSITVRVFEDGK-NLLGFD-VQTNKKKVTQAQELDYLTRHYLVKNKKLY 202

QY	171	NSDSFGGKVQRGLIVFHSSEGSTVSYDLFAQOQYPD--TLRIYRDNKTINSENHLIDL 228
Db	203	EFNN--SPYETGYIKFIENENG-FWYDMMPAPGDPFQSKYLMYNDNKNKVDKVKIEV 259
QY	229	YLYT 232
Db	260	YLYT 263
RESULT 11		
S29659		
exotoxin type A precursor (allele 1) - Streptococcus pyogenes phage T12		
N:Alternate names: erythrogenic toxin; scarlet fever toxin		
C:Species: Streptococcus pyogenes phage T12		
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999		
C:Accession: S29659; S18782; S18784; S18785; S18791; S18796; S18797; S18800		
R:Weeks, C.R.; Ferretti, J.J.		
Infect. Immun. 52, 144-150, 1986		
A:Title: Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) ge		
A:Reference number: S29659; MUID:86166804; PMID:3514452		
A:Accession: S29659		
A:Molecule type: DNA		
A:Residues: 1-251 <WEE>		
A:Cross-references: UNIPARC:UPI0000135DD7; GB:U40453; EMBL:M19350; NID:gi877426; PIDN:AA		
R:Nelson, K.; Schlievert, P.M.; Sclander, R.K.; Musser, J.M.		
J. Exp. Med. 174, 1271-1274, 1991		
A:Title: Characterization and clonal distribution of four alleles of the speA gene encodi		
A:Reference number: S18782; MUID:92044323; PMID:1940804		
A:Accession: S18782		
A>Status: nucleic acid sequence not shown; translation not shown		
A:Molecule type: DNA		
A:Residues: 9-244 <NEU>		
A:Cross-references: UNIPARC:UPI0000081BCE; EMBL:X61560; NID:g47287; PIDN:CAA43758.1; PID:		
A:Experimental source: Streptococcus pyogenes strain MGAS156 isolate Nebraska unassigned		
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991		
A:Accession: S18784		
A>Status: nucleic acid sequence not shown; translation not shown		
A:Molecule type: DNA		
A:Residues: 9-244 <NEA>		
A:Cross-references: UNIPARC:UPI0000081BCE; EMBL:X61556; NID:g47291; PIDN:CAA43754.1; PID:		
A:Experimental source: Streptococcus pyogenes strain MGAS165 isolate Minnesota unassigned		
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991		
A:Accession: S18785		
A>Status: nucleic acid sequence not shown; translation not shown		
A:Molecule type: DNA		
A:Residues: 9-244 <NEZ>		
A:Cross-references: UNIPARC:UPI0000081BCE; EMBL:X61559; NID:g47293; PIDN:CAA43757.1; PID:		
A:Experimental source: Streptococcus pyogenes strain MGAS167 isolate Texas unassigned ph		
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991		
A:Accession: S18791		
A>Status: nucleic acid sequence not shown; translation not shown		
A:Molecule type: DNA		
A:Residues: 9-244 <NEY>		
A:Cross-references: UNIPARC:UPI0000081BCE; EMBL:X61555; NID:g47309; PIDN:CAA43753.1; PID:		
A:Experimental source: Streptococcus pyogenes strain MGAS327 isolate Arizona unassigned I		
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991		
A:Accession: S18796		
A>Status: nucleic acid sequence not shown; translation not shown		
A:Molecule type: DNA		
A:Residues: 9-244 <NEO>		
A:Cross-references: UNIPARC:UPI0000081BCE; EMBL:X61557; NID:g47319; PIDN:CAA43755.1; PID:		
A:Experimental source: Streptococcus pyogenes strain MGAS493 isolate France unassigned ph		
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991		
A:Accession: S18797		
A>Status: nucleic acid sequence not shown; translation not shown		
A:Molecule type: DNA		
A:Residues: 9-244 <NEH>		
A:Cross-references: UNIPARC:UPI0000081BCE; EMBL:X61558; NID:g47321; PIDN:CAA43756.1; PID:		
A:Experimental source: Streptococcus pyogenes strain MGAS494 isolate France unassigned ph		
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991		
A:Accession: S18800		
A>Status: nucleic acid sequence not shown; translation not shown		

A:Molecule type: DNA
A:Residues: 9-228 <NES>
A:Cross-references: UNIPARC:UPI00001701AF; EMBL:X61554; NID:947327; PIDN:CAA43752.1; PIDN:CAA43752.1; PIDN:CAA43752.1
A:Experimental source: Streptococcus pyogenes strain MGAS500 isolate New Zealand unassigned
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C:Genetics:
A:Gene: speA; speA1
A:Superfamily: enterotoxin B
C:Keywords: exotoxin
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-251/Product: exotoxin type A #status predicted <MAT>

Query Match 23.9%; Score 295.5; DB 1; Length 251;
Best Local Similarity 34.2%; Pred. No. 1.1e-16;
Matches 81; Conservative 45; Mismatches 92; Indels 19; Gaps 10;

QY 4 SEINEKDLRKKSSELOALN-SNLROIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG 60
Db 25 SQEVFAQQDDPSQLHRSSLVKRNQWLYFLYEGDPVTNENKSVDDQLSHDLIN---VS 81

QY 61 HPWYNLDLVGSKDATNKYKGVLDLYGAYGYQC-AGGTPNKATCMYGGVTLHDNNRL 119
Db 82 GPNYDKLTQELKQEWATLTKDNVDIYGVVEYHLCVLCENAESACIYGGVTNHEGNHL 141

QY 120 TBEKKVPINLWIDGKQTPVDIKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKV 179
Db 142 EIPKTIWVKSIDGQ-SLSFD-IETNKNWTAQELDYKVRKYLTDNKLQYTNGP--SKY 197

QY 180 QRLGIVFHSSEGSTVSYDLFD----AQGYPDLLRIYRDNTKINSENLHIDLTYLT 232
Db 198 ETGYIKPIPKNESPFWDFPEPEFTQSKY----LMYKDNELTDSNTSQIEVYLT 250

RESULT 12
S11885
enterotoxin C3 - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S11885
R:Howe, C.J.; Hackett, S.P.; Bohach, G.A.
Mol. Gen. Genet. 220, 329-333, 1990
A:Title: Nucleotide sequence of the staphylococcal enterotoxin C3 gene: sequence comparison
A:Reference number: S11885; MUID:90220508; PMID:2325627
A:Accession: S11885
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-266 <HOV>
A:Cross-references: UNIPROT:P23313; UNIPARC:UPI00000010A4; GB:X51661; NID:946570; PIDN:CAA43752.1
C:Superfamily: enterotoxin B

Query Match 23.1%; Score 285.5; DB 2; Length 266;
Best Local Similarity 32.1%; Pred. No. 7.4e-16;
Matches 75; Conservative 49; Mismatches 91; Indels 19; Gaps 9;

QY 11 DLKKSSELOALNLSRLQIYYNEKAITENK-ESDDQFLENTLLFKGFFTGHPWYNLDLV 69
Db 37 DLHKSSEF-TGTGNNK--YLYDDHYVSVATKVSVDKFLAHDLIYNSDKLKNYDKVKT 93

QY 70 DLGSKDATNKYKGVLDLYGAYGYQC-----AGGTPNKATCMYGGVTLHDNNRLTEE 122
Db 94 ELLNEDLAKYKDEVVDVYGSYVNCYFSSKDNVGVKGTGKTCMYGGITKHEGNHFDNG 153

QY 123 --KKVPINLWIDGKQTPVDIKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVQ 180
Db 154 NLQNLVIRVY-ENKRTISFE-VQTDKKSVAQELDIKARNFLINKNLNLYEFS--SPYE 209

QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPD--TLRIYRDNTKINSENLHIDLTYLT 232
Db 210 TGYIKFIENNGNTFWYDMMPAPGDKFDQSKYLMYNDKNTVDSKSVKIEVLT 263

RESULT 13
A60114
enterotoxin C-2 precursor - Staphylococcus aureus
N:Alternate names: enterotoxin C-3 precursor
C:Species: Staphylococcus aureus
C:Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004
C:Accession: A60114; B60114; A33866
R:Bohach, G.A.; Schlievert, P.M.
Infect. Immun. 57, 2249-2252, 1989
A:Title: Conservation of the biologically active portions of staphylococcal enterotoxins
A:Reference number: A60114; MUID:89277549; PMID:2543637
A:Accession: A60114
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-266 <BOH>
A:Cross-references: UNIPROT:P34071; UNIPARC:UPI00000000DA6
A:Accession: B60114
A:Molecule type: protein
A:Residues: 28-66 <BOH2>
A:Cross-references: UNIPARC:UPI00001766F4
J. Bacteriol. 171, 4507-4510, 1989
A:Title: Nucleotide sequence of the type C-3 staphylococcal enterotoxin gene suggests the
A:Reference number: A33866; MUID:89327174; PMID:2473979
A:Accession: A33866
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-266 <COU>
A:Cross-references: UNIPARC:UPI00000000DA6; GB:M28364; NID:gi53003; PIDN:AAA26624.1; PIDN:AAA26624.1
C:Genetics:
A:Gene: entC2
C:Superfamily: enterotoxin B
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-266/Product: enterotoxin C-2 #status predicted <MAT>

Query Match 22.7%; Score 281.5; DB 2; Length 266;
Best Local Similarity 31.1%; Pred. No. 1.6e-15;
Matches 76; Conservative 50; Mismatches 99; Indels 19; Gaps 9;

QY 1 SEKSEINEKDLRKKSSELOALNLSRLQIYYNEKAITENK-ESDDQFLENTLLFKGFFTG 59
Db 27 AESQPDPTPDELHKSSEF-TGTGNNK--YLYDDHYVSVATKVSVDKFLAHDLIYNSDK 83

QY 60 GHPWYNLDLVGSKDATNKYKGVLDLYGAYGYQC-----AGGTPNKATCMYGGVT 112
Db 84 KLNKYDKVKTTELLNEDLAKYKDEVVDVYGSYVNCYFSSKDNVGVKGTGKTCMYGGIT 143

QY 113 LHDNNRLTEE--KKVPINLWIDGKQTPVDIKVTSKKEVTVOELDQARHYLHGKFGLY 170
Db 144 KHGHNHFDNGNLQNLVIRV-ENKRTISFE-VQTDKKSVAQELDIKARNFLINKNLNLY 201

QY 171 NSDSFGKVQVORGLIVFHSSEGSTVSYDLFDAQGYPD--TLRIYRDNTKINSENLHIDL 228
Db 202 EFNS--SPYETGYIKFIENNGNTFWYDMMPAPGDKFDQSKYLMYNDKNTVDSKSVKIEV 259

QY 229 YLYT 232
Db 260 HLTT 263

RESULT 14
S18789
exotoxin A precursor (allele 4) - Streptococcus pyogenes (strain MGAS262 isolate Caliform
N:Alternate names: scarlet fever toxin
C:Species: Streptococcus pyogenes
A:Variety: strain MGAS262 isolate California
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jul-2004
C:Accession: S18789
J.Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A:Title: Characterization and clonal distribution of four alleles of the speA gene encodi
A:Reference number: S18782; MUID:92044323; PMID:1940804
A:Accession: S18789
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18792
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEO>
A;Cross-references: UNIPARC:UPI00000BEA6A; EMBL:X61565; NID:g47311; PIDN:CAA43763.1; PID
A;Experimental source: strain MGAS480 isolate Yugoslavia unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18795
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEH>
A;Cross-references: UNIPARC:UPI00000BEA6A; EMBL:X61566; NID:g47317; PIDN:CAA43764.1; PID
A;Experimental source: strain MGAS492 isolate United Kingdom unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18799
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NES>
A;Cross-references: UNIPARC:UPI00000BEA6A; EMBL:X61567; NID:g47325; PIDN:CAA43765.1; PID
A;Experimental source: strain MGAS496 isolate Germany unassigned phage
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C;Genetics:
A;Gene: speA2
C;Superfamily: enterotoxin B
C;Keywords: exotoxin
F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F;23-236/Product: exotoxin type A (fragment) #status predicted <MAT>

Query Match 22.0%; Score 272.5; DB 2; Length 236;
Best Local Similarity 33.3%; Pred. No. 7.2e-15;
Matches 77; Conservative 43; Mismatches 92; Indels 19; Gaps 10;

QY 4 SESEINEKDLKKSELORNAL-SNLRLQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG 60
DB 17 SQEVFAQQDDPSQLHSSLVKLNLIYFYEGDPVTHENVKSVQDQLSHDLIYN---VS 73

QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYYGQC-AGGTPNKATACMYGGVTLHDNNRL 119
DB 74 GPYDKLKTQKQEWATLFPKDNVDIYSVEYHYLCVLCENASRSACIYGVTHNENHL 133

QY 120 TEKKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGYNSDFGGKV 179
DB 134 EIPKIVKVSIDGIG-SLSFD-IETNKMTVAQELDYKVRKYLTONKQLYTNGP--SKY 189

QY 180 QRLGLVHSSGSESTVSVDLFD----AQGYPTLLRIYRDNKTINSENHLI 226
DB 190 ETGYIKRPIPKNKESFWDFPPEFTQSKY----LMIYKDNLTDSNTSQI 236

RESULT 17
ENSAC1
enterotoxin C-1 precursor - Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 15-Nov-1984 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004
C;Accession: S06356; A01816
R;Bohach, G.A.; Schlievert, P.M.
Mol. Gen. Genet. 209, 15-20, 1987
A;Title: Nucleotide sequence of the staphylococcal enterotoxin C1 gene and relatedness
A;Reference number: S06356; MUID:88038352; PMID:2823067
A;Accession: S06356
A;Molecule type: DNA
A;Residues: 1-266 <BOH>
A;Cross-references: UNIPROT:P01553; UNIPARC:UPI000012A22B; EMBL:X05815; NID:g46566; PIDN
R;Schmidt, J.J.; Spero, L.
J. Biol. Chem. 258, 6300-6306, 1983
A;Title: The complete amino acid sequence of Staphylococcal enterotoxin C-1.
A;Reference number: A01816; MUID:83213327; PMID:6189824
A;Accession: A01816
A;Molecule type: protein
A;Residues: 28-75, 'IL', 78-176, 'N', 178-266 <SCH>
A;Cross-references: UNIPARC:UPI0000173636
C;Genetics:

A;Gene: entC1
C;Superfamily: enterotoxin B
C;Keywords: enterotoxin
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-266/Product: enterotoxin C-1 #status experimental <MAT>
F;120-137/Disulfide bonds: #status experimental

Query Match 21.5%; Score 266.5; DB 1; Length 266;
Best Local Similarity 30.5%; Pred. No. 2.6e-14;
Matches 74; Conservative 51; Mismatches 101; Indels 17; Gaps 8;

QY 1 SEKSEINEKDLKKSELORNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 27 AESQDPPTDELHAKSKF-TGLMENNKVLYDDHYVSATKVK-SVDKFLAHDLLIYNISDKK 84
QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYYGQC-----AGGTPNKATACMYGGVTL 113
DB 85 LKNYDKVTLELNEGLAKYKDEVDVYGSNYYVYFSSKDNVGVKVTGGTKCMYGGITK 144

QY 114 HNNRLTEE--KKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYN 171
DB 145 HEGNHFDNGLQNLVLRVY-ENKRNITISPE-VQTDKKSVTQAELDIKARFNLINKKNLYE 202

QY 172 SDSFGGKVGRLIVFHSSGSESTVSVDLFDAGQGYPD--TLLRIYRDNKTINSENHLIDLY 229
DB 203 FNS--SPYETGYIKFTIENNGTFWYDMPPAPGDFDQSKYLMYNDNKTVDKSKVIEVH 260
QY 230 LYT 232
DB 261 LYT 263

RESULT 18
G89968
extracellular enterotoxin type G precursor [imported] - Staphylococcus aureus (strain N31)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: G89968
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: G89968
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-258 <KUR>
A;Cross-references: UNIPROT:O85382; UNIPARC:UPI000012A276; GB:BA000018; PID:g13701617; P
A;Experimental source: strain N315
C;Genetics:
A;Gene: seg
C;Superfamily: enterotoxin B

Query Match 20.6%; Score 255.5; DB 2; Length 258;
Best Local Similarity 29.1%; Pred. No. 2e-13;
Matches 71; Conservative 49; Mismatches 83; Indels 41; Gaps 11;

QY 11 DLKKSELORN--ALSNLRQIYY---YNEKAITENKESDDQFLENTLLFKGFFTGHPWYN 65
DB 33 ELNKVSDYKNNKGTGMGNVNNLYTSPPEVGRGVINSR----QFLSHDLIFP---IEYKSYN 85
QY 66 DLLAVDLGSKDATNKYKGGKVDLYGAYYGQCA-----GGTPNKATACMYGGVTL 113
DB 86 EVKTELENTLANNYKDKKVDIFGVFYFTCIIPKSEPDINQNFSG-----CMYGGLTTF 140

QY 114 H--DNNRLTEEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYN 171
DB 141 NSSENER---DKLITVQVTDNRQSLG--FTITTNKMVTIQELDYKARHWTKEKKLYE 195

QY 172 SDSFGGKVGRLIVFHSSGSESTVSVDLFDAGQGYPDT--LLRIYRDNKTINSENHLIDL 228
DB 196 FD--GSAFESGYIKFTEKNNTSFWFDLPKRELVPFVPPKFLNIYGDNKVDSKSKMEV 253

QY 229 YLYT 232
Db 254 FLNT 257

RESULT 19
A26152
streptococcal pyrogenic exotoxin type A precursor - Streptococcus sp.
N:Alternate names: scarlet fever toxin; SPE type A (speA)
C:Species: Streptococcus sp.
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A26152
R:Johnson, L.P.; I:Italian, J.J.; Schlievert, P.M.
Mol. Gen. Genet. 203, 354-356, 1986
A:Title: Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to Sta
A:Reference number: A26152; MUID:86284313; PMID:3526093
A:Accession: A26152
A:Molecule type: DNA
A:Residues: 1-250 <JOH>
A:Cross-references: UNIPROT:P08095; UNIPARC:UPI000017021E
A:Superfamily: enterotoxin B
C:Keywords: exotoxin

Query Match 19.8%; Score 245; DB 1; Length 250;
Best Local Similarity 30.7%; Pred. No. 1.3e-12; Mismatches 94; Indels 22; Gaps 9;
Matches 70; Conservative 42

QY 14 KXSELQNALSNLRQIYYNEKA--IT-ENKESDDQFLENTLLFKGFFTGHPWYNDLLVD 70
Db 35 KPSQLQRSNLVKTKIYIFPMRVTLVTHENVKSDQLLSHDLIYN--VSGPNYDKLKE 91

QY 71 LSKDATNKYKGGKVDLYGAYGYQC-AGGTPNKTAAGGVTTLHNNRLTEKKVPINL 129
Db 92 LKNQEMATLFDKNVDIYGYVYHLCYLCENAEASCLYGGVTNHEGNHLEIPKKIWKV 151

QY 130 WDGKOT-TVPIDKVTSKKEVTVQELDLQARHLHGKFGLYNSDSFGKGKVGORGLIVFHS 188
Db 152 SDIGIQLSFDEIQKNG-----NCSRISYTVRKLTNDKQLYNGP--SKYETGIYKFTP 205

QY 189 SEGSTVSYDLFD----AQGGYPTLLRIYRDNKNTINSENHLHDLYLT 232
Db 206 KNKESFWDFPFPEPTQSKY----LMYKDNETLDSNTSQIEVLYLT 249

RESULT 20
A89942
hypothetical protein SA1430 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: A89942
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: A89942
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-157 <KUR>
A:Cross-references: UNIPROT:Q99TP7; UNIPARC:UPI00000CAD54; GB:BA0000018; PID:gl3701400; F
A:Superfamily: enterotoxin B
C:Keywords: exotoxin

Query Match 16.2%; Score 201; DB 2; Length 157;
Best Local Similarity 35.8%; Pred. No. 2.8e-09; Mismatches 53; Indels 2; Gaps 2;
Matches 42; Conservative 21

QY 1 SEKSEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 42 TNSASALEYSDLHHSKFSKRLSNK-KMSFINPTQL-ENKNTNDRLLKHDLLFHDMEYN 99

QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTAAGGVTTLHNNR 118
Db 100 VASKDKFVPEPENEALSKKFINKNDIYAGSYSECHGGATNKTCQSGVTLSDNNK 157

RESULT 21
A89969
enterotoxin YENT2 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: A89969
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: A89969
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <KUR>
A:Cross-references: UNIPROT:Q99T49; UNIPARC:UPI00000CAD54; GB:BA0000018; PID:gl3701619; P
A:Experimental source: strain N315
C:Genetics:
A:Gene: yent2

Query Match 15.9%; Score 197; DB 2; Length 136;
Best Local Similarity 34.1%; Pred. No. 5e-09; Mismatches 51; Indels 10; Gaps 5;
Matches 46; Conservative 28

QY 103 KTACMYGGVTLHNNRLTEKKV--PINLWI--DGKQTTVPIDKVKTSKKEVTVOELDL 157
Db 2 KTCMYGGVTEHDGQIDKNSTDNHNLILKIVYERNLSLFD-IPTNKNITAEIDY 60

QY 158 QARHYLHGKFGLYNSDSFGKGKVGORGLIVFHSSEGSTVSYDLFDAQQ--YPTDLLRIYRD 215
Db 61 KVRNLLKHLKLYEFNS--SPVETGYIKFIEGSHGFWYDLMPESGKFKFYPTKYLIIYND 118

QY 216 NKTINSENHLHDLYL 230
Db 119 NKTVESKSNVVEHL 133

RESULT 22
A30509
exotoxin C precursor - Streptococcus pyogenes
C:Species: Streptococcus pyogenes
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C:Accession: A30509
R:Goshorn, S.C.; Schlievert, P.M.
Infect. Immun. 56, 2518-2520, 1988
A:Title: Nucleotide sequence of streptococcal pyrogenic exotoxin type C.
A:Reference number: A30509; MUID:88314303; PMID:3045005
A:Accession: A30509
A:Molecule type: DNA
A:Residues: 1-235 <GOS>
A:Cross-references: UNIPROT:PI3380; UNIPARC:UPI000017022C; GB:M35514; NID:gl53820; PID:N
C:Superfamily: enterotoxin B
C:Keywords: exotoxin

Query Match 14.8%; Score 183.5; DB 2; Length 235;
Best Local Similarity 25.8%; Pred. No. 1.3e-07; Mismatches 37; Indels 65; Gaps 11;
Matches 61; Conservative 37

QY 47 FLENTLLFKGFFTG-----PW-YNDLLVDLGSKDA-----TNK 79
Db 11 FIITVILISTYFTYHQSDSKDISNVKSDLLVAYTITPYDYKDCRVNFSHTLTNIDTQK 70

QY 80 YRGK-----KVDLYGAYGYQCAGGTPNKTAAGGVTTLHNNRL 119
Db 71 YRGKDYIISSEMSYEASQKFKRDDHVDVFGFLFILNSHTG-----EYIYGGITPAQNNKV 125

Db 86 -----LLGKD-KDKYKGLGQNVFVVKELI-----DPNGRLSTVGGV 122
QY 112 TLHDNRLTEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFLYN 171
Db 123 TKQNKSSNTNHLFVNK-VYGGNLDASIDSFLINKEEVSLEKELDKIRKQLVEKGLYK 181
QY 172 SDSFGKGQVGLVIFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTIINSEN 224
Db 182 -----GTTKYGKITINLKDKEKVEDLGDK-----LQFRMGVDVLNSKDI 221

RESULT 30
G86907
exotoxin 14 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G89807
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Oi, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G89807
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-227 <KUR>
A:Cross-references: UNIPROT:Q99WH3; UNIPARC:UPI000000CAB82; GB:BA000018; PID:g13700320; E
A:Experimental source: strain N315
C:Genetics:
A:Gene: set14
C:Superfamily: toxic shock syndrome toxin

Query Match 7.8%; Score 96; DB 2; Length 227;
Best Local Similarity 26.7%; Pred. No. 1.6;
Matches 54; Conservative 28; Mismatches 76; Indels 44; Gaps 9;
QY 8 NEKDLRK--KSELQNALSLRQIYYNEKAITENKESDDQFLENTLLPKGPFTHPWYN 65
Db 33 NQKSNVNHDKREALYR-----YVTGKTMEKNISALKHGKNLRFK--FRGIKIQV 80
QY 66 DLLVDLGSKDATNKYG-----KKVDLYGAYGYQCAGT--PNKTACMGYGVTLHDN 116
Db 81 LLPGNDKSKFQQRSEGLDVFVQEKRDKHDIFY---TVGGVIQNKNTS---GVVSAPI 133
QY 117 NRLTEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFLYNSDSFG 176
Db 134 LNISEK-----GEDAFVKGYPYIKKEKITLKELDYKURKHLIEKLYKTIISKD 184
QY 177 GKVQVGLVIFHSSEGSTVSVDL 198
Db 185 GRVKISL-----KDGsfYNLDL 201

RESULT 31
G86903
cell shape determining protein [imported] - Lactococcus lactis subsp. lactis (strain IL1
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: G86903
R:Boletín, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarre, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: G86903
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-291 <STO>
A:Cross-references: UNIPROT:Q9CDI9; UNIPARC:UPI000000C6BFE; GB:AE005176; PID:g12725299; E
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: mreC

Query Match 7.6%; Score 94.5; DB 2; Length 291;
Best Local Similarity 20.7%; Pred. No. 2.8;
Matches 48; Conservative 26; Mismatches 67; Indels 91; Gaps 8;
QY 21 NALSRLQIYYNEKAIT-----ENK-----ESDQFLENTLLPKGPFTHG----- 61
Db 67 NELSNLMDTYQQNQSKTQLAKSKDDNKLGLSENKELKALKIQLTETLDTDTQTVAAV 126
QY 62 -----PWYNDLLVGLSKDATNKYKGVKVDLYGAYGYQCAGTGNKTACTMYGVTLHD 115
Db 127 ITRPSSWNTLVIDSGSKD-----GLTTGMIVWANGGVV--- 161
QY 116 NNRLTE-----EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQ 158
Db 162 -GRVTQVKNSSKVALLSKSGIDNKIPVRIESDGSPIYGLSSYDSQQEAYVVKNIDSQ 220
QY 159 ARHYLHGKFLYNSDSFGKQVQGLVIFHSSEGSTVSVDLFDAGQGYPTLL 210
Db 221 -----GRFKNGDSVFTSGLGTNSG-----SQGTPSGLL 249

RESULT 32
S70908
transferrin-binding protein 2 precursor - Haemophilus influenzae (strain SB29)
C:Species: Haemophilus influenzae
A:Variety: strain SB29
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S70908; S73321
R:Loosmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.E.
Mol. Microbiol. 19, 575-586, 1996
A:Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes
A:Reference number: S70901; MUID:96228706; PMID:8830248
A:Accession: S70908
A:Molecule type: DNA
A:Residues: 1-631 <LOO>
A:Cross-references: UNIPROT:Q48041; UNIPARC:UPI00001783A3; EMBL:U15055
A:Experimental source: strain SB29, clone DS-1090-3-2
R:Loosmore, S.M.
submitted to the EMBL Data Library, September 1994
A:Reference number: S73320
A:Accession: S73321
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-250, 'I', 252-349, 'RTDATN', 357-631 <LOW>
A:Cross-references: UNIPARC:UPI00000B271A; EMBL:U15055; MID:g1223948; PIDN:AAC43931.1; P1
A:Experimental source: strain SB29, clone DS-1090-3-2
C:Genetics:
A:Gene: tdp2
C:Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor an
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-631/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match 7.6%; Score 94.5; DB 2; Length 631;
Best Local Similarity 20.8%; Pred. No. 7.5;
Matches 52; Conservative 28; Mismatches 55; Indels 115; Gaps 11;
QY 31 YNEKAITENKESDDQFLENTL-----LFGKF-----FTGHPWYNDL----- 67
Db 202 YNRRSAISEDIDN-----LENNLNGAGLTSEFTVNFQTKLTGKLYNERETNNKLQKR 257
QY 68 ----LVDLGSKDATNKYKG-----KVDLYGAYGYQCAGTGNKTACTMY 108
Db 258 KHELYDIDADIYSNRFRGKVPKPTQKDSQEPHPTSEGTLEGGFYG-----PNGE--L 308
QY 109 GGVTFLHDNNRL-----TEEEKVPINLWIDGKQTTVPIDK-----VKTSKEV 150
Db 309 GGFKLADNRVFGVFSKAEETKDKSLRETLDGLKITFKTKTAKTAANKTDEKNF 368
QY 151 TVQELD-----LQARHYLHG-----KFG 168
Db 369 TTKDIPSGEADYLLIDNYPVPLFPPEINTNDFITSRHHKVGDKTYKVEACKNLSVYKFG 428
QY 169 LYNDSFGGK 178

Db 1194 FDYQNNNNSLVLKVNFEFSNQSABDYTVFNNGE-----ILLDDINICDYNL 1244

RESULT 36

G90559

tree-like protein [imported] - Mycoplasma pulmonis (strain UAB CTIP)

C;Species: Mycoplasma pulmonis

C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C;Accession: G90559

R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallieson, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001

A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis

A;Reference number: A99512; MUID:21267165; PMID:11353084

A;Accession: G90559

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-853 <KUR>

A;Cross-references: UNIPROT:Q98QHB; UNIPARC:UPI00000045D0; GB:AL445566; PID:g14089797; E

C;Experimental source: strain UAB CTIP

C;Genetics:

A;Gene: MYPU 3830

A;Genetic code: SGC3

Query Match 7.4%; Score 91; DB 2; Length 853;

Best Local Similarity 23.1%; Pred. No. 21;

Matches 56; Conservative 41; Mismatches 97; Indels 48; Gaps 9;

QY 4 SEINEKDLKK-SELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTGHP 62

Db 224 SNEIEKISLMKTAGFENFOLSNDVQINLSKINFFKNLELDSEYLENT----- 272

QY 63 WYNDLLVDLGSKDATNKYKGGK-----VDLYGA-YYGYOCAGGTNNKTACMYGGVT 112

Db 273 --NNINENLSKEFEKFEINKKHLKINDYFVNLSQVEEPPFELPGWASNIFKSDSTVI 330

QY 113 LHNNRLTEKKVPIN-LWIDGKQTVPI--DKVKTSKKEVTVOELDLQARHYLHGKFGY 170

Db 331 WHFNSVEEDQAKVLINKAIINSRVNSINVKXVDIEKEKFIHNFELAKKIAFGKESL- 389

QY 171 NSDSFGKQVGRGLIVFHSSSGSVSDLPDAQOQYPTDLLRIYRDNKTINSENLDLYL 230

Db 390 -----KRSSIIIFINK--STNKKDLIKLQNE-----NIKNNLINIKINNCL 428

QY 231 YT 232

Db 429 YT 430

RESULT 37

AC1553

B. subtilis YjbK protein homolog lin0964 [imported] - Listeria innocua (strain Clip11262)

C;Species: Listeria innocua

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 12-Jul-2004

C;Accession: AC1553

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluetter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AC1553

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-194 <GLA>

A;Cross-references: UNIPARC:UPI000000CC3F9; GB:AL592022; PIDN:CAC96195.1; PID:g16413423;

A;Experimental source: strain Clip11262

C;Genetics:

A;Gene: lin0964

C;Superfamily: uncharacterized stand-alone CYTH domain protein, gram-positive bacterial

Query Match 7.3%; Score 90.5; DB 2; Length 194;

Best Local Similarity 22.4%; Pred. No. 3.6;

Matches 53; Conservative 32; Mismatches 89; Indels 63; Gaps 12;

QY 3 KSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTGHP 62

Db 3 KELEIEFRNLLTYKEEYDR-----LIEDPRIKEDDFEQT-----N 37

QY 63 WYNDLLVDLGSKDATNKYKGGKVDLYGAYGYOCAGGTNNKTACMYGGVTLHDNNRLTEE 122

Db 38 FYLD-TADFGLKERNALSARIRKLETO-----YQLTLKTPEARGLM-----ETTQILAAD 85

QY 123 KKVPINLWIDGKQTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVGR 182

Db 86 QATAIT---DG--ANIPVGPVRDTLKEIGINHEDLQV-----FGLSKTIRAEKDYKKG 133

QY 183 LIVFHSS-EGSTVSYDL-----FDAQGOVDPDTLLRIYR-----DNKTINSENLIHI 226

Db 134 LLVFDKXNFVGSISDFDLEVEVSDYDKGEIKFIDLKLEYQITNHPAKNKVAFYN-HV 189

RESULT 38

AI1161

flagellar hook protein FlgE homolog lmo0697 [imported] - Listeria monocytogenes (strain I

C;Species: Listeria monocytogenes

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C;Accession: AI1161

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluetter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AI1161

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-411 <GLA>

A;Cross-references: UNIPROT:Q92DV7; UNIPARC:UPI000000556A7; GB:NC_003210; PIDN:CAC98775.1;

A;Experimental source: strain EGD-e

C;Genetics:

A;Gene: lmo0697

Query Match 7.3%; Score 90; DB 2; Length 411;

Best Local Similarity 20.9%; Pred. No. 10;

Matches 55; Conservative 39; Mismatches 81; Indels 88; Gaps 14;

QY 32 YNEKAITENKESDDQFLENTL--LPKGFTG-HPW-----YNDLLVD--LGSKDATNK 79

Db 34 YKQSVVFN----DLLYQNTMGSVAGGLYAGTNPMSPGSGSKIGAILTDYTAGSPSTGR 89

QY 80 YKGGKVDLYGAYGYOCAGGTNNKTACMYGGVTLHDNNRLTEEK----- 123

Db 90 NKDAALQGRGFFIAGNAGG--NIVYTRDGSFAVSDNNVLTTOQGVKVMGYATDKNGNVL 147

QY 124 -----KVPINLWIDGKOT-----TVPIDKVTSKKEVTVOELDLQARHYLHGKFG 169

Db 148 NGNLQPIQIPLNSAIPGATKNGSLSGNIPLD---WGEKDTISSELSVY----- 193

QY 170 YNSDSFGG--KVQRGLIVFHSSSGSVSYDL-----FDAQGOY--PD 207

Db 194 ---DNAGGKHKLQVNNKAATPDASGNVSVEYEIQMDGKALTPTPVGTGLTNYNAQGLTNPD 250

QY 208 TLLRIYRDNKTINSENLDLYL 230

Db 251 ALKNI-QINSTVNGKQVNMGLNL 272

RESULT 39

AI1520

flagellar hook protein FlgE homolog lin0705 [imported] - Listeria innocua (strain Clip11

C;Species: Listeria innocua

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: E64410
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1634 <BUL>
A;Cross-references: UNIPARC:UPI0000178A96; GB:U67532; GB:L77117; NID:gl515959; PID:gl591
C;Genetics:
A;Map position: REV816304-811400
C;Function: <DPL>
A;Description: as DNA-directed DNA polymerase, catalyzes the polymerization of DNA at th
C;Function: <EN1>
A;Description: as DNA endonuclease PI-MjaI, catalyzes the hydrolysis of internal phospho
C;Function: <EN2>
A;Description: as DNA endonuclease PI-MjaII, catalyzes the hydrolysis of internal phosph
C;Superfamily: DNA-directed DNA polymerase KOD
C;Keywords: endonuclease; hydrolase; nucleotidyltransferase; protein splicing
F;1-425/Domain: DNA-directed DNA polymerase family B extein 1 #status predicted <XT1>
F;426-794/Domain: DNA endonuclease PI-I (pol B extein 1) #status predicted <MAT2>
F;795-882/Domain: DNA-directed DNA polymerase family B extein 2 #status predicted <XT2>
F;883-1358/Domain: DNA endonuclease PI-II (pol B extein 2) #status predicted <MAT3>
F;1358-1634/Domain: DNA-directed DNA polymerase family B extein 3 #status predicted <XT3>
F;425-795/Cross-link: peptide (Arg-Ser) #status predicted
F;882-1359/Cross-link: peptide (Asn-Ser) #status predicted

Query Match 7.2%; Score 89; DB 2; Length 1634;
Best Local Similarity 22.1%; Pred. No. 69;
Matches 51; Conservative 34; Mismatches 80; Indels 66; Gaps 10;

QY 12 LRKSELRNALNRLQIYYNKAITENKESDDQFLENTLLPKGPTGHPWNLDLVL 71
Db 614 VREKGGTKAITLCAKADIVLKEILKNKE---KVLPAAIL-RGFFGEGGYVTVRRAV 669

QY 72 GSKDATNKYGGK-----VDLYGAYGYQCAGGTPNKTCMGVTLHDNRNLTTEKKVP 126
Db 670 VVNGQTNNDYDKIRFIASLLDLRLGDKYSF-----YTSYEEERGGKLRVY 713

QY 127 INLWIDGKQTTVPIDKVKTS-----KKEVTVOELDLQARHVLHGKFLYNSD----- 173
Db 714 IEIFSGK-----DLIKFSILISFTSRKNNLNEIIRKTLKIDGYDFYDLDDVCVS 766

QY 174 --SFGGKV-----QRGLIVFHSSEGS--TVSYDLFDAQQGVPTDL 209
Db 767 LESYKGEVYDLEGRPPYFANGILTHNSLYPSIIISYNI-----SPDTL 811

RESULT 43
C89888
hypothetical protein SA1011 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
R;Accession: C89888
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogun
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, R.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: C89888
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-241 <KUR>
A;Cross-references: UNIPROT:Q99UUI; UNIPARC:UPI000000CA9DE; GB:BA000018; PID:gl3700967; F
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA1011
C;Superfamily: toxic shock syndrome toxin

Query Match 7.1%; Score 88; DB 2; Length 241;
Best Local Similarity 23.9%; Pred. No. 7.6;
Matches 44; Conservative 32; Mismatches 62; Indels 46; Gaps 10;

QY 63 WYNDLVLGSKD--ATNKYKGGKVDLYG-----AYGYQ---CAGGTPNKTCMG 109
Db 84 WYSHIQV-FGSESNGINQLRNKYVDIFGKQBDTVEGYWTYDETFTGGVTPAAT----- 137

QY 110 GVTLHDNRNLTBEKKVPINLWIDGKQTTV--PIDKVKTSKKEVTVQELDLQARHVLHGK 167
Db 138 -----SSDKPVRLFYKSDKQOTIIGGHFYGKGNKPVLTLLKELDFRIRQTLINK 187

QY 168 GLYNDSFGGKQVORGLIVFHSSEGSVSYDLFDAQQGVPTDLRIYRDNKTI--NSENLHI 226
Db 188 KLYN-----GEFNKGQIKI-TADGNNTIDL-----SKKLKLTDTNRYVKNPKNAQI 233

QY 227 DLYL 230
Db 234 EVIL 237

RESULT 44
E96793
hypothetical protein F14G6.15 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-2004
C;Accession: E96793
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
ker, M.; Salzborg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: E96793
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-617 <STO>
A;Cross-references: UNIPARC:UPI0000048495; GB:AE005173; NID:g6642673; PIDN:AAF20253.1; G
C;Genetics:
A;Gene: F14G6.15
A;Map position: 1
C;Superfamily: pyrophosphate-dependent phosphofructokinase, PfpB type; 6-phosphofructokin

Query Match 7.1%; Score 88; DB 2; Length 617;
Best Local Similarity 30.2%; Pred. No. 25;
Matches 26; Conservative 9; Mismatches 35; Indels 16; Gaps 3;

QY 74 KDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMGVGT-----LHDNRNLTTEE 122
Db 412 KEGT--YKGGKFNACHTFGYQARGSLPSKFCDCYAVVLGHVCYHILAAAGLNGYMATVTN 469

QY 123 KKVPINLWIDGKQTTVPIDKVKTSKK 148
Db 470 LKSPVKNK---KCGAAPISAMMTVKR 492

RESULT 45
S73438
MG032 homolog B01_orf672 - Mycoplasma pneumoniae (strain ATCC 29342)
C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: S73438
R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
A;Reference number: S73327; MUID:97105885; PMID:8948633
A;Accession: S73438
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-672 <HIM>
A;Cross-references: UNIPROT:P75072; UNIPARC:UPI0000139F53; EMBL:AE000013; GB:U00089; NID

Db 556 EHTQSDTASAKISSNKEIHLKXLSYIRKXNSNSNFDTATNTQNTSFSGANVALIL 615
QY 114 HDNNRLTEKKVPINLWIDKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNS- 172
Db 616 ADSNK-----TLAPDRVEADLKG---NALDLKSGRG-NAKFDLYYS 653
QY 173 -----DSFGKG-----VQGLIVFH-SSEGSTVSVDLPAQOQYPTTLRIYR 214
Db 654 NDLNLVNSIDNLYNEFLQKQAVODG--VFNLISKSGLEY--FDGQIDFKNTYV---K 706
QY 215 DNKTINSENLIHD 227
Db 707 DLKGINQLISFID 719
RESULT 52
A45604
major blood-stage surface antigen Pv200 - Plasmodium vivax
C:Species: Plasmodium vivax
C:Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004
C:Accession: A45604
R:Gibson, H.L.; Tucker, J.B.; Kaelow, D.C.; Kretzli, A.U.; Collins, W.E.; Kiefer, M.C.;
Mol. Biochem. Parasitol. 50, 325-333, 1992
A:Title: Structure and expression of the gene for Pv200, a major blood-stage surface ant
A:Reference number: A45604; MUID:92158013; PMID:1371329
A:Accession: A45604
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1751 <GIB>
A:Cross-references: UNIPROT:Q26194; UNIPARC:UPI0000083C26; GB:M75674; NID:g160608; PID:9
A:Note: sequence extracted from NCBI backbone (NCBI:83591, NCBI:P:83592)
C:Superfamily: G surface protein
C:Keywords: surface antigen
Query Match 7.0%; Score 86.5; DB 2; Length 1751;
Best Local Similarity 22.9%; Pred. No. 1.2e+02;
Matches 44; Conservative 30; Mismatches 63; Indels 55; Gaps 8;
QY 2 EKSEENEKND-----LRKKSQALNLSNRQIY-----YNEKAITENKESDDQFLE 49
Db 1087 KKNKISNSKQIKKLSLKNLERRQNLNPTSVLKNYTAFFNKKRETEKKEVENTLKN 1146
QY 50 NTLIPK-----GFFTGHPWYNDLLVDLGSKOATN-----KYK-----GKKVDLYG 89
Db 1147 TELLYKXARAKYIYGEPPFLKTLSEESQKEDNYLNLEKFKVLSRLGRLGKNIIELEK 1206
QY 90 AYYGYQCAGTPNKATCMYGGVTLHDNNRLTEKKVPINLWIDKQTTVPIDKVKTSKK- 148
Db 1207 ENISYLSG-----LH--HVLTELKEILKKNKYSGNDHTKNIAAVKEALQA 1250
QY 149 -----EVTQVE 154
Db 1251 YQELIPKVTQVE 1262
RESULT 53
S78650
DNA endonuclease ai5-alpha - yeast (Saccharomyces cerevisiae) mitochondrion
N:Alternate names: protein Q0070
C:Species: mitochondrion Saccharomyces cerevisiae
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C:Accession: S78650; S78651; S27138
R:Foury, F.; Roganti, T.; Lecrenier, N.; Purnelle, B.
submitted to the Protein Sequence Database, December 1998
A:Reference number: S78634
A:Accession: S78650
A:Molecule type: DNA
A:Residues: 1-630 <FOU>
A:Cross-references: UNIPROT:Q92ZK1; UNIPARC:UPI0000091C05; EMBL:AJ011856; GSPDB:GN00017;
A:Experimental source: strain FY1679, isogenic derivative of strain S288C
R:Foury, F.; Roganti, T.; Lecrenier, N.; Purnelle, B.
FEBS Lett. 440, 325-331, 1998

A:Title: The complete sequence of the mitochondrial genome of Saccharomyces cerevisiae.
A:Reference number: Z13743; MUID:99087401; PMID:9872396
A:Accession: S78651
A:Molecule type: DNA
A:Residues: 1-630 <POU>
A:Cross-references: UNIPARC:UPI0000091C05; EMBL:AJ011856; NID:g4160362; PIDN:CAA09829.1;
A:Experimental source: strain FY1679, isogenic derivative of strain S288C
R:Hensgens, L.A.M.; Bonen, L.; de Haan, M.; van der Horst, G.; Grivell, L.A.
Cell 32, 379-389, 1983
A:Title: Two intron sequences in yeast mitochondrial COX1 gene: homology among URF-contain
A:Reference number: S27138; MUID:83129428; PMID:6297792
A:Accession: S27138
A:Molecule type: DNA
A:Residues: 241-630 <HEN>
A:Cross-references: UNIPARC:UPI00001787C6; EMBL:J01477
A:Experimental source: strain KLI4-4A
C:Genetics:
A:Gene: SGD:A15 ALPHA; SCAI5alpha; MIPS:Q0070
A:Cross-references: SGD:S0007265
A:Genome: mitochondrion
A:Genetic code: SG2
C:Superfamily: DNA endonuclease I-SceII; COI intron 9 protein homology; cytochrome-c oxid
C:Keywords: mitochondrion
F:241-324/Region: cox1 exon 5-alpha encoded
F:325-630/Region: cox1 intron encoded
Query Match 6.9%; Score 86; DB 2; Length 630;
Best Local Similarity 19.5%; Pred. No. 3;
Matches 56; Conservative 35; Mismatches 86; Indels 110; Gaps 14;
QY 2 EKSEENEKDKKKGELQNALNSRQIYIYNEKAITENKESDDQPLENTLFPKGFFTGH 61
Db 331 DKQKQKXKLIRYQKMNW---NMKTYLNNNNMIMWNN-----MYKG----- 370
QY 62 PWYNDLLVDLGSKOATNKYKKVDLYGAYGY---QCAG-----GTPNKTAC 106
Db 371 -----NLVDYPRSNRYIQPNINKELVYGVNLESVCVGMPTTYNIVKHMVGIPNNILY 425
QY 107 MYGGVTLHDNNRLTEKKVPINLWIDKQTTVPIDKVKTSKKEV---TVQELDLQAR--- 160
Db 426 IMTGILLTDG-----WID-----YTSKXDLKKTIMEINCRFLKQ 461
QY 161 -----HY-----LHGKFGLYNSDSFGKQVQGL-----IVF 186
Db 462 SMHSEYLMYVFWLISHYCMSPKMKIAKVKGK--SYNQLF---YTRSLPCFTILRYMF 516
QY 187 HSSEGSTVSVDLPAQOQYPTTLRIYRDNKNTINSENLIHDLYYTT 233
Db 517 YNGRVKIVPNLYDLL-NYESLAHIMCDGSFVKGGGLYLNLSQFTT 562
RESULT 54
AG1749
glycosidase homolog lin2540 [imported] - Listeria innocua (strain Clip11262)
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AG1749
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duesurget, O.; Entian, K.D.; Fsihi, H.,
Science 294, 849-852, 2001
A:Authors: Krefit, J.; Kuhn, M.; Kunst, P.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative Genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AG1749
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1090 <GLA>
A:Cross-references: UNIPROT:Q928J2; UNIPARC:UPI000000C8DB; GB:AL592022; PIDN:CAC97767.1;
A:Experimental source: strain Clip11262
C:Genetics:
A:Gene: lin2540

A:Gene: tra1077C

Query Match 6.8%; Score 84; DB 2; Length 272;
Best Local Similarity 21.5%; Pred. No. 19;
Matches 42; Conservative 30; Mismatches 67; Indels 56; Gaps 7;

QY 5 EEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTGHPWY 64
DB 19 ERNVKDELTEKMLK-----IRQ-----EHANAGYRPMRELLKQRGTHVNHKKV 62

QY 65 NDLLVDLGSKDATNKYKGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKK 124
DB 63 QRLMKKGLRVTSYWHKSRK-----YNSYKGKGVTAKN-----KLHRRFR----- 103

QY 125 VPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKQVQRGLI 184
DB 104 -----TSIPHQKITDTTPEKYVEDGQKKCYLNPYIALFNSE-----VI 143

QY 185 VPH-SSEGSTVSVDL 198
DB 144 SYHISKQPSYQSIDI 158

RESULT 65
F70339
Glycerol kinase - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: F70339
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Oviatt, J.

Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: F70339
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-492 <AQP>
A:Cross-references: UNIPROT:O66746; UNIPARC:UPI0000056365; GB:AE000690; NID:92983100; PMID:92983100; P11111
A:Title: Cloning and nucleotide sequence determination of the entire mec DNA of pre-methicillin-resistant strain VFS
A:Experimental source: strain VFS
C:Genetics: glpK
A:Gene: glpK
C:Superfamily: xylulokinase

Query Match 6.8%; Score 84; DB 2; Length 492;
Best Local Similarity 25.7%; Pred. No. 39;
Matches 61; Conservative 30; Mismatches 74; Indels 72; Gaps 15;

QY 9 EKDLRKSELQNALSNLRQ---IYYNEKAITENKESDDQFLENTLLFKGFTGHPWYN 65
DB 44 EQDPLELWAVRKSLSSEVIQQVGLKEINSIGITNQRE-----TVILWDXETGRPVYN 95

QY 66 DLL-VDLGSKDATNKYKGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKK 124
DB 96 AILWQDLRTEDIC---RKLSEYSEYIKENT-----GLLLHPYFSASK--- 134

QY 125 VPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGK--FGLYNS-----DSFGK 178
DB 135 --VN-WI-----IENVGVKKDTE-----RGKVIQGTVDTWILWNLGTGK 171

QY 179 VQVGLIVFHSSEGSTVSVD-LFDAQG-QYPTDLLRIYRONKNTINSE-NLHIDLILYLT 232
DB 172 V-----HKTEFSPNASRLLFNIRKLEYDDELLKIFRIPKNIPLFVNNESSLFGYT 221

RESULT 66
T41863
chitinase chi-A orf126 - Bombyx mori nuclear polyhedrosis virus (isolate T3)
C:Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV
A:Variety: Isolate T3
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
R:Gomi, S.; Majima, K.; Maeda, S.

J. Gen. Virol. 80, 1323-1337, 1999
A:Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.
A:Reference number: Z22020; MUID:99281911; PMID:1035780
A:Accession: T41863
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-552 <KAM>
A:Cross-references: UNIPROT:O92482; UNIPARC:UPI00000F4295; EMBL:L33180; NID:g3745835; P11111
A:Experimental source: isolate T3
C:Superfamily: Serratia marcescens chitinase

Query Match 6.8%; Score 84; DB 2; Length 552;
Best Local Similarity 24.3%; Pred. No. 45;
Matches 45; Conservative 23; Mismatches 69; Indels 48; Gaps 11;

QY 32 YNEKAI---TENKESDDQFLENTLLFKGFTGHPWYNLLVDLGSKDATNKYKGKVDLY 88
DB 359 YDKIAVNVYAEQAQKSLDKIFLMTYDFKG-----AWSN---TDLGYQTTVYAFPSWNSSELY 410

QY 89 GAYGYQC---AGGTPNKT---ACMYG---GVTLHDN-NRLTEKKVPIN-LWIDGKQT 136
DB 411 TTHYAVDALLEGQVDPNKIIIVGAVYGRGWTGVTNNGNYFSGTNGPVGSTWEDG--- 467

QY 137 TVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKQVQRGLIYVHSESEGSTVS 196
DB 468 -----VDYRQIQKDLNNY-----VYTFDS-----AAQASYVFDKSKGDLISF 505

QY 197 DLFDA 201
DB 506 DSVD 510

RESULT 67
T44118
penicillin-binding protein 2 [imported] - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T44118
R:Ito, T.; Katayama, Y.; Hiramatsu, K.
Antimicrob. Agents Chemother. 43, 1449-1458, 1999
A:Title: Cloning and nucleotide sequence determination of the entire mec DNA of pre-methicillin-resistant strain N315
A:Reference number: Z22733; MUID:99278010; PMID:10348769
A:Accession: T44118
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-668 <ITO>
A:Cross-references: UNIPROT:Q54113; UNIPARC:UPI00000DA0B7; EMBL:D86934; PIDN:BAA82220.1
A:Experimental source: strain N315
C:Genetics: mecA
A:Note: mecA
C:Superfamily: penicillin-binding protein 2B

Query Match 6.8%; Score 84; DB 2; Length 668;
Best Local Similarity 20.0%; Pred. No. 57;
Matches 63; Conservative 45; Mismatches 87; Indels 120; Gaps 15;

QY 4 SEINEKDLRKSE---LQNALSNLRQIYYNEK-----YDKLQHEGQYRVITVDONSNTIAHTLIE 39
DB 261 SEELKQKEYKGYKDDAVIGKKGLEKL-----YDKLQHEGQYRVITVDONSNTIAHTLIE 315

QY 40 NKESDDQFLENTLLFKGFTGHPWYNLLVDLGSKDATNKYKGKVDL-----YGAYGY 94
DB 316 KKKKGKQIQLTIDAK---VQKSIYNNMKNDYSGGTAHPQTGELLALVSTPSYDV--- 369

QY 95 QCAGGTPNKTACMYGGVTLHDNNRLTEKKVP-INLWIDGKQTTVP--IDKVKTSKKEVT 151
DB 370 -----PMY-GMSNEEYNKLTEDKKEPLLNKF---QITTSFGTQKILTAMIGLN 415

QY 152 VQELDLQARHYLHGKFGLYNSDSFGG----- 177
DB 416 NKTLDKTSYKIDGK-GWQKQKSWGVNTRVEVNVNGNIDLKQALESSNIPFARVALEL 474

QY 178 ---KVQVGLIVFHSSEGSTVSVDLFDQAQ-----GQ-----YPTDLLRI 212

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 15, 2006, 20:08:30 ; Search time 76.7226 Seconds
(without alignments)
2142.628 Million cell updates/sec

Title: US-09-900-766-7
Perfect score: 1238
Sequence: 1 SEKSEINEKDLKKSELR.....RDNKTINSENHIDLYLTYT 233

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 segs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : UniProt 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1238	100.0	257	1	ETXE STAAU
2	1023	82.6	257	1	ETXA STAAU
3	1023	82.6	257	1	ETXA STAAU
4	1023	82.6	257	2	O6G7Y7 STAAU
5	1023	82.6	260	2	Q931M4 STAAU
6	1018	82.2	261	2	Q5P8P6 STAAU
7	1013	81.8	257	2	Q6GFAB STAAU
8	994	80.3	260	2	Q99SU3 STAAU
9	971	78.4	219	2	Q6XZB9 STAAU
10	837	67.6	268	2	Q761S7 STAAU
11	830	67.0	288	2	O85217 STAAU
12	825	66.6	154	2	Q6R2G0 STAAU
13	663	53.6	258	1	ETXD STAAU
14	496	40.1	152	2	Q6R2F9 STAAU
15	492.5	39.8	234	2	O5HFG0 STAAC
16	490.5	39.6	229	2	O6G8W7 STAAU
17	490.5	39.6	229	2	O8NW97 STAAU
18	461.5	37.3	258	2	Q9EZM4 STAAU
19	461.5	37.3	258	2	Q7A2Q6 STAAU
20	461.5	37.3	258	2	Q7A4X1 STAAU
21	446.5	36.1	251	2	O6YCN3 STAAU
22	446.5	36.1	251	2	O6GFM1 STAAU
23	414	33.4	254	2	O6GFN7 STAAU
24	387.5	31.3	260	2	Q7A4W6 STAAU
25	387.5	31.3	260	2	Q99T46 STAAU
26	387.5	31.3	261	2	Q9EZM8 STAAU
27	381	30.8	179	2	O52075 9ZZZZ
28	366	29.6	217	2	O8RR76 STAAU
29	366	29.6	241	1	ETXH STAAU
30	366	29.6	241	1	ETXH STAAU
31	366	29.6	241	2	Q6VAM8 STAAU

32	366	29.6	241	2	Q6GD45 STAAU	Q6gd45	staphylococ
33	348.5	28.2	242	2	Q7X0E8 STAAU	Q7x0e8	staphylococ
34	348.5	28.2	242	2	Q6GFM9 STAAU	Q6gfm9	staphylococ
35	341.5	27.6	225	2	Q8VVM1 STRPY	Q8vwm1	streptococ
36	340.5	27.5	243	2	Q7X0E7 STAAU	Q7x0e7	staphylococ
37	339.5	27.4	242	2	O5DIJ9 STAAU	O5dij9	staphylococ
38	339.5	27.4	242	2	O8S383 STAAU	O8s383	staphylococ
39	339.5	27.4	242	2	Q7A2Q5 STAAU	Q7a2q5	staphylococ
40	339.5	27.4	242	2	Q7A4W8 STAAU	Q7a4w8	staphylococ
41	337.5	27.3	218	2	O52T95 STAAU	O52t95	staphylococ
42	337	27.2	240	2	Q9POL7 STAAU	Q9pol7	staphylococ
43	337	27.2	240	2	Q7A2N9 STAAU	Q7a2n9	staphylococ
44	337	27.2	240	2	Q7A4K9 STAAU	Q7a4k9	staphylococ
45	336.5	27.2	209	2	O52TA0 STAAU	O52ta0	staphylococ
46	336	27.1	240	2	O8NXJ5 STAAU	O8nxj5	staphylococ
47	335.5	27.1	210	2	O52T97 STAAU	O52t97	staphylococ
48	335.5	27.1	218	2	O8RR75 STAAU	O8rr75	staphylococ
49	335.5	27.1	225	2	O9L921 STRPE	O9l921	streptococ
50	334.5	27.0	225	2	Q99Z21 STRPY	Q99z21	streptococ
51	332.5	26.9	242	2	Q7X0E6 STAAU	Q7x0e6	staphylococ
52	320	25.8	239	2	Q7A4W7 STAAU	Q7a4w7	staphylococ
53	320	25.8	239	2	Q99T47 STAAU	Q99t47	staphylococ
54	319.5	25.8	242	2	O6G7U1 STAAU	O6g7u1	staphylococ
55	319.5	25.8	242	2	O8NVN3 STAAU	O8nvn3	staphylococ
56	318.5	25.7	256	2	O8VLM7 STAAU	O8vlm7	staphylococ
57	316.5	25.6	242	2	Q93CC6 STAAU	Q93cc6	staphylococ
58	316.5	25.6	242	2	O5HHJ9 STAAC	O5hhj9	staphylococ
59	316	25.5	239	2	Q9EZM7 STAAU	Q9ezm7	staphylococ
60	312	25.2	86	2	O711S9 STAIN	O711s9	staphylococ
61	310	25.0	242	2	O6G7U0 STAAU	O6g7u0	staphylococ
62	310	25.0	242	2	O8NVN2 STAAU	O8nvn2	staphylococ
63	309	25.0	163	2	O6R2F8 STAAU	O6r2f8	staphylococ
64	309	25.0	242	2	O54476 STAAU	O54476	staphylococ
65	309	25.0	242	2	Q93CC5 STAAU	Q93cc5	staphylococ
66	309	25.0	242	2	O5HHK0 STAAC	O5hhk0	staphylococ
67	302	24.4	239	2	O6GFM8 STAAC	O6gfm8	staphylococ
68	300.5	24.3	250	2	Q5MAA8 STAAU	Q5maa8	staphylococ
69	300.5	24.3	266	1	ETXB STAAU	F01552	staphylococ
70	300.5	24.3	266	2	O7BBY8 STAAU	O7bby8	staphylococ
71	300.5	24.3	266	2	O5HHH9 STAAC	O5hhh9	staphylococ
72	299.5	24.2	239	2	O5MAB7 STAAU	O5mab7	staphylococ
73	298	24.1	261	2	O6YCN4 STAAU	O6ycn4	staphylococ
74	298	24.1	261	2	Q6GFN0 STAAC	Q6gfn0	staphylococ
75	296.5	23.9	256	2	O5XC17 STRP6	O5xc17	streptococ
76	295.5	23.9	251	1	SPEA STRP8	P62561	streptococ
77	295.5	23.9	251	1	SPEA STRPY	P62560	streptococ
78	295	23.8	177	2	O6R1Y7 STAAU	O6r1y7	staphylococ
79	294.5	23.8	251	2	O8K6K5 STRP3	O8k6k5	streptococ
80	291.5	23.5	261	2	O6XXM3 STAAU	O6xxm3	staphylococ
81	290.5	23.5	261	2	O6XXM5 STAAU	O6xxm5	staphylococ
82	288.5	23.3	261	2	O6XXM4 STAAU	O6xxm4	staphylococ
83	285.5	23.1	239	2	O6E531 STAAU	O6e531	staphylococ
84	285.5	23.1	239	2	O6E532 STAAU	O6e532	staphylococ
85	285.5	23.1	266	1	ENTC3 STAAU	F0a013	staphylococ
86	285.5	23.1	266	1	ENTC3 STAAU	F0a015	staphylococ
87	285.5	23.1	266	2	O54A76 STAAU	O54a76	staphylococ
88	285.5	23.1	266	2	O6E535 STAAU	O6e535	staphylococ
89	284.5	22.9	239	2	O05157 STAIN	O05157	staphylococ
90	283.5	22.9	239	2	O8NXJ6 STAAU	O8nxj6	staphylococ
91	283.5	22.8	239	2	O6E533 STAAU	O6e533	staphylococ
92	282.5	22.8	239	2	ENTC2 STAAU	F34071	staphylococ
93	281.5	22.7	266	1	O53X04 STAAU	O53x04	staphylococ
94	281.5	22.7	266	2	O6X2E6 STAAU	O6x2e6	staphylococ
95	280.5	22.7	239	2	O6ST49 STAAU	O6st49	staphylococ
96	280.5	22.7	239	2	O54696 STRPY	O54696	streptococ
97	279.5	22.6	236	2	Q9F0L6 STAAU	Q9f0l6	staphylococ
98	279.5	22.6	271	2	Q9F0L6 STRPY	P97163	streptococ
99	278.5	22.5	236	2	O53678 STAAU	O53678	staphylococ
100	278.5	22.5	239	2	Q938P4 STRAQ	Q938p4	staphylococ
101	277.5	22.4	222	2	O985Z4 STRPY	O985z4	streptococ
102	277.5	22.4	222	2	O985Z4 STRPY	Q985z4	streptococ
103	277.5	22.4	234	2	Q9R5X4 STAP	Q9r5x4	staphylococ
104	277.5	22.4	236	2	Q54779 STRPY	Q54779	streptococ

105	276.5	22.3	222	2	Q9R931_STRPY	Q9r931 streptococc	178	217	17.5	240	2	Q8P2R5_STRP8	Q8p2r5 streptococc
106	272.5	22.0	236	2	Q57453_STRPY	Q57453 streptococc	179	216	17.4	210	2	Q9K2G9_STRPY	Q9k2g9 streptococc
107	272.5	22.0	239	2	Q06534_STAAU	Q06534 staphylococc	180	214	17.3	234	2	Q76FM2_STRDY	Q76fm2 streptococc
108	269.5	21.8	260	2	Q54971_STRPY	Q54971 streptococc	181	213	17.2	234	2	Q76FM3_STRDY	Q76fm3 streptococc
109	267.5	21.6	260	2	Q54738_STRPY	Q54738 streptococc	182	208	16.8	234	2	Q76FNO_STRREQ	Q76fn0 streptococc
110	267.5	21.6	260	2	Q54739_STRPY	Q54739 streptococc	183	205	16.6	234	2	Q76FM5_STRREQ	Q76fm5 streptococc
111	267.5	21.6	260	2	Q79X14_STRP3	Q79x14 streptococc	184	203	16.4	234	2	Q76FM7_STRREQ	Q76fm7 streptococc
112	266.5	21.5	266	1	ENTC1_STAAU	P01553 staphylococc	185	201	16.2	257	2	Q7A5A7_STAAU	Q7a5a7 staphylococc
113	264.5	21.4	258	2	Q7X0E4_STAAU	Q7X0e4 staphylococc	186	201	16.2	157	2	Q95TP7_STAAU	Q95tp7 staphylococc
114	264.5	21.4	258	2	Q6GFN2_STAAU	Q6GFn2 staphylococc	187	199	16.1	234	2	Q76FM0_STRREQ	Q76fm0 streptococc
115	262.5	21.2	233	2	Q52T98_STAAU	Q52t98 staphylococc	188	199	16.1	236	2	Q9L920_9STRE	Q9l920 streptococc
116	262.5	21.2	258	2	Q9ZNF2_STAAU	Q9Znf2 staphylococc	189	198	16.0	234	2	Q76FM9_STAAU	Q76fm9 streptococc
117	259.5	21.0	222	2	Q6XZE7_STAAU	Q6xze7 staphylococc	190	197	15.9	136	2	Q7A4X0_STAAU	Q7a4x0 staphylococc
118	258.5	20.9	258	2	Q5D1K7_STAAU	Q5d1k7 staphylococc	191	197	15.9	136	2	Q99T49_STAAU	Q99t49 staphylococc
119	256.5	20.7	264	2	Q764P6_STAIN	Q764p6 staphylococc	192	197	15.9	195	2	Q6VCN2_STAAU	Q6vcn2 staphylococc
120	256	20.7	209	2	Q9RQ05_STRPY	Q9rq05 streptococc	193	197	15.9	234	2	Q8G9K7_STRREQ	Q8g9k7 streptococc
121	255.5	20.6	233	2	Q8RR77_STAAU	Q8rr77 staphylococc	194	197	15.9	234	2	Q9JRR3_STRREQ	Q9jrr3 streptococc
122	255.5	20.6	258	1	ETXG_STAAU	P0a017 staphylococc	195	197	15.9	236	1	SPEH_STRPY	Q9x5c8 streptococc
123	255.5	20.6	258	1	ETXG_STAAU	P0a018 staphylococc	196	193	15.6	232	2	Q7BAE3_STRPY	Q7bae3 streptococc
124	255.5	20.6	258	1	ETXG_STAAU	Q7X0e5 staphylococc	197	187	15.1	256	2	Q9S1H9_STRPY	Q9s1h9 streptococc
125	255.5	20.6	258	2	Q7X0E5_STAAU	Q7X0e5 staphylococc	198	187	15.1	256	2	Q9X9R8_STRPY	Q9x9r8 streptococc
126	255.5	20.6	258	2	Q9EZM3_STRPY	Q9ezm3 staphylococc	199	185	14.9	235	1	SPEC_STRP6	Q5xb82 streptococc
127	253	20.4	209	2	Q5Q043_STRPY	Q5q043 streptococc	200	185	14.9	235	1	SPEC_STRP8	Q8nxx2 streptococc
128	253	20.4	209	2	Q9LAD8_STRPY	Q9lad8 streptococc	201	185	14.9	235	1	SPEC_STRPY	P13380 streptococc
129	253	20.4	209	2	Q9LAE0_STRPY	Q9lae0 streptococc	202	180	14.5	235	1	SPEC_STRPY	P13380 streptococc
130	251.5	20.3	259	2	Q76LS8_STAAU	Q76ls8 staphylococc	203	168	13.6	206	2	Q6LD36_STRPY	Q6ld36 streptococc
131	251	20.3	209	2	Q9LAC6_STRPY	Q9lac6 streptococc	204	163	13.2	206	2	Q54512_STRPY	Q54512 streptococc
132	251	20.3	209	2	Q9LAD1_STRPY	Q9lad1 streptococc	205	160.5	13.0	108	2	Q9EZM5_STAAU	Q9ezm5 staphylococc
133	250.5	20.2	258	2	Q79IV2_STAAU	Q79iv2 staphylococc	206	144	11.6	62	2	Q7A5A8_STAAU	Q7a5a8 staphylococc
134	249	20.1	209	2	Q9LAC4_STRPY	Q9lac4 streptococc	207	144	11.6	62	2	Q99TP8_STAAU	Q99tp8 staphylococc
135	249	20.1	209	2	Q9LAE1_STRPY	Q9lae1 streptococc	208	138	11.1	96	2	Q5XE11_STRP6	Q5xe11 streptococc
136	249	20.1	233	2	Q76WJ7_STRPY	Q76wj7 streptococc	209	135	10.9	259	2	Q70EW3_9STRE	Q70ew3 streptococc
137	248.5	20.1	258	2	Q5D1K4_STAAU	Q5d1k4 staphylococc	210	135	10.9	259	2	Q5W1M5_9STRE	Q5w1m5 streptococc
138	247.5	20.0	220	2	Q79AQ0_STRPY	Q79aq0 streptococc	211	135	10.9	262	2	Q8P0S0_STRP8	Q8p0s0 streptococc
139	247	20.0	209	2	Q9LAC5_STRPY	Q9lac5 streptococc	212	134.5	10.9	98	2	Q5XC18_STRP6	Q5xc18 streptococc
140	247	20.0	223	2	Q52TA2_STAAU	Q52ta2 staphylococc	213	134	10.8	227	2	Q849U3_STRPY	Q849u3 streptococc
141	246	19.9	209	2	Q9LAC7_STRPY	Q9lac7 streptococc	214	134	10.8	262	2	Q70EW2_9STRE	Q70ew2 streptococc
142	245.5	19.8	159	2	Q6R2G1_STAAU	Q6r2g1 staphylococc	215	134	10.8	262	2	Q5W1M4_9STRE	Q5w1m4 streptococc
143	245.5	19.7	214	2	Q6XZE8_STAAU	Q6xze8 staphylococc	216	130	10.5	259	2	Q938J1_9CAUD	Q938j1 temperate p
144	244.5	19.7	258	2	Q7WS59_STAAU	Q7ws59 staphylococc	217	127.5	10.3	62	2	Q8NYV9_STAAU	Q8nyv9 staphylococc
145	244	19.7	209	2	Q9LAD2_STRPY	Q9lad2 streptococc	218	126	10.2	209	2	Q879B0_STRP3	Q879b0 streptococc
146	244	19.7	209	2	Q9LAD6_STRPY	Q9lad6 streptococc	219	126	10.2	233	2	Q849U4_STRPY	Q849u4 streptococc
147	243.5	19.7	201	2	Q4ZJR6_STRPY	Q4zjr6 streptococc	220	123	9.9	132	2	Q9EZM6_STAAU	Q9ezm6 staphylococc
148	243	19.6	197	2	Q7WY99_STRCB	Q7wy99 streptococc	221	123	9.9	133	2	Q7A4W9_STAAU	Q7a4w9 staphylococc
149	243	19.6	233	2	Q6VB17_STRCB	Q6vb17 streptococc	222	123	9.9	133	2	Q99T48_STAAU	Q99t48 staphylococc
150	242	19.5	209	2	Q5Q044_STRPY	Q5q044 streptococc	223	122	9.9	156	2	Q71US9_STRPY	Q71us9 streptococc
151	242	19.5	209	2	Q5Q045_STRPY	Q5q045 streptococc	224	120	9.7	883	2	Q71YD4_PLABE	Q71yad4 plasmodium
152	242	19.5	209	2	Q9LAD9_STRPY	Q9lad9 streptococc	225	118.5	9.6	156	2	Q7BTR4_STRPY	Q7btr4 streptococc
153	242	19.5	233	2	Q8N289_STRP8	Q8n289 streptococc	226	116.5	9.4	231	2	Q9RN32_STAAU	Q9rn32 staphylococc
154	241	19.5	209	2	Q9LAC9_STRPY	Q9lac9 streptococc	227	116	9.4	231	2	Q92FS5_STAAU	Q92fs5 staphylococc
155	241	19.4	209	2	Q9LAD4_STRPY	Q9lad4 streptococc	228	116	9.4	231	2	Q6GJP2_STAAP	Q6gjp2 staphylococc
156	239	19.3	209	2	Q9LAC3_STRPY	Q9lac3 streptococc	229	115.5	9.3	180	2	Q5XBU3_STRP6	Q5xbu3 streptococc
157	239	19.3	209	2	Q9LAC8_STRPY	Q9lac8 streptococc	230	114.5	9.2	231	2	Q6C588_STAAU	Q6c588 staphylococc
158	239	19.3	258	2	Q5X9R9_STRP6	Q5x9r9 streptococc	231	114.5	9.2	231	2	Q8NY48_STAAU	Q8ny48 staphylococc
159	238	19.2	256	2	Q9S1H8_STRPY	Q9s1h8 streptococc	232	114	9.2	231	2	Q9RN33_STAAU	Q9rn33 staphylococc
160	237.5	19.2	180	2	Q6DTL6_STRPY	Q6dtl6 streptococc	233	113.5	9.2	1400	2	Q86AL1_DICDI	Q86al1 dictyostelli
161	237	19.1	209	2	Q9LAD5_STRPY	Q9lad5 streptococc	234	113	9.1	232	2	Q7A7H2_STAAU	Q7a7h2 staphylococc
162	234	18.9	179	2	Q56D15_STRPY	Q56d15 streptococc	235	113	9.1	232	2	Q99WH4_STAAU	Q99wh4 staphylococc
163	234	18.9	209	2	Q9LAD7_STRPY	Q9lad7 streptococc	236	112.5	9.1	237	2	Q8P0R9_STRP8	Q8p0r9 streptococc
164	233	18.8	209	2	Q9LAD3_STRPY	Q9lad3 streptococc	237	111.5	9.0	443	2	Q5HL39_STAEQ	Q5hl39 staphylococc
165	232	18.7	233	2	Q99XW1_STRPY	Q99xw1 streptococc	238	111.5	9.0	443	2	Q8CM25_STAEQ	Q8cm25 staphylococc
166	231.5	18.7	180	2	Q6DTL4_STRPY	Q6dtl4 streptococc	239	111.5	9.0	1158	2	Q4N1Y5_THEPA	Q4niy5 thelleria p
167	231	18.7	209	2	Q9LAD0_STRPY	Q9lad0 streptococc	240	109.5	8.8	680	2	Q4Z2H5_PLABE	Q4z2h5 plasmodium
168	228	18.4	180	2	Q56D03_STRPY	Q56d03 streptococc	241	109	8.8	232	2	Q9ZFS4_STAAU	Q9zfs4 staphylococc
169	228	18.4	183	2	Q6DTL3_STRPY	Q6dtl3 streptococc	242	109	8.8	232	2	Q6C5C6_STAAU	Q6c5c6 staphylococc
170	227	18.3	259	2	Q936G4_STAAU	Q936g4 staphylococc	243	109	8.8	232	2	Q6GJPI_STAAU	Q6gjpi staphylococc
171	226.5	18.3	178	2	Q56D04_STRPY	Q56d04 streptococc	244	109	8.8	232	2	Q5HIP4_STAAU	Q5hip4 staphylococc
172	224	18.1	183	2	Q6DTL5_STRPY	Q6dtl5 streptococc	245	109	8.8	232	2	Q8NY46_STAAU	Q8ny46 staphylococc
173	221	17.9	180	2	Q4ZJR7_STRPY	Q4zjr7 streptococc	246	108.5	8.7	1176	2	Q4U991_THEAN	Q4u991 thelleria a
174	220.5	17.8	131	2	Q7CEP2_STRP3	Q7cep2 streptococc	247	107.5	8.7	234	1	TSST_STAAU	P06886 staphylococc
175	220	17.8	234	1	SPEG_STRP3	Q8k8g7 streptococc	248	105.5	8.5	234	2	Q8RSX9_STAAU	Q8rsx9 staphylococc
176	218	17.6	183	2	Q6DTL1_STRPY	Q6dtl1 streptococc	249	105.5	8.5	234	2	Q54462_STAAU	Q54462 staphylococc
177	217	17.5	234	1	SPEG_STRPY	Q9x5c7 streptococc	250	105.5	8.5	234	2	Q7A2N8_STAAU	Q7a2n8 staphylococc

251	105.5	8.5	234	2	Q7A4K7_STAAN	Q7A4k7 staphylococ	RT
252	105	8.5	226	2	Q5HIP9_STAAC	Q5hip9 staphylococ	RL
253	104	8.4	226	2	Q6GC64_STAAS	Q6gc64 staphylococ	RN
254	104	8.4	226	2	Q8NV54_STAAM	Q8nv54 staphylococ	RP
255	104	8.4	553	2	Q4N6P4_THEPA	Q4n6p4 theileria p	RX
256	104	8.4	582	2	Q4XXJ3_PLACH	Q4xxj3 plasmodium	RA
257	103.5	8.4	2232	2	Q7RR88_PLAAS	Q7rr88 plasmodium	RT
258	103	8.3	1147	2	Q8KERO_FUSNU	Q8kero fusobacteri	RL
259	102.5	8.3	967	2	Q4XZHV_PLACH	Q4xzhv plasmodium	CC
260	102	8.2	232	2	Q8NY47_STAAM	Q8ny47 staphylococ	CC
261	102	8.2	234	2	Q6GC57_STAAS	Q6gc57 staphylococ	CC
262	101.5	8.2	771	2	Q7RG71_PLAYO	Q7rg71 plasmodium	CC
263	101	8.2	232	2	Q7A7H3_STAAN	Q7a7h3 staphylococ	CC
264	101	8.2	232	2	Q99WH5_STAAM	Q99wh5 staphylococ	CC
265	101	8.2	238	2	Q8L3E1_STRDY	Q8l3e1 streptococ	CC
266	101	8.2	569	2	Q8I2T6_PLAF7	Q8i2t6 plasmodium	CC
267	100.5	8.1	608	2	Q7R9Z2_PLAYO	Q7r9z2 plasmodium	CC
268	100	8.1	279	2	Q4X8R2_PLACH	Q4x8r2 plasmodium	CC
269	100	8.1	2251	2	Q8IKB6_PLAF7	Q8ikb6 plasmodium	CC
270	99.5	8.0	231	2	Q7A7H4_STAAN	Q7a7h4 staphylococ	CC
271	99.5	8.0	231	2	Q99WH6_STAAM	Q99wh6 staphylococ	CC
272	99.5	8.0	602	2	Q8IB95_PLAF7	Q8ib95 plasmodium	CC
273	99.5	8.0	733	2	Q7R9I8_PLAYO	Q7r9i8 plasmodium	CC
274	99.5	8.0	1811	2	Q8I1L76_PLAF7	Q8i1l76 plasmodium	CC
275	98.5	8.0	234	2	Q9F0L4_STAAN	Q9f0l4 staphylococ	CC
276	98.5	8.0	468	2	Q4L3O8_STAAN	Q4l3o8 staphylococ	DR
277	98.5	8.0	611	2	Q4XFQ2_PLACH	Q4xfq2 plasmodium	DR
278	97.5	7.9	655	2	Q4YMT7_PLABE	Q4ymt7 plasmodium	DR
279	97.5	7.9	1636	2	Q4XZ26_PLACH	Q4xz26 plasmodium	DR
280	97	7.8	232	2	Q6GC59_STAAS	Q6gc59 staphylococ	DR
281	97	7.8	232	2	Q8NY49_STAAM	Q8ny49 staphylococ	DR
282	97	7.8	463	2	Q7V2X1_PROMP	Q7v2x1 prochloroco	DR
283	97	7.8	614	2	Q4YW78_PLABE	Q4yw78 plasmodium	DR
284	96.5	7.8	588	2	Q4N8F6_THERPA	Q4n8f6 theileria p	DR
285	96.5	7.8	617	2	Q69W78_ORYSA	Q69w78 oryza sativ	DR
286	96.5	7.8	632	2	Q4W333_9CAUD	Q4w333 streptococ	DR
287	96.5	7.8	1100	2	Q55F96_DICDI	Q55f96 dictyosteli	DR
288	96	7.8	227	2	Q6GC55_STAAS	Q6gc55 staphylococ	DR
289	96	7.8	227	2	Q5HIP3_STAAC	Q5hip3 staphylococ	KW
290	96	7.8	227	2	Q7A7H1_STAAN	Q7a7h1 staphylococ	FT
291	96	7.8	227	2	Q8NV45_STAAM	Q8nv45 staphylococ	FT
292	96	7.8	227	2	Q99WH3_STAAM	Q99wh3 staphylococ	FT
293	96	7.8	495	2	Q7RDT5_PLAYO	Q7rdt5 plasmodium	FT
294	95.5	7.7	150	1	RS192_THEVO	Q97cu4 thermoplas	FT
295	95.5	7.7	1307	2	Q4YVS2_PLABE	Q4yvs2 plasmodium	FT
296	95	7.7	709	2	Q4HM91_CAMLA	Q4hm91 campylobact	FT
297	94.5	7.6	291	2	Q9CDI9_LACIA	Q9cdi9 lactococcus	FT
298	94.5	7.6	402	2	Q5HN31_STAEO	Q5hn31 staphylococ	FT
299	94.5	7.6	402	2	Q8CRU1_STAEP	Q8cru1 staphylococ	FT
300	94.5	7.6	820	1	GORK_ARATH	Q94a76 arabidopsis	FT

enterotoxin gene.";
J. Bacteriol. 170:2954-2960 (1988).
[2]
3D-STRUCTURE MODELING.
MEDLINE=96022987; PubMed=7552730;
Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
RT "Residues defining V beta specificity in staphylococcal
enterotoxins.";
Nat. Struct. Biol. 2:680-686 (1995).
CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication
staphylococcal food poisoning syndrome. The illness characterized
by high fever, hypotension, diarrhea, shock, and in some cases
death.
CC -!- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
for the toxin interaction with MHC class II (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
family.

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removed.

EMBL; M21319; AAA26617.1; -; Genomic_DNA.
DR PIR; A28179; A28179.
DR PDB; 1SBE; Model; @=28-257.
DR InterPro; IPR006177; Bcrl tox.
DR InterPro; IPR006123; Stap/Strep toxin.
DR InterPro; IPR006126; Staph/Strept tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF02876; Stap_Strep_tox_C; 1.
DR Pfam; PF01123; Stap_Strep_toxin; 1.
DR PRINTS; PR00279; BACTETOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW 3D-structure; Antigen; Direct protein sequencing; Enterotoxin;
Metal-binding; Signal; Superantigen; Toxin; Zinc.
FT SIGNAL 1 27
FT CHAIN 28 257 Enterotoxin type E.
FT METAL 211 211 Zinc (By similarity).
FT METAL 249 249 Zinc (By similarity).
FT METAL 251 251 Zinc (By similarity).
FT HELIX 33 35
FT HELIX 39 41
FT STRAND 42 42
FT TURN 46 47
FT HELIX 48 51
FT HELIX 52 54
FT STRAND 59 64
FT TURN 66 67
FT STRAND 69 69
FT TURN 73 74
FT STRAND 75 79
FT TURN 83 84
FT STRAND 90 94
FT HELIX 98 104
FT TURN 105 106
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FT TURN 118 119
FT STRAND 128 132
FT STRAND 135 137
FT TURN 139 140
FT STRAND 142 142
FT STRAND 152 152
FT STRAND 154 155
FT TURN 156 157
FT STRAND 163 163
FT STRAND 171 171
FT STRAND 173 175
FT HELIX 176 190

ALIGNMENTS

RESULT 1	ETXE_STAAN	STANDARD;	PRT;	257 AA.
AC	P12933;			
DT	01-JAN-1990 (Rel. 13, Created)			
DT	01-JAN-1990 (Rel. 13, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Enterotoxin type E precursor (SEE).			
GN	Name=entE;			
OS	Staphylococcus aureus.			
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.			
OX	NCBI_TaxID=1280;			
RN	[1]			
RC	NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 28-74.			
RP	STRAIN=MJB265;			
RX	MEDLINE=88257005; PubMed=3384800;			
RA	Couch J.L., Soltis M.T., Betley M.J.;			
RT	"Cloning and nucleotide sequence of the type E staphylococcal			

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FT TURN 191 191
FT STRAND 203 211
FT STRAND 219 221
FT STRAND 227 227
FT HELIX 234 239
FT STRAND 242 244
FT TURN 245 247
FT STRAND 249 257
SQ SEQUENCE 257 AA; 29358 MW; 27EDA94B97770CE3 CRC64;

Query Match 100.0%; Score 1238; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.2e-93;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSKSELQNALSNLRQIYYNEKAITENKSGDDQFLENTLLFKGFPTG 60
DB 25 SEKSEINEKDLRKSKSELQNALSNLRQIYYNEKAITENKSGDDQFLENTLLFKGFPTG 84
QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTCMYGCVTLHDNNRLT 120
DB 85 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTCMYGCVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTYQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTYQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVPHSSEGSTVSVDLFDAGQYPTLLRIYRDNKTNSENLHIDLILYTT 233
DB 205 RGLIVPHSSEGSTVSVDLFDAGQYPTLLRIYRDNKTNSENLHIDLILYTT 257

RESULT 2
ETXA STAAU
ID ETXA STAAU STANDARD; PRT; 257 AA.
AC POA0L2; P13163;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Enterotoxin type A precursor (SEA).
GN Name=entA;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PRI337;
RX MEDLINE=88086892; PubMed=3335483;
RA Betley M.J., Mekalanos J.J.;
RT "Nucleotide sequence of the type A staphylococcal enterotoxin gene.";
RL J. Bacteriol. 170:34-41(1988).
RN [2]
RP PROTEIN SEQUENCE OF 25-257.
RX MEDLINE=87222293; PubMed=3584106;
RA Huang I.-Y., Hughes J.L., Bergdoll M.S., Schantz E.J.;
RT "Complete amino acid sequence of staphylococcal enterotoxin A.";
RL J. Biol. Chem. 262:7006-7013(1987).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95354648; PubMed=7628431;
RA Schad E.M., Zaitseva I., Zaitsev V.N., Dohlsten M., Kalland T.,
RA Schlievert P.M., Ohlendorf D.H., Svensson L.A.;
RT "Crystal structure of the superantigen staphylococcal enterotoxin type A.";
RL EMBO J. 14:3292-3301(1995).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=97113025; PubMed=8943278; DOI=10.1074/jbc.271.50.32212;
RA Sundstrom M., Hallen D., Svensson A., Schad E., Dohlsten M.,
RA Abrahamson L.;
RT "The Co-crystal structure of staphylococcal enterotoxin type A with Zn2+ at 2.7-A resolution. Implications for major histocompatibility complex class II binding.";
RL J. Biol. Chem. 271:32212-32216(1996).
RN [5]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=96022967; PubMed=7552730;
RA Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
RT "Residues defining V beta specificity in staphylococcal enterotoxins.";
RL Nat. Struct. Biol. 2:680-686(1995).
RN [6]
RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
RX MEDLINE=97334373; PubMed=9191070; DOI=10.1006/jmbi.1997.1023;
RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
RT "A structural and functional comparison of staphylococcal enterotoxins A and C2 reveals remarkable similarity and dissimilarity.";
RL J. Mol. Biol. 269:270-280(1997).
CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication staphylococcal food poisoning syndrome. The illness characterized by high fever, hypotension, diarrhea, shock, and in some cases death.
CC -!- COPACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary for the toxin interaction with MHC class II.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MISCELLANEOUS: This toxin seems to be coded by a bacteriophage.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC -----
DR EMBL; M18970; AAA26681.1; -; Genomic_DNA.
DR PIR; A28664; A28664.
DR PDB; 1DQY; X-ray; A=25-257.
DR PDB; 1ESF; X-ray; A/B=25-257.
DR PDB; 1I4G; X-ray; A/B=25-257.
DR PDB; 1I4H; X-ray; A/B=25-257.
DR PDB; 1LO5; X-ray; D=25-257.
DR PDB; 1SEA; Model; @=25-257.
DR PDB; 1SXT; X-ray; A/B=25-257.
DR SMR; POA0L2; 25-257.
DR InterPro; IPR006177; Bcrl tox.
DR InterPro; IPR006123; Stap/Strep toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF02876; Stap_Strep_tox_C; 1.
DR Pfam; PF01123; Stap_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR 3D-structure; Antigen; Direct protein sequencing; Enterotoxin; Metal-binding; Signal; Superantigen; Toxin; Zinc.
FT SIGNAL 1 24
FT CHAIN 25 257 Enterotoxin type A.
FT METAL 211 211 Zinc.
FT METAL 249 249 Zinc.
FT METAL 251 251 Zinc.
FT DISULFID 120 130
FT CONFLICT 242 242
FT HELIX 33 35 T -> S (in Ref. 2).
FT HELIX 39 41
FT TURN 44 45
FT HELIX 46 55
FT STRAND 59 65
FT STRAND 75 78
FT TURN 79 80
FT STRAND 90 94
FT TURN 98 104
FT TURN 105 106
FT STRAND 109 114
FT STRAND 116 116
FT HELIX 117 119

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FT TURN 122 123
FT TURN 126 132
FT STRAND 128 132
FT STRAND 135 137
FT STRAND 139 140
FT STRAND 142 148
FT STRAND 151 155
FT TURN 156 157
FT STRAND 158 160
FT TURN 164 165
FT STRAND 168 171
FT STRAND 173 175
FT HELIX 176 191
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FT TURN 246 247
FT STRAND 249 255
SQ SEQUENCE 257 AA; ADEBF5BCA1F14677 CRC64;

Query Match 82.6%; Score 1023; DB 1; Length 257;
Best Local Similarity 82.0%; Pred. No. 6e-76;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTD 84

QY 61 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLT 120
DB 85 HSWYNLLVDFDSKDIDVYKGVLDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLT 144

QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKXEVTVQELDLQARHYLHGKFLYNSDFGKVKQ 180
DB 145 EEKVPINLWIDGKQNTVLETVKTNKQNTVQELDLQARHYLHGKFLYNSDFGKVKQ 204

QY 181 RGLIVPHSSEGSTVSYDLFDAQOQYPTLLRIYRDNKTINSENHLDLYLTT 233
DB 205 RGLIVPHSTEPSVYDYLFGAQOQYNTLLRIYRDNKTINSENHLDLYLTS 257

RESULT 3
ID ETXA STAAW STANDARD; PRT; 257 AA.
AC POA0LJ; P13163;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Enterotoxin type A precursor (SEA).
GN Name=entA; OrderedLocusNames=MW1889;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Chii L.,
RA Yamanoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
acquired MRSA."
RL Lancet 359:1819-1827(2002).
CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication
CC staphylococcal food poisoning syndrome. The illness characterized
CC by high fever, hypotension, diarrhea, shock, and in some cases

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CC death (By similarity).
CC -!- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
CC for the toxin interaction with MHC class II (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; BA000033; BAB95754.1; -; Genomic_DNA.
CC SMR; POA0LJ; 25-257.
CC InterPro; IPR006177; Bcrl tox.
CC InterPro; IPR006123; Staph/Strep toxin.
CC InterPro; IPR006126; Staph/Strep tox.
CC InterPro; IPR006173; Staph tox OB.
CC Pfam; PF02876; Staph_Strip_tox_C; 1.
CC DR PF01123; Staph_Strip_toxin; 1.
CC PRINTS; PR00279; BACTRLTOXIN.
CC PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
CC PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
CC KW Antigen; Complete proteome; Enterotoxin; Metal-binding; Signal;
CC Superantigen; Toxin; Zinc.
CC FT SIGNAL 1 24 By similarity.
CC FT CHAIN 25 257 Enterotoxin type A.
CC FT METAL 211 211 Zinc (By similarity).
CC FT METAL 249 249 Zinc (By similarity).
CC FT METAL 251 251 Zinc (By similarity).
CC FT DISULFID 120 130 By similarity.
CC SQ SEQUENCE 257 AA; 29669 MW; ADEBF5BCA1F14677 CRC64;

Query Match 82.6%; Score 1023; DB 1; Length 257;
Best Local Similarity 82.0%; Pred. No. 6e-76;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTD 84

QY 61 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLT 120
DB 85 HSWYNLLVDFDSKDIDVYKGVLDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLT 144

QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKXEVTVQELDLQARHYLHGKFLYNSDFGKVKQ 180
DB 145 EEKVPINLWIDGKQNTVLETVKTNKQNTVQELDLQARHYLHGKFLYNSDFGKVKQ 204

QY 181 RGLIVPHSSEGSTVSYDLFDAQOQYPTLLRIYRDNKTINSENHLDLYLTT 233
DB 205 RGLIVPHSTEPSVYDYLFGAQOQYNTLLRIYRDNKTINSENHLDLYLTS 257

RESULT 4
ID Q6GY7 STAAAS PRELIMINARY; PRT; 257 AA.
AC Q6GY7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Enterotoxin type A.
GN OrderedLocusNames=SAS1872;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,

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RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.,
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791 (2004).
DR EMBL; BX571857; CAG43678.1; -; Genomic_DNA.
DR SMR; Q67Y7; 25-257.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0003405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006173; Staph/Strep toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 257 AA; 29669 MW; ADEBF5BCAIF14677 CRC64;

Query Match 82.6%; Score 1023; DB 2; Length 257;
Best Local Similarity 82.0%; Pred. No. 6e-76;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOARNLSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOAGTALGNLQIYYNEKAKTENKESHDOFLQHTILFKGFFTD 84
QY 61 HPWYNDLLVLDGSKDATNKGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDIVKYGKKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTPVIDKVTSSKEVTVQELDLQARHYLHGFGLYNSDSFGKVKQ 180
DB 145 EEKVPINLWIDGKQNTVPLETVKTKNKNVTVOELDLQARRYLQEKYLYNSDVDFGKVKQ 204
QY 181 RGLIVPHSSEGSVSVLDLFDAGQYPTDILLRIYRDKNKTINSENHLHLDVLYTT 233
DB 205 RGLIVPHSTEPSVNYDLFQAQGYNSLTLLRIYRDKNKTINSENHMDIYLYTS 257

RESULT 5
Q931M4 STAAAM PRELIMINARY; PRT; 260 AA.
AC Q931M4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin P.
GN Names-sep; OrderedLocusNames-SAV1948;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Iwanaga H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshino K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240 (2001).
DR EMBL; BA000017; BAB58110.1; -; Genomic_DNA.

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DR HSSP; PI3163; 1LO5.
DR SMR; Q931M4; 28-260.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0003405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep toxin.
DR InterPro; IPR006173; Staph/Strep toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 260 AA; 30016 MW; 15C2D36270FA8241 CRC64;

Query Match 82.6%; Score 1023; DB 2; Length 260;
Best Local Similarity 82.0%; Pred. No. 6.1e-76;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOARNLSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 28 SEKSEINEKDLRKSELOAGTALGNLQIYYNEKAKTENKESHDOFLQHTILFKGFFTD 87
QY 61 HPWYNDLLVLDGSKDATNKGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
DB 88 HSWYNDLLVDFDSKDIVKYGKKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 147
QY 121 EEKVPINLWIDGKQTTPVIDKVTSSKEVTVQELDLQARHYLHGFGLYNSDSFGKVKQ 180
DB 148 EEKVPINLWIDGKQNTVPLETVKTKNKNVTVOELDLQARRYLQEKYLYNSDVDFGKVKQ 207
QY 181 RGLIVPHSSEGSVSVLDLFDAGQYPTDILLRIYRDKNKTINSENHLHLDVLYTT 233
DB 208 RGLIVPHSTEPSVNYDLFQAQGYNSLTLLRIYRDKNKTINSENHMDIYLYTS 260

RESULT 6
Q5PSP6 STAAU PRELIMINARY; PRT; 261 AA.
AC Q5PSP6;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Enterotoxin A (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 13565;
RA Wang L., Zhang S., Yu M.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY827552; AAV84102.1; -; Genomic_DNA.
DR SMR; Q5PSP6; 28-260.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0003405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006173; Staph/Strep toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
FT NON TER 261
SQ SEQUENCE 261 AA; 30144 MW; 36B6F7EDFA8AD9B3 CRC64;

Query Match 82.2%; Score 1018; DB 2; Length 261;
Best Local Similarity 81.5%; Pred. No. 1.6e-75;
Matches 190; Conservative 18; Mismatches 25; Indels 0; Gaps 0;

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QY 1 SEKSEINEKDLRKKSLOALNSLRQIYYNEKAITENKESDDQPLENTLLFKGFFTG 60
DB 28 SEKSEINEKDLRKKSLOALNSLRQIYYNEKAITENKESDDQPLENTLLFKGFFTD 87
QY 61 HPWYNDLLVDLGSKDATNKYKGGVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
DB 88 HSWYNDLLVDFSDKDIIVDKYKGGVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 147
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
DB 148 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSVDFGKVKQ 207
QY 181 RGLIVHSSSGSTSVSYDLFDAQOQYPTLLRIYRDNKNTINSENHLHIDLXYLYTT 233
DB 208 RGLIVHTSTEPSVYDLFDAQOQYNSNTLLRIYRDNKNTISSENHHDIDYLYTS 260
RESULT 7
Q6GFA8 STAAAR PRELIMINARY; PRT; 257 AA.
AC Q6GFA8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Enterotoxin type A.
GN OrderedLocusNames=SA2043;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Feltham T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571856; CAG41028.1; -; Genomic_DNA.
DR SNR; Q6GFA8; 25-257.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin_C; 1.
DR PRINTS; PR00279; BACTRITOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Complete proteome.
SQ SEQUENCE 257 AA; 29674 MW; 56B0A6D952EDFD4 CRC64;
Query Match 81.8%; Score 1013; DB 2; Length 257;
Best Local Similarity 81.5%; Pred. No. 4e-75;
Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKSLOALNSLRQIYYNEKAITENKESDDQPLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKSLOALNSLRQIYYNEKAITENKESDDQPLENTLLFKGFFTN 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFSDKDIIVDKYKGGVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 144
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QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSVDFGKVKQ 204
QY 181 RGLIVHSSSGSTSVSYDLFDAQOQYPTLLRIYRDNKNTINSENHLHIDLXYLYTT 233
DB 205 RGLIVHTSTEPSVYDLFDAQOQNSNTLLRIYRDNKNTINSENHHDIDYLYTS 257
RESULT 8
Q99SU3 STAAAR PRELIMINARY; PRT; 260 AA.
AC Q99SU3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin P.
GN Name=sep; OrderedLocusNames=SA1761;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=2311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekinizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Shiba T.,
RA Kanehisa M., Yamashita A., Ohnita K., Furuya K., Hiramatsu K.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL; BA000018; BAB43036.1; -; Genomic_DNA.
DR FIK; C89984; C89984.
DR HSP; P13163; ISXT.
DR SNR; Q99SU3; 28-260.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin_C; 1.
DR PRINTS; PR00279; BACTRITOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Complete proteome.
SQ SEQUENCE 260 AA; 29708 MW; 087C5B4BC028CFDB CRC64;
Query Match 80.3%; Score 994; DB 2; Length 260;
Best Local Similarity 79.0%; Pred. No. 1.5e-73;
Matches 184; Conservative 17; Mismatches 32; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKSLOALNSLRQIYYNEKAITENKESDDQPLENTLLFKGFFTG 60
DB 28 SEKSEINEKDLRKKSLOALNSLRQIYYNEKAITENKESDDQPLENTLLFKGFFTN 87
QY 61 HPWYNDLLVDLGSKDATNKYKGGVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
DB 88 HSWYNDLLVDFSDKDIIVDKYKGGVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 147
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
DB 148 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSVDFGKVKQ 207
QY 181 RGLIVHSSSGSTSVSYDLFDAQOQYPTLLRIYRDNKNTINSENHLHIDLXYLYTT 233
DB 208 RGLIEFHPSSGSDSVYDLFDAQOQYPTQLRIYRDNKNTIKSKNMHIDYLYTT 260
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RESULT 9	
Q6XZE9 STAAU PRELIMINARY;	PRT; 219 AA.
AC Q6XZE9;	
DT 05-JUL-2004 (TrEMBLrel. 27, Created)	
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)	
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)	
DE Enterotoxin sea variant (Fragment).	
OS Staphylococcus aureus.	
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.	
OX NCBI_TaxID=1280;	
RN [1]	
RP NUCLEOTIDE SEQUENCE.	
RC STRAIN=3208;	
RX MEDLINE=22943091; PubMed=14580397; DOI=10.1016/S0890-8508(03)00058-6;	
RA Leteire C., Perelle S., Dillasser F., Fach P.;	
RT "A strategy based on 5' nuclease multiplex PCR to detect enterotoxin	
RL Mol. Cell. Probes 17:227-235(2003).	
DR EMBL; A196686; AAP37183.1; -; Genomic_DNA.	
DR SMR; Q6XZE9; 2-219.	
DR GO; GO:0005576; C:extracellular region; IEA.	
DR GO; GO:0009405; P:pathogenesis; IEA.	
DR InterPro; IPR006177; Bcrl tox.	
DR InterPro; IPR006123; Staph/Strep toxin.	
DR InterPro; IPR006173; Staph/Strep toxin.	
DR Pfam; PF01123; Staph/Strep toxin; 1.	
DR Pfam; PF02876; Staph/Strep toxin; 1.	
DR PRINTS; PR00279; BACTRLTOXIN.	
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.	
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.	
FT NON TER 1	
FT NON TER 219	
SQ SEQUENCE 219 AA; 25264 MW; DE8F38AEB652FC89 CRC64;	
Query Match 78.4%; Score 971; DB 2; Length 219;	
Best Local Similarity 82.6%; Pred. No. 9.4e-72;	
Matches 180; Conservative 17; Mismatches 21; Indels 0; Gaps 0;	
QY 9 EKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLNTLLFKGFFTGHPWYNDLL 68	
DB 2 EKDLHKSELQVALNLRQIYYNHKAITENKESDNQFLQHTLPNGFFTDHPWYNDLL 61	
QY 69 VDLGSKDATNKYKGVLDLYGAYGYQCAGGTPTNKACMYGGVTLHDNNRLTEKKVPIN 128	
DB 62 VDPFDSKVLADKYKGVLDLYGAYGYQCAGGTPTNKACMYGGVTLHDNNRLTEKKVPIN 121	
QY 129 LMTDGKQTVPTDKVTSKEVTQELDQARHLYHGKFGLYNSDSFGKGVORGLIVFHS 188	
DB 122 LMLDGGKQTVPLETVTKNKKEVTQELDQARHLYHGKFGLYNSDTFDGKVORGLIVFHT 181	
QY 189 SEGTSVSYDLFDAQGYPTTLRIYRDNKTINSENLIH 226	
DB 182 STEPSVNYDLFGAQGYNTLLRIYRDNKTINSENHI 219	
RESULT 10	
Q76LS7 STAAU PRELIMINARY;	PRT; 268 AA.
AC Q76LS7;	
DT 05-JUL-2004 (TrEMBLrel. 27, Created)	
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)	
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)	
DE Enterotoxin J.	
GN Name=sej;	
OS Staphylococcus aureus.	
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.	
OX NCBI_TaxID=1280;	
RN [1]	
RP NUCLEOTIDE SEQUENCE.	
RA Omoe K., Hu D., Nakane A., Shinagawa K.;	
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.	
Query Match 67.0%; Score 830; DB 2; Length 268;	
Best Local Similarity 65.4%; Pred. No. 1.3e-60;	
Matches 151; Conservative 38; Mismatches 42; Indels 0; Gaps 0;	
QY 3 KSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLNTLLFKGFFTGHP 62	
DB 27 KNETKEKNLHKSELSSITLNNLRHIYFFNEKGISEKIMTEDQFLDYTLTFKSPFISHS 86	
QY 63 WYNDDLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPTNKACMYGGVTLHDNNRLTBE 122	
DB 87 QYNDDLVDQFDSKETVWPKGVLDLYGSYGQCSGKGNKTACMYGGVTLHENNQLYDT 146	
QY 123 KKVPTNLMTDGKQTVPTDKVTSKEVTQELDQARHLYHGKFGLYNSDSFGGKVOR 182	
DB 147 KKIPINLMTDSIRTVVPLDIVTKNKKVTVQELDQARYYHLHKQYNLYNPSFTGGKIQ 206	
QY 183 LIVFHSSEGTSVSYDLFDAQGYPTTLRIYRDNKTINSENLIHIDLTYTT 233	
DB 207 LIVFHSKEPLVSYDLFVNVIGYPPKLLKIYQDNKLIENSENNHIDIYLYTS 257	
RESULT 11	
O85217 STAAU PRELIMINARY;	PRT; 268 AA.
AC O85217;	
DT 01-NOV-1998 (TrEMBLrel. 08, Created)	
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)	
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
DE Enterotoxin J.	
GN Name=sej;	
OS Staphylococcus aureus.	
OG Plasmid p1845.	
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.	
OX NCBI_TaxID=1280;	
RN [1]	
RP NUCLEOTIDE SEQUENCE.	
RC STRAIN=KSI1410;	
RX MEDLINE=99052098; PubMed=9835033;	
RA Zhang S., Iandolo J.J., Stewart G.C.;	
RT "The enterotoxin D plasmid of Staphylococcus aureus encodes a second	
RL FEMS Microbiol. Lett. 168:227-233(1998).	
DR EMBL; AF053140; AAC78590.1; -; Genomic_DNA.	
DR HSSP; P13183; IESF.	
DR GO; GO:0005576; C:extracellular region; IEA.	
DR GO; GO:0009405; P:pathogenesis; IEA.	
DR InterPro; IPR006177; Bcrl tox.	
DR InterPro; IPR006123; Staph/Strep toxin.	
DR InterPro; IPR006126; Staph/Strep toxin.	
DR InterPro; IPR006173; Staph/Strep toxin.	
DR Pfam; PF01123; Staph/Strep toxin; 1.	
DR Pfam; PF02876; Staph/Strep toxin; 1.	
DR PRINTS; PR00279; BACTRLTOXIN.	
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.	
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.	
KW Plasmid.	
SQ SEQUENCE 268 AA; 31230 MW; ACSF3546060ACE22 CRC64;	

Best Local Similarity 64.9%; Pred. No. 4.8e-60;
Matches 150; Conservative 38; Mismatches 43; Indels 0; Gaps 0;

QY 3 KSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLKGFPTGHP 62
DB 27 KNETIKERLKHKKSELSITLNNRHLYFPNEKIGSEKIMTBDQFLDYTLFLKSPFISHS 86
QY 63 WYNDLLVLDGSDATNKYKGGKVDLYGAYGYQCAGGTENKTKACMYGGVTLHDNNRLTPE 122
DB 87 QYNDLLVQFDSKETVKNFKGQVDLYGSGYFQCSGKFNKTKACMYGGVTLHNNQLYDT 146
QY 123 KKVPINLWIDGQTTVPIDKVKTSKEVTVQELDLQARHLYHGKFGLYNSDSFGGKVGQ 182
DB 147 KKIPINLWIDSRTVVPIDKVKTSKEVTVQELDLQARHLYHGKFGLYNSDSFGGKVGQ 206
QY 183 LIVFHSSEGSTVSYDLFDAQGGVPTLLRIYRDNKTINSNLHIDLILYTT 233
DB 207 LIVFHTSKEPLSYDLFNVIGYQFDKLLKIYQDNKIIESNHNHIDIYLYTS 257

RESULT 12
Q6R2G0 STAAU PRELIMINARY; PRT; 154 AA.
AC Q6R2G0;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DE Enterotoxin E (Fragment).
OS Staphylococcus aureus subsp. aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=46170;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN-ATCC 27664;
RX PubMed=1513181; DOI=10.1128/JCM.42.5.2134-2143.2004;
RA Sergeev N., Volokhov D., Chizhikov V., Rasooly A.;
RT "Simultaneous analysis of multiple staphylococcal enterotoxin genes by an oligonucleotide microarray assay";
RL J. Clin. Microbiol. 42:2134-2143(2004).
DR EMBL; AY518387; AAR99635.1; -; Genomic_DNA.
DR HSSP; PI3380; 1AN8.
DR SMR; Q6R2G0; 3-154.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bcrl tox.
DR InterPro; IPR006123; Stap/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_toxin; 1.
DR PRINTS; PR00279; BACTLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT NON_TER 154
FT NON_TER 154
SQ SEQUENCE 154 AA; 17390 MW; 10D2329E23F0C74F CRC64;

Query Match 66.6%; Score 825; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 6.3e-60;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 ATNKYGGKVDLYGAYGYQCAGGTENKTKACMYGGVTLHDNNRLTTEKKVPINLWIDGKQ 135
DB 1 ATNKYGGKVDLYGAYGYQCAGGTENKTKACMYGGVTLHDNNRLTTEKKVPINLWIDGKQ 60
QY 136 TTVPIDKVKTSKEVTVQELDLQARHLYHGKFGLYNSDSFGGKVGRLIVFHSSEGSTVS 195
DB 61 TTVPIDKVKTSKEVTVQELDLQARHLYHGKFGLYNSDSFGGKVGRLIVFHSSEGSTVS 120
QY 196 YDLFDAQGGVPTLLRIYRDNKTINSNLHIDL 229
DB 121 YDLFDAQGGVPTLLRIYRDNKTINSNLHIDL 154

RESULT 13
ETXD STAAU STANDARD; PRT; 258 AA.
AC P20723;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Enterotoxin type D precursor (SED).
GN Name=entD;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89359112; PubMed=2549000;
RA Bayles K.W., Tandolo J.J.;
RT "Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin D";
RT J. Bacteriol. 171:4799-4806(1989).
RN [2]
RP NUCLEOTIDE SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RC STRAIN-ATCC 23235;
RX MEDLINE=97157473; PubMed=9003758;
RA Sundstroem M., Abrahmsen L., Antonsson P., Mehindate K., Mourad W., Dohlsten M.;
RT "The crystal structure of staphylococcal enterotoxin type D reveals Zn2+-mediated homodimerization";
RT EMBO J. 15:6832-6840(1996).
RL CC
CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication staphylococcal food poisoning syndrome. The illness characterized by high fever, hypotension, diarrhea, shock, and in some cases death.
CC -!- SUBUNIT: Homodimer; zinc-dependent.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC
CC EMBL; M28521; AAB06195.1; -; Genomic_DNA.
DR PIR; A33953; A33953.
DR HSSP; PI3163; LSXT.
DR InterPro; IPR006177; Bcrl tox.
DR InterPro; IPR006123; Stap/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF02876; Staph_strep_toxin; 1.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR PRINTS; PR00279; BACTLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Antigen; Enterotoxin; Metal-binding; Signal; Superantigen; Toxin;
Zinc
FT SIGNAL 1 25
FT CHAIN 26 258 Enterotoxin type D.
FT METAL 212 212 Zinc.
FT METAL 250 250 Zinc.
FT METAL 252 252 Zinc.
FT VARIANT 114 114 P -> A (in strain ATCC 23235).
FT SEQUENCE 258 AA; 29746 MW; 4F7C6A28D42597FD CRC64;
Query Match 53.6%; Score 663; DB 1; Length 258;
Best Local Similarity 54.5%; Pred. No. 2.5e-46;
Matches 126; Conservative 35; Mismatches 70; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLKGFPTG 60
DB 26 NENIDSVKELHKKSELSSTALNNMKHSYADKNPIIGENKSTGQFLENTLLKRPFTD 85

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QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTAACMYGGVTLHDNNRLT 120
Db 86 LINFEDLLNFNSKEMAQHFKGNVDVPIRISYNCYGGEIDRTACTYGGVTPHEGNKLUK 145
QY 121 EEKQVPINLWIDGKQTTPIDKVTSSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 146 ERKKIPINLWINGVQKEVSLDRKVDQTKNVTQELDAQARRYLQKDLKLYNNDTLGGKIQ 205
QY 181 RGLIVFHSSEGSTVSYDLDFDAQGYPTDLLRIYRDNKTINSNLHIDLILY 231
Db 206 RKGIFDSSDGSKVSVDLFDVKGDFPEKQLRIYSDNKTLSLTHEHLHIDLILY 256

RESULT 14
QSR2F9 STAAU
ID Q6R2F9 STAAU PRELIMINARY; PRT; 152 AA.
AC Q6R2F9;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Enterotoxin D (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NTCC 10656;
RX PubMed=1513181; DOI=10.1128/JCM.42.5.2134-2143.2004;
RA Sergeev N., Velokhov D., Chizhikov V., Rasooly A.;
RT "Simultaneous analysis of multiple staphylococcal enterotoxin genes by
an oligonucleotide microarray assay.";
RL J. Clin. Microbiol. 42:2134-2143(2004).
DR EMBL; AY518386; AAR95636.1; -; Genomic_DNA.
DR HSP; F13380; IAN8.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_tox C; 1.
DR Pfam; PF02876; Staph_strep_tox C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT NON_TER 152
SQ SEQUENCE 152 AA; 17514 MW; F0354318924CB739 CRC64;

Query Match 40.1%; Score 496; DB 2; Length 152;
Best Local Similarity 59.9%; Pred. No. 7.3e-33;
Matches 91; Conservative 22; Mismatches 39; Indels 0; Gaps 0;

QY 80 YKGGKVDLYGAYGYQCAGGTPNKTAACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTP 139
Db 1 FSKKNVDVVAIRYSYNCYGGEIDRTACTYGGVTPHEGNKLKERKKIPINLWINGVQKVS 60

QY 140 IDKVTSSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRLIVFHSSEGSTVSYDLF 199
Db 61 LDKVQTDKKNVTVQELDAQARRYLQKDLKLYNNDTLGGKIQRGKIEFSDSDGSKVSYDLF 120

QY 200 DAQGYPTDLLRIYRDNKTINSNLHIDLILY 231
Db 121 DVKGDFPEKQLRIYSDNKTLSLTHEHLHIDLILY 152

RESULT 15
QSHFG0 STAAC
ID QSHFG0 STAAC PRELIMINARY; PRT; 234 AA.
AC QSHFG0;
DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)

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DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
DE Enterotoxin type A, putative.
GN OrderedLocusNames=SACOL1657;
OS Staphylococcus aureus (strain COL).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=93062;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15774886; DOI=10.1128/JB.187.7.2426-2438.2005;
RA Gill S.R., Fouts D.E., Archer G.L., Mongodin E.F., DeBoy R.T.,
RA Ravel J., Paulsen I.T., Kolonay J.F., Brinkac L.M., Beanan M.J.,
RA Haddad R.J., Daugherty S.C., Madupu R., Angiuoli S.V., Durkin A.S.,
RA Haft D.H., Vamathevan J.J., Khouri H., Utterback T.R., Lee C.,
RA Dimitrov G., Jiang L., Qin H., Weidman J., Tran K., Kang K.H.,
RA Hance I.R., Nelson K.E., Fraser C.M.;
RT "Insights on evolution of virulence and resistance from the complete
genome analysis of an early methicillin-resistant Staphylococcus
RT aureus strain and a biofilm-producing methicillin-resistant
RT Staphylococcus epidermidis strain.";
RL J. Bacteriol. 187:2426-2438(2005).
DR EMBL; CP000046; AAW38273.1; -; Genomic_DNA.
DR TIGR; SACOL1657; -.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_tox C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 234 AA; 27337 MW; 16613BEFEF94AF1D CRC64;

Query Match 39.8%; Score 492.5; DB 2; Length 234;
Best Local Similarity 39.8%; Pred. No. 2.4e-32;
Matches 92; Conservative 48; Mismatches 86; Indels 5; Gaps 3;

QY 1 SEKSEINEKDLRKSELRNALSRLRIQYYNEKAITENKESDDOFLNTLLFKGFFTG 60
Db 7 TNSAIAEYSDLHHKSKFDSKRLSNAK-MSFINPTQL-ENKNTDRLKHLDFHDMFVN 64

QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTAACMYGGVTLHDNNRLT 120
Db 65 DWWKDFKVEFENEALSCKFKINKDIDIFAGNYGYCHGAGATNKTQCSYGGVILSDNNKYD 124

QY 121 EEKQVPINLWIDGKQTTPIDKVTSSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 125 DYKNIPCNLWIDGHQTEIETAVTKTKKIVTTQELVQLRNLNKKYKLYEQ---GGDIV 181

QY 181 RGLIVFHSSEGSTVSYDLDFDAQGYPTDLLRIYRDNKTINSNLHIDLILY 231
Db 182 KGYVKYNDDEQNVEYDFYNLNGEYGREVLKMYADNKTINSKDLHLDIYLF 232

RESULT 16
QSG8W7 STAA
ID QSG8W7 STAA PRELIMINARY; PRT; 229 AA.
AC QSG8W7;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Putative enterotoxin.
GN OrderedLocusNames=SAS1538;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,

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Db 32 EVDKKDLKKSDLSKLFNLTS--YYTD--ITWQLDESINKISTDQLLNTILKKNIDIS 87
Qy 61 HPWYNLLVLDGSKDATNKYGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
Db 88 VLKTSLSLKVEFNSSDLANQFKGNIDYGLYFGNKCGLTEKTSCLYGGVTIHDGNQLD 147
Qy 121 BEKKVPINLWIDGKQTTVPIDKVKTSKVTVOELDLQARHYLHGKGLYNSDSFGKVKQ 180
Db 148 EEKVGIVNFKDGVQOEGFV--IKTKAKVTVOELDTKRVFKLENLYKYNKDT--GNIQ 203
Qy 181 RGLIVFHS--SEGSTVSYDLFDAQQGVPTDLLRIYRDNKTINSENHLIDLYL 231
Db 204 KGCIFPHSHNQDSFYDLYNVKSGVGAEFFQFYSDNRTVSSNVHIDVFLY 256

RESULT 19
Q7A2Q6 STAAH
ID Q7A2Q6 STAAH PRELIMINARY; PRT; 258 AA.
AC Q7A2Q6; 2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Enterotoxin.
GN Name=sen; OrderedLocusNames=SAV1825;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL; BA000017; BAB57987.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bcrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph Strep toxin; 1.
DR Pfam; PF02876; Staph Strep tox C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Complete proteome.
KW Complete proteome.
SQ SEQUENCE 258 AA; 29676 MW; 8A6C074F3E1F82D2 CRC64;

Query Match 37.3%; Score 461.5; DB 2; Length 258;
Best Local Similarity 41.2%; Pred. No. 9.6e-30;
Matches 96; Conservative 45; Mismatches 77; Indels 15; Gaps 6;

Qy 6 EINEKDLRKSELRNALSRLRIYYNEKAIT-----ENKESDDQFLENTLLFKGFFTG 60
Db 32 EVDKKDLKKSDLSKLFNLTS--YYTD--ITWQLDESINKISTDQLLNTILKKNIDIS 87
Qy 61 HPWYNLLVLDGSKDATNKYGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
Db 88 VLKTSLSLKVEFNSSDLANQFKGNIDYGLYFGNKCGLTEKTSCLYGGVTIHDGNQLD 147
Qy 121 BEKKVPINLWIDGKQTTVPIDKVKTSKVTVOELDLQARHYLHGKGLYNSDSFGKVKQ 180
Db 148 EEKVGIVNFKDGVQOEGFV--IKTKAKVTVOELDTKRVFKLENLYKYNKDT--GNIQ 203
Qy 181 RGLIVFHS--SEGSTVSYDLFDAQQGVPTDLLRIYRDNKTINSENHLIDLYL 231
Db 204 KGCIFPHSHNQDSFYDLYNVKSGVGAEFFQFYSDNRTVSSNVHIDVFLY 256

RESULT 21
Q6YCN3 STAAU
ID Q6YCN3 STAAU PRELIMINARY; PRT; 251 AA.
AC Q6YCN3; 2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Enterotoxin SEN variant.
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Db 204 KGCIFPHSHNQDSFYDLYNVKSGVGAEFFQFYSDNRTVSSNVHIDVFLY 256

RESULT 20
Q7A4X1 STAAH
ID Q7A4X1 STAAH PRELIMINARY; PRT; 258 AA.
AC Q7A4X1; 2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Enterotoxin Sen.
GN Name=sen; OrderedLocusNames=SA1643;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL; BA000018; BAB42911.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bcrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph Strep toxin; 1.
DR Pfam; PF02876; Staph Strep tox C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Complete proteome.
KW Complete proteome.
SQ SEQUENCE 258 AA; 29676 MW; 8A6C074F3E1F82D2 CRC64;

Query Match 37.3%; Score 461.5; DB 2; Length 258;
Best Local Similarity 41.2%; Pred. No. 9.6e-30;
Matches 96; Conservative 45; Mismatches 77; Indels 15; Gaps 6;

Qy 6 EINEKDLRKSELRNALSRLRIYYNEKAIT-----ENKESDDQFLENTLLFKGFFTG 60
Db 32 EVDKKDLKKSDLSKLFNLTS--YYTD--ITWQLDESINKISTDQLLNTILKKNIDIS 87
Qy 61 HPWYNLLVLDGSKDATNKYGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
Db 88 VLKTSLSLKVEFNSSDLANQFKGNIDYGLYFGNKCGLTEKTSCLYGGVTIHDGNQLD 147
Qy 121 BEKKVPINLWIDGKQTTVPIDKVKTSKVTVOELDLQARHYLHGKGLYNSDSFGKVKQ 180
Db 148 EEKVGIVNFKDGVQOEGFV--IKTKAKVTVOELDTKRVFKLENLYKYNKDT--GNIQ 203
Qy 181 RGLIVFHS--SEGSTVSYDLFDAQQGVPTDLLRIYRDNKTINSENHLIDLYL 231
Db 204 KGCIFPHSHNQDSFYDLYNVKSGVGAEFFQFYSDNRTVSSNVHIDVFLY 256

RESULT 21
Q6YCN3 STAAU
ID Q6YCN3 STAAU PRELIMINARY; PRT; 251 AA.
AC Q6YCN3; 2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Enterotoxin SEN variant.
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OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1] NUCLEOTIDE SEQUENCE.
RP STRAIN=382F;
RC MEDLINE=22692404; PubMed=12807452;
RX DOI=10.1046/j.1365-2672.2003.01957.x;
RA Letetere C., Perelle S., Dilasser F., Fach P.;
RT "Identification of a new putative enterotoxin SEU encoded by the egc
RT cluster of Staphylococcus aureus.";
RL J. Appl. Microbiol. 95:38-43(2003).
DR EMBL: AY158703; AA017733.1; -; Genomic DNA.
DR GO: GO:0005576; C:extracellular region; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR006177; Bcrl tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR Pfam: PF01123; Staph Strp toxin; 1.
DR Pfam: PF02876; Staph Strp tox C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH STREP TOXIN 1; UNKNOWN_1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 251 AA; 28806 MW; 1E2966FBBF86BA40 CRC64;

Query Match 36.1%; Score 446.5; DB 2; Length 251;
Best Local Similarity 39.5%; Pred. No. 1.6e-28;
Matches 92; Conservative 49; Mismatches 77; Indels 15; Gaps 6;

QY 6 EINEKDLRKSEIQRNLSNLRIQIYYNEKAIT-----ENKESDDQFLENTLFGKFFTG 60
Db 25 DVDKNDLKKKSDIDSSKFLNLT--YYTD--ITWQDESINKISTDQLLNNTIILKIDIS 80
QY 61 HPWYNLLVDLGSKDATNKYKGVLDYGYVQCAGGTPNKTACWGGVTLHNNRLT 120
Db 81 VLKTSLSKVEFNSSDLANQFKGNIDYGLYGNKCVGLTEERTSLCYGGVTIYDGNQLD 140
QY 121 EEKKVPINLWIDGKQTTPIDKVKTSKKEVTQELDQARHYLHGKFGLYNSDSFGKVK 180
Db 141 EERVIGNVFVKGIQEGFV--IKTKAKVTQVELDTKVRKLENLYKIYNKDT--GNIQ 196
QY 181 RGLVIFHSS--EGSTVSYDLFDAQQGVPTDLRIYRDNKTINSENLHIDLYLY 231
Db 197 KGCIFHNNHQNQSFYDLYNKGSGAEFFQFYSNRTVSSNVHIDVELY 249

RESULT 22
Q6GFN1 STAAAR PRELIMINARY; PRT; 251 AA.
AC Q6GFN1;
DT 05-JUL-2004 (T-EMBLrel. 27, Created).
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Enterotoxin.
GN OrderedLocusNames=SAR1917;
OS Staphylococcus aureus (strain MSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15213324; DOI=10.1073/pnas.04025211101;
RA Holden M.T.G., Feil E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL: BX571856; CAG40907.1; -; Genomic DNA.
DR GO: GO:0005576; C:extracellular region; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR006177; Bcrl tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR Pfam: PF01123; Staph Strp toxin; 1.
DR Pfam: PF02876; Staph Strp tox C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH STREP TOXIN 1; UNKNOWN_1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 251 AA; 28806 MW; 1E2966FBBF86BA40 CRC64;

Query Match 36.1%; Score 446.5; DB 2; Length 251;
Best Local Similarity 39.5%; Pred. No. 1.6e-28;
Matches 92; Conservative 49; Mismatches 77; Indels 15; Gaps 6;

QY 6 EINEKDLRKSEIQRNLSNLRIQIYYNEKAIT-----ENKESDDQFLENTLFGKFFTG 60
Db 25 DVDKNDLKKKSDIDSSKFLNLT--YYTD--ITWQDESINKISTDQLLNNTIILKIDIS 80
QY 61 HPWYNLLVDLGSKDATNKYKGVLDYGYVQCAGGTPNKTACWGGVTLHNNRLT 120
Db 81 VLKTSLSKVEFNSSDLANQFKGNIDYGLYGNKCVGLTEERTSLCYGGVTIYDGNQLD 140
QY 121 EEKKVPINLWIDGKQTTPIDKVKTSKKEVTQELDQARHYLHGKFGLYNSDSFGKVK 180
Db 141 EERVIGNVFVKGIQEGFV--IKTKAKVTQVELDTKVRKLENLYKIYNKDT--GNIQ 196
QY 181 RGLVIFHSS--EGSTVSYDLFDAQQGVPTDLRIYRDNKTINSENLHIDLYLY 231
Db 197 KGCIFHNNHQNQSFYDLYNKGSGAEFFQFYSNRTVSSNVHIDVELY 249

RESULT 22
Q6GFN1 STAAAR PRELIMINARY; PRT; 251 AA.
AC Q6GFN1;
DT 05-JUL-2004 (T-EMBLrel. 27, Created).
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Enterotoxin.
GN OrderedLocusNames=SAR1917;
OS Staphylococcus aureus (strain MSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15213324; DOI=10.1073/pnas.04025211101;
RA Holden M.T.G., Feil E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";

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QY 59 TGHFW-----YNDLLVGLGSKDATNKYKKVDLYGAYGYQCAGGTPNKTACMYGV 111
Db 85 ---NWLDDGISAEFKOLKVEFSSAISKEFLGKTVDYGVYKAKHGEHQVDTACTYGGV 141
QY 112 TLHNNRLTEKKVPINLWIDGKQTTPIDKVKTSKEVTQBELDQARHYLHGKFLYN 171
Db 142 TPHNNKLSPEKNGVAVYKDNVNVNFTI--VTTDKKKVTAQELDIKVRTKLNAYKLY- 198
QY 172 SDSFGKVGKGLVFIHSSSEGSTVS--YDLFDAQGVYPTDILLRIYRDNKTINSNLHIDLY 229
Db 199 -DRMTSDVQKGYIKFHSHEKSFYDLYFIKGNLPDQVLYQNDKNTIDSSDYHIDVY 257
QY 230 LYT 232
Db 258 LFT 260

RESULT 26
Q9EZM8 STAAU PRELIMINARY; PRT; 261 AA.
AC Q9EZM8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SEO.
GN Name=seo;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A900322;
RX MEDLINE=20571956; PubMed=11123352;
RA Jarraud S., Peyrat M.A., Lim A., Tristan A., Bes M., Mougel C.,
RA Etienne J., Vandenesch F., Bonneville M., Lina G.;
RT "egc, a highly prevalent operon of enterotoxin gene, forms a putative
RT nursery of superantigens in Staphylococcus aureus.";
RL J. Immunol. 166:669-677(2001).
DR EMBL; AF285760; AAG36951.1; -; Genomic_DNA.
DR HSSP; Q54971; 1BXT.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin_C; 1.
DR PRINTS; P00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 261 AA; 29949 MW; 24DA4DD766288EC CRC64;

Query Match 31.3%; Score 387.5; DB 2; Length 261;
Best Local Similarity 39.9%; Pred. No. 1.2e-23;
Matches 97; Conservative 31; Mismatches 86; Indels 29; Gaps 8;

QY 8 NEKD-----LRKKSLEQNALSLRQIYYNE----KAITENKESDDQFLENTLLFKGPF 58
Db 30 NEEDPKIESLCKSSVDPTALHNDYINRRTTVKSIIVSTTE---KFLDPDLLFKSI- 85
QY 59 TGHFW-----YNDLLVGLGSKDATNKYKKVDLYGAYGYQCAGGTPNKTACMYGV 111
Db 86 ---NWLDDGISAEFKOLKVEFSSAISKEFLGKTVDYGVYKAKHGEHQVDTACTYGGV 142
QY 112 TLHNNRLTEKKVPINLWIDGKQTTPIDKVKTSKEVTQBELDQARHYLHGKFLYN 171
Db 143 TPHNNKLSPEKNGVAVYKDNVNVNFTI--VTTDKKKVTAQELDIKVRTKLNAYKLY- 199
QY 172 SDSFGKVGKGLVFIHSSSEGSTVS--YDLFDAQGVYPTDILLRIYRDNKTINSNLHIDLY 229
Db 200 -DRMTSDVQKGYIKFHSHEKSFYDLYFIKGNLPDQVLYQNDKNTIDSSDYHIDVY 258
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QY 230 LYT 232
Db 259 LFT 261

RESULT 27
Q52075 9ZZZZ PRELIMINARY; PRT; 179 AA.
ID Q52075;
AC Q52075;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin D.
GN Name=virc2;
OS Plasmid pIB485.
OG Plasmid pIB485.
OC other sequences; plasmids.
OX NCBI_TaxID=2565;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89359112; PubMed=2549000;
RA Bayles K.W., Iandolo J.J.;
RA "Genetic and molecular analyses of the gene encoding staphylococcal
RT enterotoxin D.";
RL J. Bacteriol. 171:4799-4806(1989).
DR EMBL; M94872; AAA98133.1; -; Genomic_DNA.
DR HSSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin_C; 1.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
KW Plasmid.
SQ SEQUENCE 179 AA; 20564 MW; 579FFE811BC08747 CRC64;

Query Match 30.8%; Score 381; DB 2; Length 179;
Best Local Similarity 48.7%; Pred. No. 2.6e-23;
Matches 73; Conservative 24; Mismatches 53; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELEQNALSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 26 NENIDSVEKEKELKKSELSSTALNNMKHSYADKNPIIGENKSTGDOFLENTLLYKKFFTD 85
QY 61 HPWYNDLLVGLGSKDATNKYKKVDLYGAYGYQCAGGTPNKTACMYGVTLHNNRLT 120
Db 86 LINFEDLLINFNSKEMAQHFKSNVDVYPIRYSINCYGGEIDRTACTYGGVTPHEGNLKL 145
QY 121 EKKKVPINLWIDGKQTTPIDKVKTSKEV 150
Db 146 ERKKIPINLWINGVQKEVSLDKVQTDKKNL 175

RESULT 28
Q8RR76 STAAU PRELIMINARY; PRT; 217 AA.
ID Q8RR76;
AC Q8RR76;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin H (Fragment).
GN Name=seh;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21871379; PubMed=11880405; DOI=10.1128/JCM.40.3.857-862.2002;
RA Onoe K., Ishikawa M., Shimoda Y., Hu D.L., Ueda S., Shinagawa K.;
RT "Detection of seg, seh, and sel genes in Staphylococcus aureus
RT isolates and determination of the enterotoxin productivities of S.
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RT aureus isolates Harboring seg, seh, or sel genes.";
RL J. Clin. Microbiol. 40:857-862(2002).
DR EMBL; AB060536; BAB85990.1; -, Genomic_DNA.
DR HSSP; Q53585; IEWC.
DR SMR; QBR76; 2-213.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; BcTrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR Pfam; PF01123; Staph_Strep_toxin_OB.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 217 AA; 25143 MW; A8A44E23F1DE80D CRC64;

Query Match 29.6%; Score 366; DB 2; Length 217;
Best Local Similarity 37.9%; Pred. No. 5.6e-22;
Matches 85; Conservative 46; Mismatches 81; Indels 12; Gaps 7;

QY 10 KDLRKSELRNALNLRIQYIYNEKAITENKESDDQPLENTLLFKGFTGHPWYNDLLV 69
DB 1 EDLHDKSELTDLALAN--AYGQYNHPFIKENIKSDEISGEKDLIFRN--QGDSG-NDLRV 55

QY 70 DLGSKDATNKYKGVKVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLTEKKVPINL 129
DB 56 KPATADLAQKFNKNVDIYGASFYKCEKISENSELYGGTTL-NSEKLAQERVIGANV 114

QY 130 WIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVGQGLIVFHS 189
DB 115 WVDGIQKETEL--IRTNKNVTLOELDIKIRKILSDKYKIYKDS---EISKGLIEFDMK 169

QY 190 EGSTVSYDLFDAQQGYPTDLLRIYRDNKTINSENL-HIDLXYLT 232
DB 170 TPRDYSFDIYDLKGENDYEDIKYEDNKTILKSDDISHDVNLVT 213

RESULT 29
ETXH STAAW
ID ETXH STAAW STANDARD; PRT; 241 AA.
AC P0A0L9; Q53585;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DE Enterotoxin type H precursor (SEH).
GN Name=entH; Synonyms=seh;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE, PARTIAL PROTEIN SEQUENCE, AND CHARACTERIZATION.
RC STRAIN=D4508;
RX MEDLINE=95053699; PubMed=7964453; DOI=10.1084/jem.180.5.1675;
RA Ren K., Bannan J.D., Pancholi V., Cheung A.L., Robbins J.C.,
RA Fischetti V.A., Zabriskie J.B.;
RT "Characterization and biological properties of a new staphylococcal
RT exotoxin.";
RL J. Exp. Med. 180:1675-1683(1994).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.69 ANGSTROMS).
RX PubMed=10986116; DOI=10.1006/jmbi.2000.4093;
RA Haekansson M., Petersson K., Nilsson H., Forsberg G., Bjoerk P.,
RA Antonsson P., Svensson L.A.;
RT "The crystal structure of staphylococcal enterotoxin H: implications
RT for binding properties to MHC class II and TcR molecules.";
RL J. Mol. Biol. 302:527-537(2000).
CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication
CC staphylococcal food poisoning syndrome. The illness characterized
CC by high fever, hypotension, diarrhea, shock, and in some cases
CC death.
CC -!- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
CC for the toxin interaction with MHC class II.

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CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U11702; AAA19777.1; -, Genomic_DNA.
CC PDB; 1ENF; X-ray; A=26-237.
CC PDB; 1EMC; X-ray; A=26-239.
CC PDB; 1R77; X-ray; A/B=25-241.
CC SMR; P0A0M0; 26-237.
CC InterPro; IPR006177; BcTrl tox.
CC InterPro; IPR006123; Staph/Strep toxin.
CC InterPro; IPR006126; Staph/Strep tox.
CC InterPro; IPR006173; Staph_tox_OB.
CC Pfam; PF02876; Staph_Strep_toxin_C; 1.
CC Pfam; PF01123; Staph_Strep_toxin; 1.
CC PRINTS; PR00279; BACTRLTOXIN.
CC PROSITE; PS00277; STAPH_STREP_TOXIN_1; FALSE NEG.
CC PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW 3D-structure; Antigen; Direct protein sequencing; Enterotoxin;
KW Metal-binding; Signal; Superantigen; Toxin; Zinc.
FT SIGNAL 1 24
FT CHAIN 25 241 Enterotoxin type H.
FT METAL 230 230 Zinc.
FT METAL 232 232 Zinc.
FT DISULFID 106 116
FT SEQUENCE 241 AA; 27859 MW; 70F77985877616CE CRC64;

Query Match 29.6%; Score 366; DB 1; Length 241;
Best Local Similarity 37.9%; Pred. No. 6.4e-22;
Matches 85; Conservative 46; Mismatches 81; Indels 12; Gaps 7;

QY 10 KDLRKSELRNALNLRIQYIYNEKAITENKESDDQPLENTLLFKGFTGHPWYNDLLV 69
DB 25 EDLHDKSELTDLALAN--AYGQYNHPFIKENIKSDEISGEKDLIFRN--QGDSG-NDLRV 79

QY 70 DLGSKDATNKYKGVKVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLTEKKVPINL 129
DB 80 KPATADLAQKFNKNVDIYGASFYKCEKISENSELYGGTTL-NSEKLAQERVIGANV 138

QY 130 WIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVGQGLIVFHS 189
DB 139 WVDGIQKETEL--IRTNKNVTLOELDIKIRKILSDKYKIYKDS---EISKGLIEFDMK 193

QY 190 EGSTVSYDLFDAQQGYPTDLLRIYRDNKTINSENL-HIDLXYLT 232
DB 194 TPRDYSFDIYDLKGENDYEDIKYEDNKTILKSDDISHDVNLVT 237

RESULT 30
ETXH STAAW
ID ETXH STAAW STANDARD; PRT; 241 AA.
AC P0A0L9; Q53585;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Enterotoxin type H precursor (SEH).
GN Name=entH; Synonyms=seh; OrderedLocusNames=MW0051;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwana N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-

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RT acquired MRSA.";
RL Lancelot 359:1819-1827(2002).
CC -1- FUNCTION: Staphylococcal enterotoxins cause the intoxication
CC staphylococcal food poisoning syndrome. The illness characterized
CC by high fever, hypotension, diarrhea, shock, and in some cases
CC death (By similarity).
CC -1- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
CC for the toxin interaction with MHC class II (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC ENBL; BA000033; BAB93916.1; -; Genomic_DNA.
DR SMR; POA0L9; 26-237.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox_OB.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Antigen; Complete proteome; Enterotoxin; Metal-binding; Signal;
KW Superantigen; toxin; zinc.
FT SIGNAL 1 24 By similarity.
FT CHAIN 25 241 Enterotoxin type H.
FT METAL 230 230 Zinc (By similarity).
FT METAL 232 232 Zinc (By similarity).
FT DISULFID 106 116 By similarity.
FT SEQUENCE 241 AA; 27859 MW; 70f77985877616CE CRC64;

Query Match 29.6%; Score 366; DB 1; Length 241;
Best Local Similarity 37.9%; Pred. No. 6.4e-22;
Matches 85; Conservative 46; Mismatches 81; Indels 12; Gaps 7;

QY 10 KDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTGHPWYNDLLV 69
DB 25 EDLHDKSELTDLALAN--AYQYNHPFIKENIKSDEISGEKDLIFRN--QDMSG-NDLRV 79

QY 70 DLGSKDATNKYKGVLDYGVYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINL 129
DB 80 KFTADLAQKFKNVVDIYGASFYKCEKISENISECLYGGTTL-NSEKLAQERVIGANV 138

QY 130 WIDGKQTTVPIDKVTSKSEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQGVORGLIVPHSS 189
DB 139 WVDGIQKETEL--IRTNKNVTLQELDKIRKILSDKYKIYYKDS---EISKGLIEFDMK 193

QY 190 EGSTVSVDLFDAGQYQPTDLLRIYRDNKTINSENH-HIDLVLVLT 232
DB 194 TPRDYSFDIYDLKGENDYEDKIYEDNKTLSDDISHIDVNLVLT 237

RESULT 31
Q6VAM8 STAAU PRELIMINARY; PRT; 241 AA.
AC Q6VAM8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Enterotoxin H precursor.
GN Name=seh;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.

Q6VAM8 STAAU PRELIMINARY; PRT; 241 AA.
AC Q6VAM8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Enterotoxin H precursor.
GN Name=seh;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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RC STRAIN=FRI 137;
RA Gul'ko L.B., Voyushin K.E., Fluer F.S., Okorokova N.A., Krivenko M.S.,
RA Veiko V.P., Debabov V.G.;
RT "The Obtaining of the Tumor-Addressed Genetically Engineered Drug for
RT Cancer Immunotherapy. II. Cloning a Gene of the pro-Enterotoxin H (seh)
RT from Staphylococcus aureus, its Expression in Escherichia coli.
RT Investigation of the Enterotoxin H Secretion by E. coli Cells.";
RL Biotechnology 6:72-78(2003).
DR ENBL; AY345144; AAQ63188.1; -; Genomic_DNA.
DR SMR; Q6VAM8; 26-237.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006173; Staph tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT SIGNAL 1 24 Potential.
FT CHAIN 25 241 enterotoxin H.
FT SEQUENCE 241 AA; 27831 MW; 70EBA8418C9ECCFE CRC64;

Query Match 29.6%; Score 366; DB 2; Length 241;
Best Local Similarity 37.9%; Pred. No. 6.4e-22;
Matches 85; Conservative 46; Mismatches 81; Indels 12; Gaps 7;

QY 10 KDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTGHPWYNDLLV 69
DB 25 EDLHDKSELTDLALAN--AYQYNHPFIKENIKSDEISGEKDLIFRN--QDMSG-NDLRV 79

QY 70 DLGSKDATNKYKGVLDYGVYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINL 129
DB 80 KFTADLAQKFKNVVDIYGASFYKCEKISENISECLYGGTTL-NSEKLAQERVIGANV 138

QY 130 WIDGKQTTVPIDKVTSKSEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQGVORGLIVPHSS 189
DB 139 WVDGIQKETEL--IRTNKNVTLQELDKIRKILSDKYKIYYKDS---EISKGLIEFDMK 193

QY 190 EGSTVSVDLFDAGQYQPTDLLRIYRDNKTINSENH-HIDLVLVLT 232
DB 194 TPRDYSFDIYDLKGENDYEDKIYEDNKTLSDDISHIDVNLVLT 237

RESULT 32
Q6GD45 STAAU PRELIMINARY; PRT; 241 AA.
AC Q6GD45;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Enterotoxin H.
GN Name=seh; OrderedLocusNames=SAS0051;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinovitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571857; CAG41819.1; -; Genomic_DNA.

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DR	SMR; Q6GD45; 26-237.	RL	J. Appl. Microbiol. 95:38-43 (2003).
DR	GO; GO:0005576; C:extracellular region; IEA.	DR	EMBL; AY291444; RAP78524.2; -; Genomic DNA.
DR	GO; GO:0009405; P:pathogenesis; IEA.	DR	EMBL; AY920264; AAX11328.1; -; Genomic DNA.
DR	InterPro; IPR006177; Bctrl tox.	DR	EMBL; AY920265; AAX11329.1; -; Genomic DNA.
DR	InterPro; IPR006123; Staph/Strep toxin.	DR	EMBL; AY920269; AAX11333.1; -; Genomic DNA.
DR	InterPro; IPR006173; Staph tox_OB.	DR	EMBL; AY158703; AAO17731.1; -; Genomic DNA.
DR	Pfam; PF01123; Staph_Strp_toxin; 1.	DR	EMBL; AY920263; AAX11327.1; -; Genomic DNA.
DR	Pfam; PF02876; Staph_Strp_tox_C; 1.	DR	HSSP; PI3380; 1AN8.
DR	PRINTS; PR00279; BACTRLTOXIN.	DR	GO; GO:0005576; C:extracellular region; IEA.
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.	DR	GO; GO:0009405; P:pathogenesis; IEA.
KW	Complete proteome.	DR	InterPro; IPR006177; Bctrl tox.
SQ	SEQUENCE 241 AA; 27858 MW; 70F77985877616CE CRC64;	DR	InterPro; IPR006123; Staph/Strep toxin.
Query Match 29.6%; Score 366; DB 2; Length 241;		DR	InterPro; IPR006173; Staph tox_OB.
Best Local Similarity 37.9%; Pred. No. 6.4e-22;		DR	Pfam; PF02876; Staph_Strp_tox_C; 1.
Matches 85; Conservative 46; Mismatches 81; Indels 12; Gaps 7;		DR	PRINTS; PR00279; BACTRLTOXIN.
		DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
		SQ	SEQUENCE 242 AA; 27950 MW; 5935658E21C4C89C CRC64;
		Query Match 28.2%; Score 348.5; DB 2; Length 242;	
		Best Local Similarity 36.6%; Pred. No. 1.8e-20;	
		Matches 87; Conservative 37; Mismatches 77; Indels 37; Gaps 9;	
QY	10 KDLRKSELRNLSLRQIYYNEKAITENKESDDQFLNTLLPKGFTGHPWYNDLLV 69	QY	8 NEKDLRKSELRN-ALSNLRQIY----YYNEKAITENKESDDQFLNTLLPKGFTGHP 62
DB	25 EDLHDKSELTDLALN--AYQYNHFFIKENIKSDEISGEKDLIFRN--QGDSG-NDLRV 79	DB	17 NIKDL---SYAOGDIGVGNLRNFYTKYDIDLKGVTDKNLPANQLE-----FSTG-- 64
QY	70 DLGSKDATNKKYKKGVLDLYGAYGYQCAGGTPNKTAQMYGGVTLHDNNRLTEKKVPINL 129	QY	63 WYNDLVDLGSKDATNKKYKKGVLDLYGAYGYQCAGGTPNKTAQMYGGVTLHDNNRLTEE 122
DB	80 KFTADLAQKFKKNQVDIYGASFYKCEKISENSECLYGGTTL-NSEKLAQERVIGANV 138	DB	65 -TNDLISENNWDEISKPKGKMDIFGIDYNGPC-----KTKYMYGGATL-SGQYLNSA 116
QY	130 WIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQRLIVFHS 189	QY	123 KKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFG-KG--- 178
DB	139 WVDGIQKETEL--IRTNKKNVTLQELDIKIRKTLSDKYIYKDS---BISKGLIFDMK 193	DB	117 RKPIPNLWINGKHKTISTDKIATNKKLVTAQELDVKLRRYLOEYNIYGHNNNGKKEYG 176
QY	190 EGSTVSVDLFDAGQVDPDTLLRIRYDNKNTINSNL-HIDLXYLT 232	QY	179 -----VQRGLIVFHSSEGSTVSVDLFDAGQVDPDTLLRIRYDNKNTINSENHLIDL 228
DB	194 TPRDVSFDIYDLKGENDYIDKIYEDNKTKSDISHIDUNLYT 237	DB	177 YKSKFYSGFNKGKVLPHLNDEKSFYDLFTYTGDLGVLFSFKIYEDNKIIESEKFLHDV 234
RESULT 33		RESULT 34	
ID	Q7X0E8 STAAU PRELIMINARY; PRT; 242 AA.	ID	Q6GFM9 STAAU PRELIMINARY; PRT; 242 AA.
AC	Q7X0E8; Q6VCN5;	AC	Q6GFM9; STAAU PRELIMINARY; PRT; 242 AA.
DT	01-OCT-2003 (TrEMBLrel. 25, Created)	DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)	DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	13-SEP-2005 (TrEMBLrel. 31, Last annotation update)	DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Enterotoxin type I (Enterotoxin type Iv) (Enterotoxin SEI variant).	DE	Enterotoxin.
GN	Name=seiv;	GN	OrderedLocusNames=SAR1919;
OS	Staphylococcus aureus.	OS	Staphylococcus aureus (strain MRSA252).
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.	OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX	NCBI_TaxID=1280;	OX	NCBI_TaxID=282458;
RN	[1]	RN	[1]
RP	NUCLEOTIDE SEQUENCE.	RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=AB-8802;	RC	STRAIN=AB-8802;
RX	PubMed=15357721; DOI=10.1111/j.1365-2672.2004.02349.x;	RX	PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA	Blattota G., Ercolini D., Pennacchia C., Fusco V., Casaburi A., Pepe O., Villani F.;	RA	Holden M.T.G., Feil E.J., Lindeay J.A., Peacock S.J., Day N.P.J., Enright M.C., Foster T.J., Moore C.E., Hurst L., Actin R., Barron A., Bason N., Bentley S.D., Chillingworth C., Chillingworth T., RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L., James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K., Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M., Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G., Spratt B.G., Parkhill J.;
RT	"PCR detection of staphylococcal enterotoxin genes in Staphylococcus spp. strains isolated from meat and dairy products. Evidence for new variants of seG and sei in S. aureus AB-8802.";	RT	"Complete genomes of two clinical Staphylococcus aureus strains: evidence for the rapid evolution of virulence and drug resistance.";
RL	J. Appl. Microbiol. 97:719-730(2004).	RL	Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
RN	[2]	RN	EMBL; BX571856; CAG40905.1; -; Genomic DNA.
RP	NUCLEOTIDE SEQUENCE.	RP	GO; GO:0005576; C:extracellular region; IEA.
RC	STRAIN=AB-8802, OM562a, A2812/98, ATCC 25923, and 7645a;	RC	GO; GO:0009405; P:pathogenesis; IEA.
RA	Blattota G., Fusco V., Villani F., von Eiff C., Becker K.;	RA	InterPro; IPR006177; Bctrl tox.
RT	"Detection and characterization of the Staphylococcus aureus enterotoxin gene cluster (egc) in strains isolated from different source (human, veterinary, food and reference).";	RA	InterPro; IPR006123; Staph/Strep toxin.
RL	Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.	RA	InterPro; IPR006173; Staph_tox_OB.
RN	[3]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=382F;		
RX	MEDLINE=22692404; PubMed=12807452;		
RA	DOI=10.1046/j.1365-2672.2003.01957.x;		
RA	Letetere C., Perelle S., Dilasser F., Fach P.;		
RT	"Identification of a new putative enterotoxin SEU encoded by the egc cluster of Staphylococcus aureus.";		


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AC Q7A205;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Extracellular enterotoxin type I.
GN Name=sei; OrderedLocNames=SAV1828;
OS Staphylococcus aureus (strain MU50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hiramatsu N., Hayashi H., Hiramatsu K.;
RA "Whole genome sequencing of meticillin-resistant Staphylococcus aureus.";
RT LANCET 357:1225-1240(2001).
RL EMBL; BA000017; BAB57990.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPRO06173; Bctrl tox.
DR InterPro; IPRO06173; Staph toxin.
DR Pfam; PF01123; Staph Strp toxin; 1.
DR Pfam; PF02876; Staph Strp toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 242 AA; 27863 MW; C5C8B4ACEE5414A8 CRC64;

Query Match 27.4%; Score 339.5; DB 2; Length 242;
Best Local Similarity 35.6%; Pred. No. 9.7e-20;
Matches 79; Conservative 36; Mismatches 74; Indels 33; Gaps 7;

QY 23 LSNLRQIY----YNEKAITENKESDDQFLENTLLFKGFFTHGHPWYNDLVLGSKDATN 78
Db 30 VGNLRFYTKHDYIDLKGVTDKNLPTANQLE-----FSTG---TNDLISENNWDEIS 79

QY 79 KYGKKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLTEKKVPINLWIDGKQTTV 138
Db 80 KFKGKKLDFIDYNGPC-----KSKYMGGATL-SGQYLNSARKIPINLWNGKHKTI 132

QY 139 PIDKVKTSKEVTQVQLDQARHYLHGKFLYNSDSFG-GK-----VORGILVF 186
Db 133 STDKIATNKKLVTAQEDVLRRLQBEYNIYGHNTGKGYKSKFYSGFNNGKVLV 192

QY 187 HSEGSTSVSYDLFDQAQGYPTDLLRIYRDNKTINSENHLIDL 228
Db 193 HLNNEKFSYDLPFTGDLGVSLFKIYEDNKIIESEKFKHLDV 234

RESULT 41
Q52T95 STAAU PRELIMINARY; PRT; 218 AA.
ID Q52T95;
AC Q52T95;
DT 13-SEP-2005 (T-EMBLrel. 31, Created)
DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)
DE Enterotoxin type I (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Fc35, and Fc30;
RA Fernandez M.M., De Marzi M.C., Berquer P., Burzyn D., Langley R.J.,
RA Piazzon I., Mariuzza R.A., Malchiodi E.L.;
RT "Binding of natural variants of staphylococcal superantigens SEG and SEI to TCR and MHC class II molecules.";
RL Mol. Immunol. 0:0-0(2005).
DR EMBL; AY961387; AAX84816.1; -; Genomic DNA.
DR EMBL; AY961381; AAX84810.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPRO06177; Bctrl tox.
DR InterPro; IPRO06173; Staph toxin.
DR Pfam; PF02876; Staph Strp toxin; 1.
DR Pfam; PF01123; Staph Strp toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1 1
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DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 240 AA; 27478 MW; 85CD62DA731C3D95 CRC64;

Query Match 27.1%; Score 336; DB 2; Length 240;
Best Local Similarity 35.3%; Pred. No. 1.9e-19;
Matches 78; Conservative 37; Mismatches 72; Indels 34; Gaps 6;

QY 25 NLRLQIY----YYNEKAITENKESDDQFLENTLLFKGFFTGHPWYND-LLVDLGSKDATNK 79
DB 32 NLRNFYTKYEVNLRKNVKNKNSPESHRL-----YSKNDTLVAEFNVEYITSD 80
QY 80 YKGGKVDLYGAYGYQCAGTGNKTAACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVP 139
DB 81 LKGNVDVFGISKY-----GSNRT--IYGVTKAENKLDSPRIIPINLIINGKHQTTV 134
QY 140 IDKVTKSKEVTVQELDQARHYLHGKFGLY-----NSDSFGKVGQVGLIVFH 187
DB 135 TKSVSVDKMWVTAQEDIVKLRLKYLQDEFNIYGHNDTGKKEYGTSSKFYSFGDKGSVWFH 194
QY 188 SSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHLIDL 228
DB 195 INDGNSFSDYDLFTYGTGLPESFLKIYDKNKTVDSTQFHLDV 235

RESULT 47
Q52T97 STAAU PRELIMINARY; PRT; 210 AA.
AC Q52T97;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Enterotoxin type I (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1] NUCLEOTIDE SEQUENCE.
RP STRAIN=rc65;
RA Fernandez M.M., De Marzi M.C., Berquer P., Burzyn D., Langley R.J.,
R Piazzon I., Mariuza R.A., Malchiodi E.L.;
RT "Binding of natural variants of staphylococcal superantigens SEG and
RT SEI to TCR and MHC class II molecules.";
RL Mol. Immunol. 0:0-0(2005).
DR EMBL; AY961385; AX48414.1; -; Genomic_DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctrl tox.
DR InterPro; IPR006173; Staph/Strep toxin.
DR InterPro; IPR006173; Staph/Strep toxin.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT NON_TER 210
SQ SEQUENCE 210 AA; 24082 MW; 15A1E489513EBBBE CRC64;

Query Match 27.1%; Score 335.5; DB 2; Length 210;
Best Local Similarity 35.9%; Pred. No. 1.7e-19;
Matches 79; Conservative 39; Mismatches 67; Indels 35; Gaps 8;

QY 26 LRQIYYNEK-----AITENKESDDQFLENTLLFKGFFTGHPWYNLLVDLGSKDATNKY 80
DB 1 LKKFLYKHDSIDSKGLIDKNLPSANQ-LE-----FSTG---INDLISESNWDEISKF 49
QY 81 KGGKVDLYGAYGYQCAGTGNKTAACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVPI 140
DB 50 KGGKLDIFGIDYNGPC-----KSKYMYGGATL-SGQYLSARKIPINLWVNGKHKTIST 102
QY 141 DKVTKSKEVTVQELDQARHYLHGKFGLYNSDSFG-GK-----VQRGGLIVFHS 188
DB 103 DKISTNKLVTAEIDVKLRLRYLQEEYNIYGHNSTGKKEYGYSKFSYGFNKGKVLFLH 162

QY 189 SEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHLIDL 228
DB 163 NDEKSFSDYDLFTYGDGVPVSFLKIYEDNKIIIESEKFLDV 202

RESULT 48
Q8RR75 STAAU PRELIMINARY; PRT; 218 AA.
AC Q8RR75;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin I (Fragment).
GN Name=sei;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1] NUCLEOTIDE SEQUENCE.
RP MEDLINE=21871379; PubMed=11880405; DOI=10.1128/JCM.40.3.857-862.2002;
RX Omoe K., Ishikawa M., Shimoda Y., Hu D.L., Ueda S., Shinagawa K.;
RA "Detection of seg, seh, and sei genes in Staphylococcus aureus
RT isolates and determination of the enterotoxin production activities of S.
RT aureus isolates Harboring seg, seh, or sei genes.";
RL J. Clin. Microbiol. 40:857-862(2002).
DR EMBL; AB060537; BAB85991.1; -; Genomic_DNA.
DR HSSP; P13380; IKTK.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006173; Staph/Strep toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 218 AA; 24909 MW; 1017728FB71BF662 CRC64;

Query Match 27.1%; Score 335.5; DB 2; Length 218;
Best Local Similarity 35.1%; Pred. No. 1.8e-19;
Matches 78; Conservative 37; Mismatches 74; Indels 33; Gaps 7;

QY 23 LSNLRQIY----YYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNLLVDLGSKDATN 78
DB 6 VGNLRFYTKHYDYLKGVTDKNLPIANQLE-----FSTG---INDLISESNWDEIS 55
QY 79 KYGKVDLYGAYGYQCAGTGNKTAACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTV 138
DB 56 KFKGKKLDIFGIDYNGPC-----KSKYMFGGATL-SGQYLSARKIPINLWVNGKHKT 108
QY 139 PIDKVTKSKEVTVQELDQARHYLHGKFGLYNSDSFG-GK-----VQRGGLIVF 186
DB 109 STDKIATNKKLVTAQEDIVKLRLRYLQEEYNIYGHNTGKKEYGYSKFSYGFNNGKVL 168
QY 187 HSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHLIDL 228
DB 169 HLNNEKSFSDYDLFTYGDGGLPVSFLKIYEDNKIIIESEKFLDV 210

RESULT 49
Q9L921 STRE PRELIMINARY; PRT; 225 AA.
AC Q9L921;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 25.7 kDa protein.
OS Streptococcus equi.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OX NCBI_TaxID=1336;
RN [1] NUCLEOTIDE SEQUENCE.

DR Pfam; PF01123; Stap_Strp_toxin; 1.
DR Pfam; PF02876; Stap_Strp_tox C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 225 AA; 25611 MW; CE0D6736CC11CC04 CRC64;

Query Match 27.0%; Score 334.5; DB 2; Length 225;
Best Local Similarity 34.4%; Pred.No. 2.3e-19;
Matches 76; Conservative 42; Mismatches 80; Indels 23; Gaps 6;

QY 25 NLRIQIYYNEKAITENKESDDQLFNTLLPKGFCTHPWN---DLLVDLGSKDATNKYK 81
| | | | :
DB 8 NLRNLSTYDPTTEVKGKINEGPPPSGLSFYKNI----PYGNSSIELKVELNSVEKANFFS 63
| | | | :
QY 82 GKKVLDLYGAYGYQCAGGTPTNKTACMYGVTLHDDNNRLTEEKVPINLWIDG---KOTTV 138
| | | | :
DB 64 GRKVDIFLEYSPPCNSNTKKNS---YGGTILSDGNRI-DKKMIPNVNFIIDFGVOOKYSYT 119
| | | | :
QY 139 PIDKVRTSKKEVTQBELDLQARHYLKHKFLY-----NSDSFGKGKVGQRLIVPHSS 189
| | | | : : : | :
DB 120 DISTGSTDKKEVTIQELDVKSRYVLQKHFNVIYGVGDVKDFGRSSRFQSGFEIGNIIIFLN 179
| | | | : : : | :
QY 190 EGSTVSVDLPDAQGVDPDTLLRIYRDNKTKINSENLHIDLXL 230
| | | | : : : | :
DB 180 SGERISYNLFDTGHGDRESMLKKYSNDKTAYSQDLHIDIYL 220
| | | | : : : | :

RESULT 51

ID Q7X0E6 STAAU PRELIMINARY; PRT; 242 AA.

AC Q7X0E6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Enterotoxin type I.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BS49;
RX PubMed=15337721; DOI=10.1111/j.1365-2672.2004.02349.x;
RA Blaiotta G., Erccolini D., Pennacchia C., Fusco V., Casaburi A.,
Pepe O., Villani F.;
RT "PCR detection of staphylococcal enterotoxin genes in Staphylococcus spp. strains isolated from meat and dairy products. Evidence for new variants of seg and sei in S. aureus AB-8802.";
RL J. Appl. Microbiol. 97:719-730(2004).
RN [2]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BS49;
RA Blaiotta G., Fusco V., Villani F., von Eiff C., Becker K.;
RT "Detection and characterization of the Staphylococcus aureus enterotoxin gene cluster (egc) in strains isolated from different source (human, veterinary, food and reference).";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR ENBL; AY291446; AAP78528.2; -; Genomic_DNA.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPRO06177; Bctrl tox.
DR InterPro; IPRO06123; Stap/Strep toxin.
DR InterPro; IPRO06173; Staph tox_OB.
DR Pfam; PF01123; Stap_Strp_toxin; 1.
DR Pfam; PF02876; Stap_Strp_tox C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 242 AA; 27858 MW; C5C3f005C28414A8 CRC64;

Query Match 26.9%; Score 332.5; DB 2; Length 242;
Best Local Similarity 35.1%; Pred.No. 3.6e-19;
Matches 78; Conservative 36; Mismatches 75; Indels 33; Gaps 7;

```
QY 23 LSNLRQIY-----YYNEKAITENKESDDQFLENTLLFKGFTGHPWYNDLLVDLGSKDATN 78
Db 30 VGNLRFYTKHDYIDLKGVTDKNLPANQLE-----FSTG-----TNDLISESNWDEIS 79
QY 79 KYGKVDLYGAYYGQAGGTGPNKTCMVGVTLLHNNRLTEKKVPINLWIDGKQTTV 138
Db 80 KFKGKLDLFGIDYNGPC-----KSKYMGGATL-SGQYLSARKIPINLWNGXHKTI 132
QY 139 PIDKVKTSKEVTVQBLDQARHYLHGKFGLYNSDFG-GK-----VQRLGIYVF 186
Db 133 STDKIATNKKLVTAQEBIDVLRRLYQBEYNIYGHNTGKGYKSKFYSGFNNGKVLV 192
QY 187 HSESGTYSVDLFDAGQVPTDLLRIYRDNKTINSENHLIDL 228
Db 193 HLNNEKSFYSYDLFTYTGHLGVPVSLKIYEDNTIIESEKFLHDV 234

RESULT 52
Q7A4W7_STAAM PRELIMINARY; PRT; 239 AA.
AC Q7A4W7;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DE Enterotoxin SEM.
GN Name-sem; OrderedLocusNames=SA1647;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacilliales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Hiyama K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL; BA000018; BAB42915.1; -; Genomic_DNA.
DR HSSP; P13380; IAN8.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctrl tox.
DR InterPro; IPR006173; Staph/Strep toxin.
DR InterPro; IPR006173; Staph/Strep toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 239 AA; 27370 MW; 5F29665125705600 CRC64;
Query Match 25.8%; Score 320; DB 2; Length 239;
Best Local Similarity 33.0%; Pred. No. 3.8e-18;
Matches 72; Conservative 40; Mismatches 78; Indels 28; Gaps 6;

QY 25 NLRQIYYNEKAITENK--ESDDQFLENTLLFKGFTGHPWYNDLLVDLGSKDATNKYKG 82
Db 28 NLRN--YGYSPYEDHQSTINPENNHLHQVLS-----MDNSTVTAEFKNVDDVKFKN 79
QY 83 KKVLDLYGAYYGQAGGTGPNKTCMVGVTLLHNNRLTEKKVPINLWIDGKQTTVPIDK 142
Db 80 HAVDVYGLSYSGYCL-----KNKYIYGVTL-AGDYLEKSRRIPIINLWNGEHQTISTDK 133
QY 143 VKTSKEVTVQBLDQARHYLHGKFGLY-----NSDSFGKVGQRLIVFHSSE 190
Db 134 VSTNKKLVTAQEBIDTKRLRYLQBEYNIYGFNDTNKGRNYGNKSKFSGSGFNAGKILFLND 193
QY 191 GSTVSYDLFDAGQVPTDLLRIYRDNKTINSENHLIDL 228
Db 194 GGSFSDYDLFDGTGQAESEFLKYNNDKVTETEKFLHDV 231

RESULT 54
Q6G7UL_STAAS PRELIMINARY; PRT; 242 AA.
AC Q6G7UL;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
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QY 191 GSTVSYDLFDAGQVPTDLLRIYRDNKTINSENHLIDL 228
Db 194 GGSFSDYDLFDGTGQAESEFLKYNNDKVTETEKFLHDV 231

RESULT 53
Q99T47_STAAM PRELIMINARY; PRT; 239 AA.
AC Q99T47;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Enterotoxin.
GN Name-sem; OrderedLocusNames=SAV1829;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacilliales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Hiyama K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL; BA000017; BAB57991.1; -; Genomic_DNA.
DR PIR; D89969; D89969.
DR HSSP; Q3RQ05; LET6.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctrl tox.
DR InterPro; IPR006173; Staph/Strep toxin.
DR InterPro; IPR006173; Staph/Strep toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 239 AA; 27370 MW; 5F29665125705600 CRC64;
Query Match 25.8%; Score 320; DB 2; Length 239;
Best Local Similarity 33.0%; Pred. No. 3.8e-18;
Matches 72; Conservative 40; Mismatches 78; Indels 28; Gaps 6;

QY 25 NLRQIYYNEKAITENK--ESDDQFLENTLLFKGFTGHPWYNDLLVDLGSKDATNKYKG 82
Db 28 NLRN--YGYSPYEDHQSTINPENNHLHQVLS-----MDNSTVTAEFKNVDDVKFKN 79
QY 83 KKVLDLYGAYYGQAGGTGPNKTCMVGVTLLHNNRLTEKKVPINLWIDGKQTTVPIDK 142
Db 80 HAVDVYGLSYSGYCL-----KNKYIYGVTL-AGDYLEKSRRIPIINLWNGEHQTISTDK 133
QY 143 VKTSKEVTVQBLDQARHYLHGKFGLY-----NSDSFGKVGQRLIVFHSSE 190
Db 134 VSTNKKLVTAQEBIDTKRLRYLQBEYNIYGFNDTNKGRNYGNKSKFSGSGFNAGKILFLND 193
QY 191 GSTVSYDLFDAGQVPTDLLRIYRDNKTINSENHLIDL 228
Db 194 GGSFSDYDLFDGTGQAESEFLKYNNDKVTETEKFLHDV 231

RESULT 54
Q6G7UL_STAAS PRELIMINARY; PRT; 242 AA.
AC Q6G7UL;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
```



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DR GO: GO:0009405; P: pathogenesis; IEA.
DR InterPro: IPR006177; Bcrl tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR008375; Staph exotoxin.
DR InterPro: IPR006173; Staph tox OB.
DR Pfam: PF01123; Staph/Strep toxin; 1.
DR Pfam: PF02876; Staph/Strep tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PRINTS: PR01800; STAPHSTREPTOXIN.
DR PROSITE: PS00277; STAPH STREP TOXIN 1; UNKNOWN_1.
DR PROSITE: PS00278; STAPH STREP TOXIN 2; 1.
SQ SEQUENCE 256 AA; 29794 MW; 9E2F13790823A7DF CRC64;

Query Match 25.7%; Score 318.5; DB 2; Length 256;
Best Local Similarity 33.8%; Pred. No. 5.5e-18;
Matches 76; Conservative 35; Mismatches 71; Indels 43; Gaps 8;

QY 25 NLRQIY--YYNEK--AITENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKY 80
DB 46 NLRNFYANPEPEKLGQVSSGNFSTSHQLE---YIDGKYTLYSQFH-----NEY 90

QY 81 KGK-----KVDLYGAYGYOCAGGTENKTKACMYGGVTLHDNNRLTBKVKVPINLWIDGKQ 135
DB 91 EAKRLKDHKVDIFGISVSGLC-----NTKYMGGITLANQN-LDKPRNIPINLWNGKQ 143

QY 136 TTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYN-----SDSFGGKVQVQGL 183
DB 144 NTISTDKVSTQKKEVTAQEDIDRLKYLQNEVNIYGFNKTGKQGYGYSKFSNGFNKGK 203

QY 184 IVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDNKTINSENHLIDL 228
DB 204 ITPHLNNEPSFTYDLFTYGTGQAESFLKIYDNDKNTIDAENFHLDV 248

RESULT 57
O93CC6 STAAU
ID Q93CC6 STAAU PRELIMINARY; PRT; 242 AA.
AC Q93CC6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Seq.
GN Names=seq;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=COL;
RX MEDLINE=21935388; PubMed=11821418; DOI=10.1074/jbc.M111661200;
RA Yarwood J.M., McCormick J.K., Paustian M.L., Orwin P.M., Kapur V.,
RA Schlievert P.M.;
RT "Characterization and expression analysis of Staphylococcus aureus
RT pathogenicity island 3. Implications for the evolution of
RT staphylococcal pathogenicity islands."
RL J. Biol. Chem. 277:13138-13147(2002).
DR EMBL; AF410775; AAL04146.1; -; Genomic_DNA.
DR HSSP; P13380; 1KTK.
DR GO: GO:0005576; C: extracellular region; IEA.
DR GO: GO:0009405; P: pathogenesis; IEA.
DR InterPro: IPR006177; Bcrl tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR008375; Staph exotoxin.
DR InterPro: IPR006173; Staph tox OB.
DR Pfam: PF01123; Staph/Strep toxin; 1.
DR Pfam: PF02876; Staph/Strep tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PRINTS: PR01800; STAPHSTREPTOXIN.
DR PROSITE: PS00277; STAPH STREP TOXIN 1; UNKNOWN_1.
DR PROSITE: PS00278; STAPH STREP TOXIN 2; 1.
SQ SEQUENCE 242 AA; 28184 MW; F6EEFD4AF8C30D85 CRC64;
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Query Match 25.6%; Score 316.5; DB 2; Length 242;
Best Local Similarity 33.8%; Pred. No. 7.6e-18;
Matches 76; Conservative 35; Mismatches 71; Indels 43; Gaps 8;

QY 25 NLRQIY--YYNEK--AITENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKY 80
DB 32 NLRNFYANPEPEKLGQVSSGNFSTSHQLE---YIDGKYTLYSQFH-----NEY 76

QY 81 KGK-----KVDLYGAYGYOCAGGTENKTKACMYGGVTLHDNNRLTBKVKVPINLWIDGKQ 135
DB 77 EAKRLKDHKVDIFGISVSGLC-----NTKYMGGITLANQN-LDKPRNIPINLWNGKQ 129

QY 136 TTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYN-----SDSFGGKVQVQGL 183
DB 130 NTISTDKVSTQKKEVTAQEDIDRLKYLQNEVNIYGFNKTGKQGYGYSKFSNGFNKGK 189

QY 184 IVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDNKTINSENHLIDL 228
DB 190 ITPHLNNEPSFTYDLFTYGTGQAESFLKIYDNDKNTIDAENFHLDV 234

RESULT 58
Q5HHJ9 STAAC
ID Q5HHJ9 STAAC PRELIMINARY; PRT; 242 AA.
AC Q5HHJ9;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Staphylococcal enterotoxin type I.
GN Names=sei; OrderedLocusNames=SACOL0887;
OS Staphylococcus aureus (strain COL)
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=93062;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15774886; DOI=10.1128/JB.187.7.2426-2438.2005;
RA Gill S.R., Fouts D.E., Archer G.L., Mongodin E.F., DeBoy R.T.,
RA Ravel J., Paulsen I.T., Kolonay J.F., Brinkac L.M., Beanan M.J.,
RA Dodson R.J., Daugherty S.C., Madupu R., Angiuoli S.V., Durkin A.S.,
RA Haft D.H., Vamathevan J.J., Khouri H., Utterback T.R., Lee C.,
RA Dimitrov G., Jiang L., Qin H., Weidman J., Tran K., Kang K.H.,
RA Hance I.R., Nelson K.E., Fraser C.M.;
RT "Insights on evolution of virulence and resistance from the complete
RT genome analysis of an early methicillin-resistant Staphylococcus
RT aureus strain and a biofilm-producing methicillin-resistant
RT Staphylococcus epidermidis strain."
RL J. Bacteriol. 187:2426-2438(2005).
DR EMBL; CP000046; AAW36440.1; -; Genomic_DNA.
DR TIGR; SACOL0887; -.
DR GO: GO:0005576; C: extracellular region; IEA.
DR GO: GO:0009405; P: pathogenesis; IEA.
DR InterPro: IPR006177; Bcrl tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR008375; Staph exotoxin.
DR InterPro: IPR006173; Staph tox OB.
DR Pfam: PF01123; Staph/Strep toxin; 1.
DR Pfam: PF02876; Staph/Strep tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PRINTS: PR01800; STAPHSTREPTOXIN.
DR PROSITE: PS00277; STAPH STREP TOXIN 1; UNKNOWN_1.
DR PROSITE: PS00278; STAPH STREP TOXIN 2; 1.
KW Complete proteome.
SQ SEQUENCE 242 AA; 28184 MW; F6EEFD4AF8C30D85 CRC64;

Query Match 25.6%; Score 316.5; DB 2; Length 242;
Best Local Similarity 33.8%; Pred. No. 7.6e-18;
Matches 76; Conservative 35; Mismatches 71; Indels 43; Gaps 8;

QY 25 NLRQIY--YYNEK--AITENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKY 80
DB 32 NLRNFYANPEPEKLGQVSSGNFSTSHQLE---YIDGKYTLYSQFH-----NEY 76
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SQ SEQUENCE 242 AA; 27848 MW; FC377CB4C9BBB4E3 CRC64;
Query Match 25.0%; Score 310; DB 2; Length 242;
Best Local Similarity 33.2%; Pred. No. 2.6e-17;
Matches 74; Conservative 39; Mismatches 76; Indels 34; Gaps 9;

QY 23 LSNLRQIY-----YNEKAITENKESDDQFLENTLLFGFTGHPWYNDLLVLDLGSKDNTN 78
DB 29 IDNLRNFYTKDFINLKDVXDN-----DTPIANQLQF-----SNESY-DLISESKDFNKS 78

QY 79 KYGKKVDLVGAYGYQCAGGTENKTCACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTV 138
DB 79 NFKGKLDVFGISYNGQC-----NTKYIYGGITA-TNEYLDKPRNIPINIWINGNHKTI 131

QY 139 PIDKVKTSKKEVTVQELDLQARHYLHGKFGLY-----NSDSFGGK-----VORGILVF 186
DB 132 STNKVSTNKKFVTAQAEIDIKLRRYLBQBEYNIYHNGTKGGEYGHKSFKYSGFNIGKVT 191

QY 187 HSSEGSTVSYDLF-DAQQVPTDLLRIYRDNKTINSENHLIDL 228
DB 192 HLNNDTFSYDLPYTGDDGLPKSFLKIYEDNKTVESEKFHLDV 234

RESULT 62
QBVM2_STAAW
ID QBVM2_STAAW PRELIMINARY; PRT; 242 AA.
AC QBVM2;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Staphylococcus enterotoxin Sek.
GN Name=sek2; OrderedlocusNames=MW1938;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359:1819-1827(2002).
DR EMBL; BA000033; BAB95803.1; -; Genomic_DNA.
DR HSSP; P13380; IKTK.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006173; Bcstr1 tox.
DR InterPro; IPR006173; Staph/Strep toxin.
DR InterPro; IPR006123; Staph/Strep toxin.
DR Pfam; PF01123; Staph Strp toxin; OB.
DR Pfam; PF02876; Staph Strp-cox C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 242 AA; 27848 MW; FC377CB4C9BBB4E3 CRC64;

Query Match 25.0%; Score 310; DB 2; Length 242;
Best Local Similarity 33.2%; Pred. No. 2.6e-17;
Matches 74; Conservative 39; Mismatches 76; Indels 34; Gaps 9;

QY 23 LSNLRQIY-----YNEKAITENKESDDQFLENTLLFGFTGHPWYNDLLVLDLGSKDNTN 78
DB 29 IDNLRNFYTKDFINLKDVXDN-----DTPIANQLQF-----SNESY-DLISESKDFNKS 78

QY 79 KYGKKVDLVGAYGYQCAGGTENKTCACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTV 138
DB 79 NFKGKLDVFGISYNGQC-----NTKYIYGGITA-TNEYLDKPRNIPINIWINGNHKTI 131

QY 139 PIDKVKTSKKEVTVQELDLQARHYLHGKFGLY-----NSDSFGGK-----VORGILVF 186
DB 132 STNKVSTNKKFVTAQAEIDIKLRRYLBQBEYNIYHNGTKGGEYGHKSFKYSGFNIGKVT 191

QY 187 HSSEGSTVSYDLF-DAQQVPTDLLRIYRDNKTINSENHLIDL 228
DB 192 HLNNDTFSYDLPYTGDDGLPKSFLKIYEDNKTVESEKFHLDV 234

RESULT 63
QB2F8_STAAU
ID QB2F8_STAAU PRELIMINARY; PRT; 163 AA.
AC QB2F8;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Enterotoxin Q (Fragment).
OS Staphylococcus aureus subsp. aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=46170;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 27664;
RX PubMed=15131181; DOI=10.1128/JCM.42.5.2134-2143.2004;
RA Sergeev N., Volokhov D., Chizhikov V., Rasooly A.;
RT "Simultaneous analysis of multiple staphylococcal enterotoxin genes by
RT an oligonucleotide microarray assay."
RL J. Clin. Microbiol. 42:2134-2143(2004).
DR EMBL; AY518389; AAR99637.1; -; Genomic_DNA.
DR HSSP; P13380; IAN8.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bcstr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR008375; Staph-exotoxin.
DR InterPro; IPR006173; Staph-cox_OB.
DR Pfam; PF01123; Staph Strp toxin; 1.
DR Pfam; PF02876; Staph Strp-cox C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PR01800; STAPHSTREP_TOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT NON_TER 163
SQ SEQUENCE 163 AA; 19011 MW; C4F7B02D47D600F3 CRC64;

Query Match 25.0%; Score 309; DB 2; Length 163;
Best Local Similarity 37.7%; Pred. No. 1.9e-17;
Matches 63; Conservative 27; Mismatches 53; Indels 24; Gaps 4;

QY 78 NKYKGK-----KVDLYGAYGYQCAGGTENKTCACMYGGVTLHDNNRLTEKKVPINLWID 132
DB 4 NEYEAKLKHKVDIFGISYGLC-----NTKYMGGITLANQN-LDKPRNIPINLWVN 56

QY 133 GKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYN-----SDSFGGKQV 180
DB 57 GKQTTISTDKVSTQKKEVTAQAEIDIKLRYLBQBEYNIYHNGTKGGEYGHKSFKYSGFN 116

QY 181 RGLIVHSSEGSTVSYDLFPAQCYQPTDLLRIYRDNKTINSENHLIDL 227
DB 117 KGKITFHLNNEPSFTYDLPYTGQAESEFLKIYEDNKTVESEKFHLD 163

RESULT 64
OS4476_STAAU
ID OS4476_STAAU PRELIMINARY; PRT; 242 AA.
AC OS4476;
DT 01-JUN-1998 (T-EMBLrel. 06, Created)
DT 01-JUN-1998 (T-EMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Staphylococcus enterotoxin K.
GN Name=entk;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
```



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Qy 23 LSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLVLDLGSKDATNKYKG 82
Db 29 IDNLRNFTYTKDFVLDKDVNDNTPIANQLQF-----SNESY-DLISESKDFNKFNSFKG 82
Qy 83 KKVLDLYGAVYGYQCAGGTGPNKTAGYGVTLHDNNRLTEEEKVPINLWIDGKQTTVPIDK 142
Db 83 KKLDFVFGISYNGQC-----NTKYIYGGVTA-TNEYLDKGRNIPINIWINGNKHKTISTNK 135
Qy 143 VKTSKKEVTYQELDLQARHYLHGKFGLY-----NSDSFGGK-----VORGIVFHSSE 190
Db 136 VSTNKKFVTAQEIADVLRKLYQEBYNIYGHNGTKKGEYGHKSKFYSGFNIGKVTFFLNN 195
Qy 191 GSTVSYDLF-DAQQYQPDTLRIYRDKNKTINSENHLIDL 228
Db 196 NDTFSYDLFTGDDGLPKSLKIYEDNKTVESEKFHLDV 234

RESULT 67
Q6GFM8 STAA8
ID Q6GFM8 STAA8 PRELIMINARY; PRT; 239 AA.
AC Q6GFM8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Enterotoxin.
GN OrderedLocusNames=SARI920;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
NUCLEOTIDE SEQUENCE.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Fellwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgensen K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
RA Spratt B.G., Parkhill J.,
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571856; CAG40906.1; -; Genomic.DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; BcTrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR Pfam; PF01123; Staph Strp toxin; 1.
DR Pfam; PF02876; Staph Strp toxin C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 239 AA; 27410 MW; 74ABCTAEAF3FBF CRC64;

Query Match 24.4%; Score 302; DB 2; Length 239;
Best Local Similarity 33.0%; Pred. No. 1.2e-16;
Matches 72; Conservative 40; Mismatches 78; Indels 28; Gaps 7;

Qy 25 NLRQIYYNEKAIT-ENKESDDQFLENTLLFKGFFTGHPWYNDLLVLDLGSKDATNKYKG 82
Db 28 NLRN--YVGSYPIDHQINPDNNRLSHQLVFS-----KDNSTVTAEFKNVEDVKFKFN 79
Qy 83 KKVLDLYGAVYGYQCAGGTGPNKTAGYGVTLHDNNRLTEEEKVPINLWIDGKQTTVPIDK 142
Db 80 RAVDVIYGLSYSGYCL-----KNKYMYGGVTL-AGDYLEKGRGIPINLWVNGLNKLTISTDK 133
Qy 143 VKTSKKEVTYQELDLQARHYLHGKFGLYNSD-----SFGGK-----VORGIVFHSSE 190
Db 134 VSTNKKIVTAQEIITKLRRYLOEBYNIYGFNDTNKGRNYGTGKSFPSGFTGKISFHLND 193
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Qy 191 GSTVSYDLFPAQQYQPDTLRIYRDKNKTINSENHLIDL 228
Db 194 GTSFSYDLFTGTGQAESFLKIYDNKNTVETDKFHLDV 231

RESULT 68
Q5MAA8 STAAU
ID Q5MAA8 STAAU PRELIMINARY; PRT; 250 AA.
AC Q5MAA8;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Enterotoxin B (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
NUCLEOTIDE SEQUENCE.
RC STRAIN=CMCC 26075;
RA Wang L., Zhang S., Yu M.;
RT "Nucleotide sequence of enterotoxin b gene from Staphylococcus
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV856382; AAW21709.1; -; Genomic.DNA.
DR SNR; Q5MAA8; 12-250.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; BcTrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph Strp toxin; 1.
DR Pfam; PF02876; Staph Strp toxin C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 250 AA; 29489 MW; DB64A76A441B952 CRC64;

Query Match 24.3%; Score 300.5; DB 2; Length 250;
Best Local Similarity 33.6%; Pred. No. 1.6e-16;
Matches 82; Conservative 47; Mismatches 96; Indels 19; Gaps 8;

Qy 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 11 AESQDPKPDDELHKSKF-TGLMENMKVLYDDNNHVSAL-NVKSIDQFLYFDLIYSIKDTK 68
Qy 61 HPWYNDLLVLDLGSKDATNKYKGKVDLYGAVYGYQC-----AGGTGPNKTCMYGG 110
Db 69 LGNYDNRVFEKKNLADKDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRTCMYGG 128
Qy 111 VTLDHNNRLTEEEKVPINLWIDGKQTTVPIDKVKTSKKEVTYQELDLQARHYLHGKFGLY 170
Db 129 VTEHNGQLDKYRSITVRVFEDEGK-NLLSFD-VQTNKKKVTAEQELDYLTRHYLVKNKKLY 186
Qy 171 NSDSFGKGVORGIVFHSSEGSTVSYDLFPAQQYQPD--TLLRIYRDKNKTINSENHLIDL 228
Db 187 EFNN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDNKNMVDKSKVIEV 243
Qy 229 YLYT 232
Db 244 YLYT 247

RESULT 69
ETXB STAAU
ID ETXB STAAU STANDARD; PRT; 266 AA.
AC P01552;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Enterotoxin type B precursor (SEB).
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GN Name=entB;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=86168029; PubMed=3957869;
 RA Jones C.L., Khan S.A.;
 RT "Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.";
 RL J. Bacteriol. 166:29-33 (1986).
 RN [2]
 RP NUCLEOTIDE SEQUENCE OF 40-91.
 RX MEDLINE=85298255; PubMed=3898073;
 RA Ranelli D.M., Jones C.L., Johns M.B., Mussey G.J., Khan S.A.;
 RT "Molecular cloning of staphylococcal enterotoxin B gene in Escherichia coli and Staphylococcus aureus.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:5850-5854 (1985).
 RN [3]
 RP PROTEIN SEQUENCE OF 28-266 (S-6).
 RX MEDLINE=71007902; PubMed=5470821;
 RA Huang I.-Y., Bergdoll M.S.;
 RT "The primary structure of staphylococcal enterotoxin B. 3. The cyanogen bromide peptides of reduced and aminoethylated enterotoxin B, and the complete amino acid sequence.";
 RL J. Biol. Chem. 245:3518-3525 (1970).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=93063291; PubMed=1436058; DOI=10.1038/359801a0;
 RA Swaminathan S., Furey W.F. Jr., Fletcher J., Sax M.;
 RT "Crystal structure of staphylococcal enterotoxin B, a superantigen.";
 RL Nature 359:801-806 (1992).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II.
 RX MEDLINE=94203282; PubMed=8152483; DOI=10.1038/368711a0;
 RA Jardezy T.S., Brown J.H., Gorga J.C., Stern L.J., Urban R.G., Chi Y.I., Stauffer C., Strominger J.L., Wiley D.C.;
 RT "Three-dimensional structure of a human class II histocompatibility molecule complexed with superantigen.";
 RL Nature 368:711-718 (1994).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH TCR.
 RX MEDLINE=9906298; PubMed=9881971; DOI=10.1016/S1074-7613(00)80846-9;
 RA Li H., Llera A., Tsuchiya D., Leder L., Ysern X., Schlievert P.M., Karjalainen K., Mariuzza R.A.;
 RT "Three-dimensional structure of the complex between a T cell receptor beta chain and the superantigen staphylococcal enterotoxin B.";
 RL Immunity 9:807-816 (1998).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
 RX MEDLINE=98181012; PubMed=9514739; DOI=10.1006/jmbi.1997.1577;
 RA Papageorgiou A.C., Tranter H.S., Acharya K.R.;
 RT "Crystal structure of microbial superantigen staphylococcal enterotoxin B at 1.5-A resolution: Implications for superantigen recognition by MHC class II molecules and T-cell receptors.";
 RL J. Mol. Biol. 277:61-79 (1998).
 CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication staphylococcal food poisoning syndrome. The illness characterized by high fever, hypotension, diarrhea, shock, and in some cases death.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 CC -----
 CC ENBL; M11118; AAA89550.1; -; Genomic_DNA.
 DR PIR; S27360; ENSAB6.
 DR PDB; 1D5M; X-ray; C=28-266.

DR PDB; 1D5X; X-ray; C=28-266.
 DR PDB; 1D5Z; X-ray; C=28-266.
 DR PDB; 1D6E; X-ray; C=28-266.
 DR PDB; 1GOZ; X-ray; A/B=28-266.
 DR PDB; 1SBB; X-ray; B/D=28-266.
 DR PDB; 1SE3; X-ray; @=28-266.
 DR PDB; 1SE4; X-ray; @=28-266.
 DR PDB; 1SEB; X-ray; D/H=29-262.
 DR PDB; 2SEB; X-ray; D=28-266.
 DR PDB; 3SEB; X-ray; @=28-265.
 DR InterPro; IPR006177; Bcrl toxin.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep tox.
 DR InterPro; IPR006173; Staph tox OB.
 DR Pfam; PF02876; Staph_Strep_toxin_C; 1.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW 3D-structure; Antigen; Direct protein sequencing; Enterotoxin; Signal;
 KW Superantigen; Toxin.
 FT SIGNAL 1 27 Enterotoxin type B.
 FT CHAIN 28 266
 FT DISULFID 120 140 DDN -> NND (in Ref. 3).
 FT CONFLICT 56 58 DQFLYFDLI -> NEFFDLIYL (in Ref. 3).
 FT CONFLICT 69 77 Missing (in Ref. 3).
 FT CONFLICT 118 118 DIN -> NID (in Ref. 3).
 FT CONFLICT 128 130 QTD -> ENT (in Ref. 3).
 FT CONFLICT 133 135 NG -> GN (in Ref. 3).
 FT CONFLICT 149 150 Y -> YY (in Ref. 3).
 FT CONFLICT 156 156 QE -> EQ (in Ref. 3).
 FT CONFLICT 185 186 D -> N (in Ref. 3).
 FT CONFLICT 233 233 DN -> ND (in Ref. 3).
 FT CONFLICT 246 247
 FT STRAND 29 29
 FT HELIX 41 43
 FT STRAND 44 44
 FT TURN 48 48
 FT HELIX 49 52
 FT HELIX 53 55
 FT STRAND 60 66
 FT STRAND 69 69
 FT TURN 73 74
 FT STRAND 75 78
 FT TURN 83 85
 FT STRAND 90 94
 FT HELIX 98 104
 FT TURN 105 106
 FT STRAND 108 113
 FT TURN 116 116
 FT TURN 118 119
 FT TURN 127 128
 FT STRAND 138 142
 FT STRAND 145 147
 FT TURN 149 150
 FT STRAND 152 165
 FT TURN 166 167
 FT STRAND 168 179
 FT STRAND 181 183
 FT HELIX 184 199
 FT TURN 209 218
 FT TURN 219 220
 FT STRAND 221 226
 FT STRAND 232 232
 FT HELIX 237 241
 FT HELIX 242 246
 FT STRAND 249 251
 FT TURN 252 254
 FT STRAND 255 263
 SQ SEQUENCE 266 AA; 31436 MW; B6D417F61CF018B0 CRC64;
 Query Match 24.3%; Score 300.5; DB 1; Length 266;
 Best Local Similarity 33.6%; Pred. No. 1.8e-16;

Matches 82; Conservative 47; Mismatches 96; Indels 19; Gaps 8;	
QY 1	SEKSEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 27	AEQQPDKPELHKSKF-TGLMENMKVLYDDNHVSAT-NVKSIDQFLYFDLIYSIKDTK 84
QY 61	HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTCMYGG 110
Db 85	LGNYDNVRVEPKNKLADKYKVDVFGVANYYYQCYFSKKTNDINSHQTDKRKTCMYGG 144
QY 111	VTLDHNNRLTEEEKVPIINLWDGKQTTVPIDKVKTSKKEVTQVELDQARHYLHGKFGY 170
Db 145	VTEHNGNQLDKYRSITVRVFDGK-NLLSPD-VQTNKKKVTQAQELDYLTRHYLVNKKLY 202
QY 171	NSDSFGGKVGRLIVFHSSEGSTVSYDLFDAQGGYPD--TLRLYRNKNTINSNLHIDL 228
Db 203	EFNN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDNMKVDKVKIEV 259
QY 229	YLYT 232
Db 260	YLT 263
RESULT 70	
Q7BBY8 STAAU PRELIMINARY; PRT; 266 AA.	
AC Q7BBY8	Seb.
DT 10-MAY-2005	(Tremblrel. 30, Created)
DT 10-MAY-2005	(Tremblrel. 30, Last sequence update)
DT 10-MAY-2005	(Tremblrel. 30, Last annotation update)
DE	Staphylococcus aureus
GN	NCBI_TaxID=1280;
OS	Staphylococcus aureus
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus
OX	NCBI_TaxID=1280;
RP	NUCLEOTIDE SEQUENCE
RC	STRAIN=COL;
RX	MSDLNE=21935389; PubMed=11821418; DOI=10.1074/jbc.M111661200;
RA	Yarwood J.M., McCormick J.K., Paustian M.L., Orwin P.M., Kapur V.,
RT	"Characterization and expression analysis of Staphylococcus aureus
RT	pathogenicity island 3. Implications for the evolution of
RT	staphylococcal pathogenicity islands."
RL	J. Biol. Chem. 277.13138-13147(2002).
DR	EMBL; AF410775; AAL04126.1; Genomic DNA.
SQ	SEQUENCE 266 AA; 31436 MW; B6D417F61CF018B0 CRC64;
Query Match 24.3%; Score 300.5; DB 2; Length 266;	
Best Local Similarity 33.6%; Pred. No. 1.8e-16;	
Matches 82; Conservative 47; Mismatches 96; Indels 19; Gaps 8;	
QY 1	SEKSEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 27	AEQQPDKPELHKSKF-TGLMENMKVLYDDNHVSAT-NVKSIDQFLYFDLIYSIKDTK 84
QY 61	HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTCMYGG 110
Db 85	LGNYDNVRVEPKNKLADKYKVDVFGVANYYYQCYFSKKTNDINSHQTDKRKTCMYGG 144
QY 111	VTLDHNNRLTEEEKVPIINLWDGKQTTVPIDKVKTSKKEVTQVELDQARHYLHGKFGY 170
Db 145	VTEHNGNQLDKYRSITVRVFDGK-NLLSPD-VQTNKKKVTQAQELDYLTRHYLVNKKLY 202
QY 171	NSDSFGGKVGRLIVFHSSEGSTVSYDLFDAQGGYPD--TLRLYRNKNTINSNLHIDL 228
Db 203	EFNN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDNMKVDKVKIEV 259
QY 229	YLYT 232
Db 260	YLT 263
RESULT 72	
Q5MAB7 STAAU PRELIMINARY; PRT; 239 AA.	
AC Q5MAB7	Seb.
DT 01-FEB-2005	(Tremblrel. 29, Created)

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DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Enterotoxin B (Fragment).
GN Name=seb;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 14458;
RA Kamboj D.V., Nena V., Singh L.;
RT "Enterotoxin B gene (seb) sequence of Staphylococcus aureus strain
RT ATCC14458.";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY852244; AAM19659.1; -; Genomic_DNA.
DR SMR; Q5MAB7; 1-239.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/strept tox.
DR InterPro; IPR006173; Staph/tox OB.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR Pfam; PF02876; Staph_Strp_tox_C; 1.
DR PRINTS; PR00279; BACTRUTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; UNKNOWN_1.
FT NON TER
SQ SEQUENCE 239 AA; 28368 MW; AD5566B24A2E2750 CRC64;

Query Match 24.2%; Score 299.5; DB 2; Length 239;
Best Local Similarity 33.7%; Pred. No. 1.9e-16;
Matches 82; Conservative 46; Mismatches 96; Indels 19; Gaps 8;

Qy 2 EKSEINEKDLRKSELOALNSLRQIYYNEKAITE-NKESDDOFLNTLLPKGFPTGH 61
Db 1 ESQDDPKDELDHKSKE-TGLMKNKVLDDNHVSAL-NVKSIDQFLYFDIYSIKDTKL 58

Qy 62 PWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQC-----AGTPTNKTCMYGGV 111
Db 59 GNYDNRVFEKPKDLADKYDKYDVDFGANYYYCYFSEKKTINDINSHTDKRCKMYGGV 118

Qy 112 TLHNNRLTEBKVPINLWDGKQTTVPIDKVKTSKEVTVDLQARHYLHGKFGLYN 171
Db 119 TEHNGNQLDKYRSTVRVFEDGK-NLLSFD-VQTNKKKVTAEQLDYLTRHYLVKNKKLYE 176

Qy 172 SDSFGKVGRLIVFHSEGSTVSYDLFDAQGYPD--TLRIYRDNKTINSENHLIDLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWIDMWPAPGDKFDQSKYLLMYNDNMVDSKDVKIEVY 233

Qy 230 LYT 232
Db 234 LTT 236

RESULT 73
Q6YCN4 STAAU
ID Q6YCN4 STAAU PRELIMINARY; PRT; 261 AA.
AC Q6YCN4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Enterotoxin SEU variant.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=382F;
RX MEDLINE=22692404; PubMed=12807452;
RX DOI=10.1046/j.1365-2672.2003.01957.x;
RA Leteurre C., Perelle S., Dillasser F., Fach P.;
RT "Identification of a new putative enterotoxin SEU encoded by the egc

cluster of Staphylococcus aureus.";
J. Appl. Microbiol. 95:38-43(2003).
EMBL; AY158703; AA017732.1; -; Genomic_DNA.
GO; GO:0005576; C:extracellular region; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR006123; Staph/Strep_toxin.
InterPro; IPR006126; Staph/strept tox.
InterPro; IPR006173; Staph/tox OB.
Pfam; PF01123; Staph_Strp_toxin; 1.
Pfam; PF02876; Staph_Strp_tox_C; 1.
PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 261 AA; 30547 MW; A407E960CC5974B0 CRC64;

Query Match 24.1%; Score 298; DB 2; Length 261;
Best Local Similarity 31.5%; Pred. No. 2.8e-16;
Matches 80; Conservative 49; Mismatches 79; Indels 46; Gaps 13;

Qy 3 KSEINEKDLRKSELOALNSLRQIYYNEKAITE-NKESDDOFLNTLLPKGFPTGH 61
Db 25 KPEQLN----KASEF-TGLMDNMR--YLYDDKHVSEINIKAEKFLQHDLLFK----- 70

Qy 62 PWYNDLLVDLGSK-----DATNKYKGVLDLYGAYGYQCAGGTPN-----K 103
Db 71 --INGSKID-GSKILKTEFNNSLSQYKKNKIDLFGTNYYYCYFVSADNMELNDGRLE 127

Qy 104 TACMYGGVTLHNNRLTEKKV--PINLWI---DGKQTTVPIDKVKTSKEVTVDLQ 158
Db 128 KTCMYGGVTEHDGQIDKNNSTONSHILIKVFENRSLSFD-IPNKKNITAEIDYK 186

Qy 159 ARHYLHGKFGLYNSDSFGKVGRLIVFHSEGSTVSYDLFDAQGY--YPTLLRIYRDN 216
Db 187 VRNYLLKHKLYEFNS--SPYETGYIKFIENGSHGFYDMMWPESGEKFFYPTKYLIIYDN 244

Qy 217 KTINSENHLIDLY 230
Db 245 KTVESKINSINVEVHL 258

RESULT 74
Q6GFNO STAAU
ID Q6GFNO STAAU PRELIMINARY; PRT; 261 AA.
AC Q6GFNO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Enterotoxin.
GN OrderedLocustNames=SAR1918;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Murgall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571856; CAG40904.1; -; Genomic_DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/strept tox.
DR InterPro; IPR006173; Staph/tox OB.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
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DR Pfam; PR02876; Staph_Strp_tox_C; 1.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 261 AA; 30547 MW; A407E960CC5974B0 CRC64;

Query Match      24.1%; Score 298; DB 2; Length 261;
Best Local Similarity 31.5%; Pred. No. 2.8e-16;
Matches 80; Conservative 49; Mismatches 79; Indels 46; Gaps 13;

OY 3 KSEINEKDLRKSELQNALNLRLQIYYNYNEKAITE-NKESDDQFLENTLLFKGFFTG 61
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 25 KPEQLN-----KASEF-TGLMDNMR--YLDDKHVSEINIKAEKFLQHLLEFK----- 70
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 62 PTYNDLLVLDGSK-----DATNKYKGKVDLYGAYYGYQCAGGTPN-----K 103
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 71 --INGSKID-GSKILKTEFNNSLSDKYKNKIDLFGTNYNYQCYFSADNMELNDGRLE 127
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 104 TACMYGGVTLHDNNRLTEKKV--PINLMI---DGKQTTVPIDKVKTSKKEVTVQELDLQ 158
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 128 KTCMYGGVTEHGDGNQIDKNNSDTONSHNLIKVFENERNLSFD-IPTNKKNITAEIDYK 186
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RESULT 75
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DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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RA Voyich J.M., Deleo F.R., Martin J.M., Somerville G.A., Musser J.M.;
RT "Progress toward characterization of the group A Streptococcus
RT metagenome: complete genome sequence of a macrolide-resistant serotype
RT M6 strain."
RL J. Infect. Dis. 190:727-738 (2004).
DR EMBL; CP000003; AAT86876.1; -; Genomic_DNA.
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DR GO; GO:0009405; P:pathogenesis; IEA.
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GenCore version 5.1.7
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(without alignments)
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Title: US-09-900-766-7

Perfect score:

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

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Post-processing: Minimum Match 0%

Maximum Match 100

Listing first 300 summaries

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3: /cgn2_6/ptodata/1/iaa/H_COMB.per:*

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6: /cgn2_6/ptodata/1/1aa/backilles1.pcp:"

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query %		Length	DB	ID	Description
		Match	Rel				
SUMMARIES							
1	1238	100.0	233	2	US-08-695-692B-8		Sequence 8, Appli
2	1238	100.0	257	2	US-08-486-099-112		Sequence 112, App
3	1238	100.0	257	2	US-08-360-107A-122		Sequence 122, App
4	1238	100.0	257	2	US-08-484-223B-112		Sequence 112, App
5	1238	100.0	257	2	US-08-919-597-112		Sequence 112, App
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8	1238	100.0	257	2	US-08-471-913A-112		Sequence 112, App
9	1238	100.0	257	2	US-08-485-264A-112		Sequence 112, App
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11	1238	100.0	257	2	US-08-470-896-112		Sequence 112, App
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13	1238	100.0	257	2	US-08-487-266A-112		Sequence 112, App
14	1238	100.0	257	2	US-08-484-741-112		Sequence 112, App
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170	93.5	7.6	631	2	US-08-637-654-111	Sequence 111, App	243	81.5	6.6	616	2	US-09-396-149-7	Sequence 7, Appl
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172	93	7.5	16	2	US-08-695-692B-20	Sequence 20, Appl	245	81	6.5	14	2	US-08-896-933-1	Sequence 1, Appl
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; ZIP: 10036-2711
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US/08/486,099
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-031
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-486-099-112

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Best Local Similarity 100.0%; Pred. No. 2e-118;
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RESULT 3
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; Sequence 122, Application US/08360107A
; Patent No. 6017536
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; NUMBER OF SEQUENCES: 149
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:

; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 20-DEC-1994
; APPLICATION NUMBER: US/08/360,107A
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-013
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 122:
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Best Local Similarity 100.0%; Pred. No. 2e-118;
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Db 25 SEKSEINEKDLRKSELRNALSRLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84

QY 61 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYYGQCAGGTPNKTCMYGGVTLHDNRLLT 120
Db 85 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYYGQCAGGTPNKTCMYGGVTLHDNRLLT 144

QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204

QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDNKNTINSENHLDLYTT 233
Db 205 RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDNKNTINSENHLDLYTT 257

RESULT 4
US-08-484-223B-112
; Sequence 112, Application US/08484223B
; Patent No. 6020459
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; NUMBER OF SEQUENCES: 245
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/484,223B
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7872-029
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 112:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 257 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ US-08-484-223B-112

Query Match 100.0%; Score 1238; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 2e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOARNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOARNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84

QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 121 EEKVPINLWIDGKQTTPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 145 EEKVPINLWIDGKQTTPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204

QY 181 RGLIVFHSSEGSTVSYDLFDAQOQYPTTLRIYRDNKTINSENHLDLYLYTT 233
DB 205 RGLIVFHSSEGSTVSYDLFDAQOQYPTTLRIYRDNKTINSENHLDLYLYTT 257

RESULT 5

US-08-919-597-112
/ Sequence 112, Application US/08919597
/ Patent No. 6054265
/ GENERAL INFORMATION:
/ APPLICANT: Bolognesi, Dani P.
/ APPLICANT: Matthews, Thomas J.
/ APPLICANT: Wild, Carl T.
/ APPLICANT: Barney, Shawn O.
/ APPLICANT: Lambert, Dennis M.
/ APPLICANT: Petteway, Stephen R.
/ APPLICANT: Langlois, Alphonse J.
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
/ TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
/ TITLE OF INVENTION: TRANSMISSION
/ NUMBER OF SEQUENCES: 273
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/919,597

/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/470,896
/ FILING DATE: 06-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7872-020
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 112:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 257 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ US-08-919-597-112

Query Match 100.0%; Score 1238; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 2e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOARNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOARNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84

QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 121 EEKVPINLWIDGKQTTPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 145 EEKVPINLWIDGKQTTPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204

QY 181 RGLIVFHSSEGSTVSYDLFDAQOQYPTTLRIYRDNKTINSENHLDLYLYTT 233
DB 205 RGLIVFHSSEGSTVSYDLFDAQOQYPTTLRIYRDNKTINSENHLDLYLYTT 257

RESULT 6

US-08-475-668A-112
/ Sequence 112, Application US/08475668A
/ Patent No. 6060065
/ GENERAL INFORMATION:
/ APPLICANT: Barney, Shawn O.
/ APPLICANT: Lambert, Dennis M.
/ APPLICANT: Petteway, Stephen R.
/ TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
/ TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
/ TITLE OF INVENTION: TRANSMISSION
/ NUMBER OF SEQUENCES: 211
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds LLP
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/475,668A
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.

```
;
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-475-668A-112

Query Match 100.0%; Score 1238; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 2e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 144
QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKNTINSENHLHDLYTT 233
DB 205 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKNTINSENHLHDLYTT 257

RESULT 7
US-08-485-551A-112
; Sequence 112, Application US/08485551A
; Patent No. 6068973
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; NUMBER OF SEQUENCES: 211
; TITLE OF INVENTION: TRANSMISSION
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,551A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-023
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
;

;
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-485-551A-112

Query Match 100.0%; Score 1238; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 2e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 144
QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKNTINSENHLHDLYTT 233
DB 205 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKNTINSENHLHDLYTT 257

RESULT 8
US-08-471-913A-112
; Sequence 112, Application US/08471913A
; Patent No. 6093794
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSSTEIN-BARR VIRUS
; NUMBER OF SEQUENCES: 214
; TITLE OF INVENTION: TRANSMISSION
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,913A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-030
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
;

;
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-485-551A-112
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; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-471-913A-112

Query Match      100.0%; Score 1238; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 2e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYVYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKSSELQNALSNLRQIYYVYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 EEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDKNKTINSENHLDLYLYTT 233
DB 205 RGLIVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDKNKTINSENHLDLYLYTT 257

RESULT 9
US-08-485-264A-112
; Sequence 112, Application US/08485264A
; Patent No. 6228983
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,264A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-021
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-471-913A-112

Query Match      100.0%; Score 1238; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 2e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYVYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKSSELQNALSNLRQIYYVYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 EEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDKNKTINSENHLDLYLYTT 233
DB 205 RGLIVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDKNKTINSENHLDLYLYTT 257

RESULT 10
US-08-474-349A-112
; Sequence 112, Application US/08474349A
; Patent No. 6333395
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
; NUMBER OF SEQUENCES: 517
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-024
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
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; MOLECULE TYPE: protein
US-08-474-349A-112

Query Match      100.0%; Score 1238; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 2e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSEKSELQNALSNLRQIYYNYNEKAITENKESDDQFLENTLLFKGFFTG 60
   |||||
Db 25 SEKSEINEKDLRKSEKSELQNALSNLRQIYYNYNEKAITENKESDDQFLENTLLFKGFFTG 84
   |||||

QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
   |||||
Db 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
   |||||

QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
   |||||
Db 145 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
   |||||

QY 181 RGLIVFHSSEGSTSVSYDLFDAQGYPDPTLLRIYRDKNKTINSENHLHIDLTYTT 233
   |||||
Db 205 RGLIVFHSSEGSTSVSYDLFDAQGYPDPTLLRIYRDKNKTINSENHLHIDLTYTT 257
   |||||

RESULT 11
US-08-470-896-112
; Sequence 112, Application US/08470896
; Patent No. 6479055
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonsse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,896
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELEPHONE: (212) 990-9090
; TELEFAX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-470-896-112

Query Match      100.0%; Score 1238; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 2e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSEKSELQNALSNLRQIYYNYNEKAITENKESDDQFLENTLLFKGFFTG 60
   |||||
Db 25 SEKSEINEKDLRKSEKSELQNALSNLRQIYYNYNEKAITENKESDDQFLENTLLFKGFFTG 84
   |||||

QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
   |||||
Db 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
   |||||

QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
   |||||
Db 145 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
   |||||

QY 181 RGLIVFHSSEGSTSVSYDLFDAQGYPDPTLLRIYRDKNKTINSENHLHIDLTYTT 233
   |||||
Db 205 RGLIVFHSSEGSTSVSYDLFDAQGYPDPTLLRIYRDKNKTINSENHLHIDLTYTT 257
   |||||

RESULT 12
US-08-485-546A-112
; Sequence 112, Application US/08485546A
; Patent No. 6518013
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonsse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,546A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-028
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELETYPE: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-485-546A-112

Query Match      100.0%; Score 1238; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 2e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 SEKSEINEKDLRKSELOARNLSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOARNLSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDNTNKGKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVDLGSKDNTNKGKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
DB 85 HPWYNDLLVDLGSKDNTNKGKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 204
QY 181 RGLIVFHSSEGSTSVSYDLFDAQOQYPTLLRIYRDKNKTINSENHLDLYLYTT 233
DB 205 RGLIVFHSSEGSTSVSYDLFDAQOQYPTLLRIYRDKNKTINSENHLDLYLYTT 257
RESULT 13
US-08-487-266A-112
; Sequence 112, Application US/08487266A
; Patent No. 6824783
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,266A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: protein
; MOLECULE TYPE: protein
US-08-487-266A-112
Query Match 100.0%; Score 1238; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 2e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOARNLSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOARNLSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84

QY 61 HPWYNDLLVDLGSKDNTNKGKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVDLGSKDNTNKGKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 204
QY 181 RGLIVFHSSEGSTSVSYDLFDAQOQYPTLLRIYRDKNKTINSENHLDLYLYTT 233
DB 205 RGLIVFHSSEGSTSVSYDLFDAQOQYPTLLRIYRDKNKTINSENHLDLYLYTT 257
RESULT 14
US-08-484-741-112
; Sequence 112, Application US/08484741
; Patent No. 6951717
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,741
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS: <unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-08-484-741-112
Query Match 100.0%; Score 1238; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 2e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOARNLSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOARNLSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDNTNKGKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120

Db 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKATCMYGGVTLHDNNRLT 144
QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPDTLRLRIYRDNKTINSENHLHDLYLYTT 233
Db 205 RGLIVFHSSEGSTVSVDLFDAGQGYPDTLRLRIYRDNKTINSENHLHDLYLYTT 257
RESULT 15
US-09-350-841A-1598
; Sequence 1598, Application US/09350841A
; Patent No. 6750008
; GENERAL INFORMATION:
; APPLICANT: Jeffs, Peter;
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
; FILE REFERENCE: 7872-066-999
; CURRENT APPLICATION NUMBER: US/09/350,841A
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 1946
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1598
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-350-841A-1598

Query Match 97.1%; Score 1202; DB 2; Length 254;
Best Local Similarity 98.3%; Pred. No. 9.6e-115;
Matches 230; Conservative 0; Mismatches 2; Indels 2; Gaps 2;
QY 1 SEKSEINEKDLRKXSELQARNLSNLRLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 22 SEKSEINEKDLRKXSELQARNLSNLRLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 81
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKATCMYGGVTLHDNNRLT 120
Db 82 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKATCMYGGVTLHDNNRLT 141
QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 142 EEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 200
QY 181 RGLIVFHSSEG-STVSVDLFDAGQGYPDTLRLRIYRDNKTINSENHLHDLYLYTT 233
Db 201 RGLIVFHSSEGSTVSVDLFDAGQGYPDTLRLRIYRDNKTINSENHLHDLYLYTT 254

RESULT 16
US-08-896-933-24
; Sequence 24, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-24

Query Match 94.6%; Score 1171; DB 2; Length 226;
Best Local Similarity 95.7%; Pred. No. 1.2e-111;
Matches 220; Conservative 4; Mismatches 2; Indels 4; Gaps 1;
QY 4 SEINEKDLRKXSELQARNLSNLRLQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPW 63
Db 1 SEINEKDLRKXSELQARNLSNLRLQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPW 60
QY 64 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKATCMYGGVTLHDNNRLTEEK 123
Db 61 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKATCMYGGVTLHDNNRLTEE - 119
QY 124 KVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 183
Db 120 ---VBKWIWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 176
QY 184 IVFHSSEGSTVSVDLFDAGQGYPDTLRLRIYRDNKTINSENHLHDLYLYTT 233
Db 177 IVFHSSEGSTVSVDLFDAGQGYPDTLRLRIYRDNKTINSENHLHDLYLYTT 226
RESULT 17
US-09-314-235-24
; Sequence 24, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-314-235-24

Query Match 94.6%; Score 1171; DB 2; Length 226;
Best Local Similarity 95.7%; Pred. No. 1.2e-111;
Matches 220; Conservative 4; Mismatches 2; Indels 4; Gaps 1;
QY 4 SEINEKDLRKXSELQARNLSNLRLQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPW 63
Db 1 SEINEKDLRKXSELQARNLSNLRLQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPW 60
QY 64 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKATCMYGGVTLHDNNRLTEEK 123
Db 61 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKATCMYGGVTLHDNNRLTEE - 119
QY 124 KVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 183
Db 120 ---VBKWIWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 176
QY 184 IVFHSSEGSTVSVDLFDAGQGYPDTLRLRIYRDNKTINSENHLHDLYLYTT 233
Db 177 IVFHSSEGSTVSVDLFDAGQGYPDTLRLRIYRDNKTINSENHLHDLYLYTT 226


```
RESULT 18
US-09-708-008B-24
; Sequence 24, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09708, 008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896, 933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252, 978
; PRIOR FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-708-008B-24

Query Match          94.6%; Score 1171; DB 2; Length 226;
Best Local Similarity 95.7%; Pred. No. 1.2e-111;
Matches 220; Conservative 4; Mismatches 2; Indels 4; Gaps 1;

QY 4 SEINEKDLRKSELOARNLSNRQIYYNEKAITENKESDDOFLNTLLFKGFFTGHPW 63
Db 1 SEINEKDLRKSELOARNLSNRQIYYNEKAITENKESDDOFLNTLLFKGFFTGHPW 60
QY 64 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKATACMYGGVTLHDNNRLT 123
Db 61 YNDLLVDKSGDATNKYKGGKVDLYGAYGYQCAGGTPNKATACMYGGVTLHDNNRLT 119
QY 124 KVPINLWIDGKQTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQGL 193
Db 120 ---VBKWIDGKQTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQGL 176
QY 184 IVFHSSEGSTSVSYDLFDAQOQYPTLLRIYRDKNKTINSENHLDLYTT 233
Db 177 IVFHSSEGSTSVSYDLFDAQOQYPTLLRIYRDKNKTINSENHLDLYTT 226

RESULT 19
US-08-695-692B-7
; Sequence 7, Application US/08695692B
; Patent No. 6514498
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
; APPLICANT: Johan Hansson, Terje Kalland, Lars
; APPLICANT: Abrahamson and Goran Forsberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
; TITLE OF INVENTION: AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,692B
; FILING DATE: August 12, 1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9601245-5

; FILING DATE: March 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Krieger, Paul E.
; REGISTRATION NUMBER: 25,886
; REFERENCE/DOCKET NUMBER: 41986/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-695-692B-7

Query Match          82.6%; Score 1023; DB 2; Length 233;
Best Local Similarity 82.0%; Pred. No. 1.8e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOARNLSNRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
Db 1 SEKSEINEKDLRKSELOARNLSNRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKATACMYGGVTLHDNNRLT 120
Db 61 HSWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKATACMYGGVTLHDNNRLT 120
QY 121 EEKQVPINLWIDGKQTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQ 180
Db 121 EEKQVPINLWIDGKQTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQ 180
QY 181 RGLIVFHSSEGSTSVSYDLFDAQOQYPTLLRIYRDKNKTINSENHLDLYTT 233
Db 181 RGLIVFHSSEGSTSVSYDLFDAQOQYPTLLRIYRDKNKTINSENHLDLYTT 233

RESULT 20
US-08-486-099-113
; Sequence 113, Application US/08486099
; Patent No. 6013263
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Pettaway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
; TITLE OF INVENTION: B VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,099
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-031
```

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-486-099-113

Query Match      82.6%; Score 1023; DB 2; Length 257;
Best Local Similarity 82.0%; Pred. No. 2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELORNALSNLRIQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAKTENKESHDFLOHTTLFKGFFTD 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFPSKDIDVKYKGGKVDLYGAYYGQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVTTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKQV 180
DB 145 EEKVPINLWIDGKQTTVPLETVTNKNVTVQELDLQARRYLQEKYLNLYNSDVPDGKQV 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLHIDLTYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFAGAQYNTLLRIYRDNKTINSENMHIDIYLYTS 257

RESULT 21
US-08-360-107A-123
; Sequence 123, Application US/08360107A
; Patent No. 6017536
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 149
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,107A
; FILING DATE: 20-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-360-107A-123

Query Match      82.6%; Score 1023; DB 2; Length 257;
Best Local Similarity 82.0%; Pred. No. 2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELORNALSNLRIQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAKTENKESHDFLOHTTLFKGFFTD 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFPSKDIDVKYKGGKVDLYGAYYGQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVTTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKQV 180
DB 145 EEKVPINLWIDGKQTTVPLETVTNKNVTVQELDLQARRYLQEKYLNLYNSDVPDGKQV 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLHIDLTYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFAGAQYNTLLRIYRDNKTINSENMHIDIYLYTS 257

RESULT 22
US-08-484-223B-113
; Sequence 113, Application US/08484223B
; Patent No. 6020459
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 245
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
```

; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-484-223B-113

Query Match 82.6%; Score 1023; DB 2; Length 257;
Best Local Similarity 82.0%; Pred. No. 2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKSELOKRNALSNLRQIYYVNEKAITENKESDDOPLNTLLPKGFTG 60
Db 25 SEKSEINEKDLRKSELOKRNALSNLRQIYYVNEKAITENKESDDOPLNTLLPKGFTD 84
Qy 61 HPWYNLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNLLVDFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVQ 180
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVQ 204
Qy 181 RGLIVHSSSEGSTVSYDLFDAQOQYPTLLRIYRDKNKTINSENHLIDLILYTT 233
Db 205 RGLIVHSTSTEPSVNYDLFDAQOQYNTLLRIYRDKNKTINSENHIDIYLYTS 257

RESULT 23

US-08-919-597-113
; Sequence 113, Application US/08919597
; Patent No. 6054265
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/919,597
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,896
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-919-597-113

Query Match 82.6%; Score 1023; DB 2; Length 257;
Best Local Similarity 82.0%; Pred. No. 2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKSELOKRNALSNLRQIYYVNEKAITENKESDDOPLNTLLPKGFTG 60
Db 25 SEKSEINEKDLRKSELOKRNALSNLRQIYYVNEKAITENKESDDOPLNTLLPKGFTD 84
Qy 61 HPWYNLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNLLVDFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVQ 180
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVQ 204
Qy 181 RGLIVHSSSEGSTVSYDLFDAQOQYPTLLRIYRDKNKTINSENHLIDLILYTT 233
Db 205 RGLIVHSTSTEPSVNYDLFDAQOQYNTLLRIYRDKNKTINSENHIDIYLYTS 257

RESULT 24

US-08-475-668A-113
; Sequence 113, Application US/08475668A
; Patent No. 6060065
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,668A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-475-668A-113

Db 25 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAKTENKESHDPQLQHTILFKGFFTD 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 204
QY 181 RGLIVHSSSEGSTSVSYDLFDAQOQYPTTLRIYRDKNKTINSENHLDLYLTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQOQYSNTLLRIYRDKNKTINSENHLDLYLTS 257

RESULT 27

US-08-485-264A-113
; Sequence 113, Application US/08485264A
; Patent No. 6228983
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,264A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-021
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-485-264A-113

Query Match 82.6%; Score 1023; DB 2; Length 257;
Best Local Similarity 82.0%; Pred. No. 2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAKTENKESHDPQLQHTILFKGFFTD 60
Db 25 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAKTENKESHDPQLQHTILFKGFFTD 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120

Db 85 HSWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 204
QY 181 RGLIVHSSSEGSTSVSYDLFDAQOQYPTTLRIYRDKNKTINSENHLDLYLTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQOQYSNTLLRIYRDKNKTINSENHLDLYLTS 257

RESULT 28

US-08-474-349A-113
; Sequence 113, Application US/08474349A
; Patent No. 6333395
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
; TITLE OF INVENTION: VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 517
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-024
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-474-349A-113

Query Match 82.6%; Score 1023; DB 2; Length 257;
Best Local Similarity 82.0%; Pred. No. 2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAKTENKESHDPQLQHTILFKGFFTD 60
Db 25 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAKTENKESHDPQLQHTILFKGFFTD 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDFGKQV 180
DB 145 EEKKVPINLWLDGKQNTVPLETVKTKNKNVTVOELDLQARRYLOEKYKLYNSDVFQKQV 204
QY 181 RGLIVPHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLHIDLTYTT 233
DB 205 RGLIVPHTSTEPSVNYDLFGAQGYNSNTLLRIYRDNKTINSENMHIDIYLYTS 257

RESULT 29
US-08-470-896-113
; Sequence 113, Application US/08470896
; Patent No. 6479055
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,896
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-470-896-113

Query Match 82.6%; Score 1023; DB 2; Length 257;
Best Local Similarity 82.0%; Pred. No. 2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKXSELQGTALGNLKQIYYNEKAKTENKESHQFLOHTLLFKGFFTD 84
QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDDNRLT 120
DB 85 HSWYNLLVDFPSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDDNRLT 144
QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDFGKQV 180
DB 145 EEKKVPINLWLDGKQNTVPLETVKTKNKNVTVOELDLQARRYLOEKYKLYNSDVFQKQV 204

QY 181 RGLIVPHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLHIDLTYTT 233
DB 205 RGLIVPHTSTEPSVNYDLFGAQGYNSNTLLRIYRDNKTINSENMHIDIYLYTS 257
RESULT 30
US-08-485-546A-113
; Sequence 113, Application US/08485546A
; Patent No. 6518013
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,546A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-028
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-485-546A-113
Query Match 82.6%; Score 1023; DB 2; Length 257;
Best Local Similarity 82.0%; Pred. No. 2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKXSELQGTALGNLKQIYYNEKAKTENKESHQFLOHTLLFKGFFTD 84
QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDDNRLT 120
DB 85 HSWYNLLVDFPSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDDNRLT 144
QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDFGKQV 180
DB 145 EEKKVPINLWLDGKQNTVPLETVKTKNKNVTVOELDLQARRYLOEKYKLYNSDVFQKQV 204
QY 181 RGLIVPHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLHIDLTYTT 233

Db 205 RGLIVFHTSTEPSVNYDLFGAQOQYNTLLRIYRDNKTNSNMHIDIYLYTS 257

RESULT 31

US-08-487-266A-113
; Sequence 113, Application US/08487266A
; Patent No. 6824783
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/487,266A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-487-266A-113

Query Match 82.6%; Score 1023; DB 2; Length 257;
Best Local Similarity 82.0%; Pred. No. 2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTD 84
QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACWYGGVTLHDNNRLT 120
Db 85 HSWYNLLVDFDSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKTACWYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 204
QY 181 RGLIVHSSSGSTVSYDLFDAQOQYPTLLRIYRDNKTNSNMHIDIYLYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQOQYNTLLRIYRDNKTNSNMHIDIYLYTS 257

RESULT 32

US-08-446-918A-4
; Sequence 4, Application US/08446918A

US-08-484-741-113
; Sequence 113, Application US/08484741
; Patent No. 6951717
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/484,741
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-08-484-741-113

Query Match 82.6%; Score 1023; DB 2; Length 257;
Best Local Similarity 82.0%; Pred. No. 2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTD 84
QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACWYGGVTLHDNNRLT 120
Db 85 HSWYNLLVDFDSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKTACWYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 204
QY 181 RGLIVHSSSGSTVSYDLFDAQOQYPTLLRIYRDNKTNSNMHIDIYLYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQOQYNTLLRIYRDNKTNSNMHIDIYLYTS 257

RESULT 33

US-08-446-918A-4
; Sequence 4, Application US/08446918A

```
; Patent No. 5705151
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmelle, Robyn E.
; TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,918A
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 552
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2879-29
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-446-918A-4

Query Match      82.3%; Score 1019; DB 1; Length 233;
Best Local Similarity 81.9%; Pred. No. 4.5e-96;
Matches 190; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY      2 EKSEINEKDLRKKSLOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 61
Db      2 EKSEINEKDLRKKSLOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 61

QY      62 PWYNDLLVGLSGKATNKYKGVLDYGYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
Db      62 SWYNDLLVDFDSKIDVYKGVLDYGYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121

QY      122 EKKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVOR 181
Db      122 EKKVPINLWDGKQNTVPLETKNKQNTVVOELDLQARHYLHGKFGLYNSDSFGGKVOR 181

QY      182 GLIVFHSSSGSTSYDLFDAQGYPTLLRIYRDNKNTINSENHLDLYLYTT 233
Db      182 GLIVFHTSTPSVNYDLFCAQGYNTLLRIYRDNKNTINSENHLDLYLYTS 233

RESULT 34
US-08-580-806-4
; Sequence 4, Application US/08580806
; Patent No. 5935568
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmelle, Robyn E.
; APPLICANT: Potter, Terence A.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado

; Patent No. 5705151
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmelle, Robyn E.
; TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,918A
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 552
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-29-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-580-806-4

Query Match      82.3%; Score 1019; DB 1; Length 233;
Best Local Similarity 81.9%; Pred. No. 4.5e-96;
Matches 190; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY      2 EKSEINEKDLRKKSLOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 61
Db      2 EKSEINEKDLRKKSLOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 61

QY      62 PWYNDLLVGLSGKATNKYKGVLDYGYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
Db      62 SWYNDLLVDFDSKIDVYKGVLDYGYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121

QY      122 EKKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVOR 181
Db      122 EKKVPINLWDGKQNTVPLETKNKQNTVVOELDLQARHYLHGKFGLYNSDSFGGKVOR 181

QY      182 GLIVFHSSSGSTSYDLFDAQGYPTLLRIYRDNKNTINSENHLDLYLYTT 233
Db      182 GLIVFHTSTPSVNYDLFCAQGYNTLLRIYRDNKNTINSENHLDLYLYTS 233

RESULT 35
US-08-896-933-23
; Sequence 23, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-08-896-933-23

Query Match      81.1%; Score 1003.5; DB 2; Length 232;
Best Local Similarity 81.5%; Pred. No. 1.7e-94;
Matches 190; Conservative 16; Mismatches 26; Indels 1; Gaps 1;

QY      1 SEKSEINEKDLRKKSLOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
```



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Db 1 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAKTENKESHQDPL-HTILFKGFFTD 59
QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 60 HSWYNLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 119
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVK 180
Db 120 EEKVPINLWLDGKQNTVPLETKNKNVTQELDPQARRYLQEKYNLYNSDVFQKVK 179
QY 181 RGLIVHSSSGSTVSYDLFPAQOQYPTLLRIYRDKNKTINSENLHLDLYTT 233
Db 180 RGLIVFHTSTEPSVNYDLFGAQOQYSNTLLRIYRDKNKTINSENLHLDLYTS 232
```

RESULT 36

US-09-314-235-23

; Sequence 23, Application US/09314235

; Patent No. 6338845

; GENERAL INFORMATION:

; APPLICANT: Terman, David S.

; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,

; FILE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS

; FILE REFERENCE: 09629/005004

; CURRENT APPLICATION NUMBER: US/09/314,235

; CURRENT FILING DATE: 1999-05-18

; EARLIER APPLICATION NUMBER: 08/896,933

; EARLIER FILING DATE: 1997-07-18

; EARLIER APPLICATION NUMBER: 08/252,978

; EARLIER FILING DATE: 1994-06-02

; EARLIER APPLICATION NUMBER: 07/891,718

; EARLIER FILING DATE: 1992-06-01

; EARLIER APPLICATION NUMBER: US91/00342

; EARLIER FILING DATE: 1991-01-17

; EARLIER APPLICATION NUMBER: 07/466,577

; EARLIER FILING DATE: 1990-01-17

; EARLIER APPLICATION NUMBER: 07/416,530

; EARLIER FILING DATE: 1989-10-03

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 23

; LENGTH: 232

; TYPE: PRT

; ORGANISM: Staphylococcus aureus

US-09-314-235-23

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Query Match 81.1%; Score 1003.5; DB 2; Length 232;
Best Local Similarity 81.5%; Pred. No. 1.7e-94;
Matches 190; Conservative 16; Mismatches 26; Indels 1; Gaps 1;

QY 1 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAKTENKESHQDPL-HTILFKGFFTG 60
Db 1 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAKTENKESHQDPL-HTILFKGFFTD 59
QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 60 HSWYNLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 119
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVK 180
Db 120 EEKVPINLWLDGKQNTVPLETKNKNVTQELDPQARRYLQEKYNLYNSDVFQKVK 179
QY 181 RGLIVHSSSGSTVSYDLFPAQOQYPTLLRIYRDKNKTINSENLHLDLYTT 233
Db 180 RGLIVFHTSTEPSVNYDLFGAQOQYSNTLLRIYRDKNKTINSENLHLDLYTS 232
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RESULT 37

US-09-708-008B-23

; Sequence 23, Application US/09708008B

; Patent No. 6692746

; GENERAL INFORMATION:

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; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978
; PRIOR FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-708-008B-23
```

```
Query Match 81.1%; Score 1003.5; DB 2; Length 232;
Best Local Similarity 81.5%; Pred. No. 1.7e-94;
Matches 190; Conservative 16; Mismatches 26; Indels 1; Gaps 1;

QY 1 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAKTENKESHQDPL-HTILFKGFFTG 60
Db 1 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAKTENKESHQDPL-HTILFKGFFTD 59
QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 60 HSWYNLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 119
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVK 180
Db 120 EEKVPINLWLDGKQNTVPLETKNKNVTQELDPQARRYLQEKYNLYNSDVFQKVK 179
QY 181 RGLIVHSSSGSTVSYDLFPAQOQYPTLLRIYRDKNKTINSENLHLDLYTT 233
Db 180 RGLIVFHTSTEPSVNYDLFGAQOQYSNTLLRIYRDKNKTINSENLHLDLYTS 232
```

RESULT 38

US-09-144-776B-2

; Sequence 2, Application US/09144776B

; Patent No. 6399332

; GENERAL INFORMATION:

; APPLICANT: Robert G. Ulrich,

; Mark A. Olson

; Sina Bavari

; TITLE OF INVENTION: Bacterial Superantigen

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Charles H. Harris

; STREET: US Army MRC -504 Scott Street

; MCMR-JA (Charles H. Harris-Patent

; Atty)

; CITY: FORT DETRICK

; STATE: MARYLAND

; COUNTRY: USA

; ZIP: 21702-5012

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Macintosh 7.5

; SOFTWARE: Microsoft Word 6.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/144,776B

; FILING DATE: 01-Sep-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/882,431

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Charles H. Harris

```

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431B-2

Query Match      80.8%; Score 1000; DB 2; Length 257;
Best Local Similarity 80.7%; Pred. No. 4.6e-94;
Matches 188; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY  1 SEKSEBINEKDLRKSELQARNALSNIQRQIYYVNEKAITENKESDDQFLENTLLFKGFFTG 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  25 SEKSEBINEKDLRKSELQCTALGNLQIYYVNEKAKTENKESHQFRQHTILFKGFFTD 84
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY  61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTGPNKTACMYGGVTLLHDNNRLT 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  85 HSWYNPLLRFDSQKTDVDRYKGGKVDLYGAYGYQCAGGTGPNKTACMYGGVTLLHDNNRLT 144
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY  121 EEKVPINLWIDGKQTVPIDKVKTSKEVTVOELDQARHYLHGKFLYNSDSFGKQV 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  145 EEKVPINLWIDGKQNTVPLETVKTNKNVTVOELDQARRYLOEKYKLYNSDVFGKQV 204
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY  181 RGLIVSHSGEGSTVSYDLFDAQGYPTDLLRIYRDNKNTINSENLDLYLT 233
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db  205 RGLIVFHTSTPSVNYDLFGAQGYNTLLRIYRDNKNTINSENMDIVLYTS 257
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 40
US-09-144-776B-4
; Sequence 4, Application US/09144776B
; Patent No. 639332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
;           Mark A. Olson
;           Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
;                   Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MPMC -504 Scott Street
;          MCMR-JA (Charles H. Harris-Patent
;          Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233
; TYPE: Amino Acid

```

```
/ STRANDEDNESS: Unknown
/ TOPOLOGY: Peptide
/ MOLECULE TYPE: Peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-144-776B-4

Query Match      80.5%; Score 996; DB 2; Length 233;
Best Local Similarity 80.6%; Pred. No. 1e-93;
Matches 187; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKSELQNALSNLRQIYYNNEKAITENKESDDQFLENTLLFKGPFTH 61
DB 2 EKSEINEKDLRKSELQNALSNLRQIYYNNEKAITENKESDDQFLENTLLFKGPFTH 61
QY 62 PWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLTE 121
DB 62 SWYNDLLVDFDSKDIYDKYKGGKVDLYGAYAGYQCAGGTPNKTCACMYGGVTLHDNNRLTE 121
QY 122 EKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQVOR 181
DB 122 EKKVPINLWDGKQNTVPLETVTKTKKNTVQELDLQARRYLOEKYLNLYNSDVFQKQVOR 181
QY 182 GLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHLDLYLTT 233
DB 182 GLIVFHTSTEPSVNYDLFGAGQGYSNLLRIYRDNKTINSENHLDIYLTS 233

RESULT 41
US-08-882-431B-4
/ Sequence 4, Application US/08882431B
/ Patent No. 6713284
/ GENERAL INFORMATION:
/ APPLICANT: Robert G. Ulrich,
/ APPLICANT: Mark A. Olson
/ APPLICANT: Sina Bavari
/ TITLE OF INVENTION: Bacterial Superantigen
/ TITLE OF INVENTION: Vaccines
/ NUMBER OF SEQUENCES: 25
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Charles H. Harris
/ STREET: US Army MRM -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
/ CITY: FORT DETRICK
/ STATE: MARYLAND
/ COUNTRY: USA
/ ZIP: 21702-5012
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: Apple Macintosh
/ OPERATING SYSTEM: Macintosh 7.5
/ SOFTWARE: Microsoft Word 6.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/882,431B
/ FILING DATE: June 25, 1997
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Charles H. Harris
/ REGISTRATION NUMBER: 34,616
/ REFERENCE/DOCKET NUMBER:
/ TELEPHONE: (301) 619-2065
/ TELEFAX: (301) 619-7714
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 233
/ TYPE: Amino Acid
/ STRANDEDNESS: Unknown
/ TOPOLOGY: Unknown
/ MOLECULE TYPE: Peptide
US-08-882-431B-4

Query Match      80.5%; Score 996; DB 2; Length 233;
Best Local Similarity 80.6%; Pred. No. 1e-93;
Matches 187; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKSELQNALSNLRQIYYNNEKAITENKESDDQFLENTLLFKGPFTH 61
DB 2 EKSEINEKDLRKSELQNALSNLRQIYYNNEKAITENKESDDQFLENTLLFKGPFTH 61
QY 62 PWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLTE 121
DB 62 SWYNDLLVDFDSKDIYDKYKGGKVDLYGAYAGYQCAGGTPNKTCACMYGGVTLHDNNRLTE 121
QY 122 EKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQVOR 181
DB 122 EKKVPINLWDGKQNTVPLETVTKTKKNTVQELDLQARRYLOEKYLNLYNSDVFQKQVOR 181
QY 182 GLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHLDLYLTT 233
DB 182 GLIVFHTSTEPSVNYDLFGAGQGYSNLLRIYRDNKTINSENHLDIYLTS 233

RESULT 42
US-09-350-841A-1599
/ Sequence 1599, Application US/09350841A
/ Patent No. 6750008
/ GENERAL INFORMATION:
/ APPLICANT: Jeffs, Peter;
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
/ TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
/ FILE REFERENCE: 7872-086-999
/ CURRENT APPLICATION NUMBER: US/09/350,841A
/ CURRENT FILING DATE: 1999-07-09
/ NUMBER OF SEQ ID NOS: 1946
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1599
/ LENGTH: 252
/ TYPE: PRT
/ ORGANISM: Human immunodeficiency virus type 1
US-09-350-841A-1599

Query Match      74.8%; Score 926.5; DB 2; Length 252;
Best Local Similarity 79.1%; Pred. No. 1.5e-86;
Matches 185; Conservative 16; Mismatches 26; Indels 7; Gaps 6;

QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNNEKAITENKESDDQFLENTLLFKGPFTH 60
DB 25 SEKSEINEKDLRKSELQNALSNLRQIYYNNEKAITENKESDDQFLENTLLFKGPFTH 84
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSK-IVDKY--KKCD-YGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 140
QY 121 EKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQVOR 180
DB 141 EKKVPINLWDGKQNTVPLETVTKTKKNTVQELDLQARRYLOEK-QLNLYNSDVFQKQVOR 198
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHLDLYLTT 233
DB 199 RGLIVFHTSTEPSVNYDLFGAGQGYSNLLRIYRDNKTINSENHLDIYLTS 252

RESULT 43
US-08-896-933-25
/ Sequence 25, Application US/08896933
/ Patent No. 6221351
/ GENERAL INFORMATION:
/ APPLICANT: Terman, David S.
/ TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
/ TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
/ FILE REFERENCE: 09629/005002
/ CURRENT APPLICATION NUMBER: US/08/896,933
/ CURRENT FILING DATE: 1997-07-18
/ EARLIER APPLICATION NUMBER: 08/252,978
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; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-25

Query Match      53.1%; Score 657; DB 2; Length 228;
Best Local Similarity 55.6%; Pred. No. 4.8e-59;
Matches 125; Conservative 33; Mismatches 67; Indels 0; Gaps 0;

QY 7 INEKDLRKSELQNALSNLRQIYYNKEAITENKESDDQFLENTLLFKGFTGHPWYND 66
Db 2 VKEKELHKKSLSSTALNNMKHSYADKNPIIGENKSTGDFLENTLLYKKFTDLINFED 61
QY 67 LLVLDGSKDATNKYKGGKVDLYGAYGYOCAGTGNKTCMYGGVTLHDNNRLTEKKVP 126
Db 62 LLINFNSEKEMAQHFKSKNDVVPYIRSYNICYGGEIDRTACTYGGVTPHSGNKLKERKKIP 121
QY 127 INLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQRLIVF 186
Db 122 INLWINGVQKESLDKVDQTKNVTVOELDAQARYLQKDLKLYNNDTLGGKIQRGKIEF 181
QY 187 HSSEGSTVSYDLFDAQGOVPTDLLRIYRDNKTINSENHLIDLYL 231
Db 182 DSSDGSKVSYDLFDVKGDFFPEKQLRIYSDNKTLSLSTEHLHIDIYLY 226

RESULT 44
US-09-314-235-25
; Sequence 25, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-314-235-25

Query Match      53.1%; Score 657; DB 2; Length 228;
Best Local Similarity 55.6%; Pred. No. 4.8e-59;
Matches 125; Conservative 33; Mismatches 67; Indels 0; Gaps 0;

QY 7 INEKDLRKSELQNALSNLRQIYYNKEAITENKESDDQFLENTLLFKGFTGHPWYND 66
Db 2 VKEKELHKKSLSSTALNNMKHSYADKNPIIGENKSTGDFLENTLLYKKFTDLINFED 61
QY 67 LLVLDGSKDATNKYKGGKVDLYGAYGYOCAGTGNKTCMYGGVTLHDNNRLTEKKVP 126
Db 62 LLINFNSEKEMAQHFKSKNDVVPYIRSYNICYGGEIDRTACTYGGVTPHSGNKLKERKKIP 121
QY 127 INLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQRLIVF 186
Db 122 INLWINGVQKESLDKVDQTKNVTVOELDAQARYLQKDLKLYNNDTLGGKIQRGKIEF 181
QY 187 HSSEGSTVSYDLFDAQGOVPTDLLRIYRDNKTINSENHLIDLYL 231
Db 182 DSSDGSKVSYDLFDVKGDFFPEKQLRIYSDNKTLSLSTEHLHIDIYLY 226

RESULT 45
US-09-708-008B-25
; Sequence 25, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978
; PRIOR FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-708-008B-25

Query Match      53.1%; Score 657; DB 2; Length 228;
Best Local Similarity 55.6%; Pred. No. 4.8e-59;
Matches 125; Conservative 33; Mismatches 67; Indels 0; Gaps 0;

QY 7 INEKDLRKSELQNALSNLRQIYYNKEAITENKESDDQFLENTLLFKGFTGHPWYND 66
Db 2 VKEKELHKKSLSSTALNNMKHSYADKNPIIGENKSTGDFLENTLLYKKFTDLINFED 61
QY 67 LLVLDGSKDATNKYKGGKVDLYGAYGYOCAGTGNKTCMYGGVTLHDNNRLTEKKVP 126
Db 62 LLINFNSEKEMAQHFKSKNDVVPYIRSYNICYGGEIDRTACTYGGVTPHSGNKLKERKKIP 121
QY 127 INLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQRLIVF 186
Db 122 INLWINGVQKESLDKVDQTKNVTVOELDAQARYLQKDLKLYNNDTLGGKIQRGKIEF 181
QY 187 HSSEGSTVSYDLFDAQGOVPTDLLRIYRDNKTINSENHLIDLYL 231
Db 182 DSSDGSKVSYDLFDVKGDFFPEKQLRIYSDNKTLSLSTEHLHIDIYLY 226

RESULT 46
US-09-144-776B-19
; Sequence 19, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
```

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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144, 776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-144-776B-19

Query Match 36.9%; Score 457; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 3.1e-39;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 SDDQFLENTLLFKGFTGHPWYNDLLVGLGSKDATNKYKGVLDLYGAYGYOCAGTGN 102
Db 1 SDDQFLENTLLFKGFTGHPWYNDLLVGLGSKDATNKYKGVLDLYGAYGYOCAGTGN 60

QY 103 KTACMYGGVTLHDNNRLTEKK 124
Db 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 47
US-08-882-431B-19
; Sequence 19, Application US/08882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MPMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
```

```
;
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431B-19

Query Match 36.9%; Score 457; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 3.1e-39;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 SDDQFLENTLLFKGFTGHPWYNDLLVGLGSKDATNKYKGVLDLYGAYGYOCAGTGN 102
Db 1 SDDQFLENTLLFKGFTGHPWYNDLLVGLGSKDATNKYKGVLDLYGAYGYOCAGTGN 60

QY 103 KTACMYGGVTLHDNNRLTEKK 124
Db 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 48
US-09-144-776B-17
; Sequence 17, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MPMC -504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144, 776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
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MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-144-776B-17

Query Match 32.2%; Score 399; DB 2; Length 82;
Best Local Similarity 86.6%; Pred. No. 2.7e-33;
Matches 71; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 43 SDOFLENTLLFKGFTGHPWVNDLLVGLSKDATNKYKGGKVDLYGAYGYQCAGGTN 102
DB 1 SHDQFLQHTLILFKGFTGHSWVNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTN 60

QY 103 KTACMYGGVTLHDNNRLTEKK 124
DB 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 49
US-08-882-431B-17
Sequence 17, Application US/08882431B
Patent No. 6713284
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US Army MCMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431B
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 82
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431B-17

Query Match 32.2%; Score 399; DB 2; Length 82;
Best Local Similarity 86.6%; Pred. No. 2.7e-33;
Matches 71; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 43 SDOFLENTLLFKGFTGHPWVNDLLVGLSKDATNKYKGGKVDLYGAYGYQCAGGTN 102
DB 1 SHDQFLQHTLILFKGFTGHSWVNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTN 60

QY 103 KTACMYGGVTLHDNNRLTEKK 124
DB 61 KTACMYGGVTLHDNNRLTEKK 82

Db 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 50
US-08-446-918A-2
Sequence 2, Application US/08446918A
Patent No. 5705151
GENERAL INFORMATION:
APPLICANT: Dow, Steve W.
APPLICANT: Emslie, Robyn E.
TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSES: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,918A
FILING DATE: 18-MAY-1995
CLASSIFICATION: 552
ATTORNEY/AGENT INFORMATION:
NAME: Kovarik, Joseph E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2879-29
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-446-918A-2

Query Match 24.2%; Score 300; DB 1; Length 255;
Best Local Similarity 34.0%; Pred. No. 1.9e-22;
Matches 83; Conservative 46; Mismatches 97; Indels 18; Gaps 7;

QY 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 15 SMESQDPKPKDELHKSSKFTGLMENMKVLYDDNHVSAL-NVKSIDQFLYFDLYISIKDTK 73

QY 61 HPWYNDLLVGLSKDATNKYKGGKVDLYGAYGYQC-----AGTTPNKTACMYGG 110
DB 74 LGNYDNVRVEFKNKDLADKYDKYVDVFGANYYYCYFSKKTNDINSHQTDKRKTCMYGG 133

QY 111 VTLDHNNRLTEKKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLY 170
DB 134 VTEHNGNQLDKYRSITRVFEDGK-NLLSFD-VQTNKKKVTAEQLDYLTRHYLVKNKKLY 191

QY 171 NSDSFGGKVGRLIVFHSSEGSTVSIDLFDAQGYPD--TLRLIYRDNKTINSENHLIDL 228
DB 192 EFNN--SPVETGYIKFIENENS-FWYDMMPAGDKFDQSKYLMWYNDNKNQVSKDVKIEV 248

QY 229 YLYT 232
DB 249 YLTT 252

RESULT 51
US-08-580-806-2
Sequence 2, Application US/08580806
Patent No. 5935568
GENERAL INFORMATION:


```

Query Match      23.7%; Score 293.5; DB 2; Length 240;
Best Local Similarity 33.3%; Pred.No. 8e-22;
Matches 78; Conservative 48; Mismatches 89; Indels 19; Gaps 9;

QY 11 DLKXKSELQNALSNLRQIYYVNEKAITENK-ESDQOFLENTLLFKGFFTGHPWYNDLLV 69
DB 10 DLHKSEF-TGTGWNK--LYDDHVVSATKVSVDKFLAHDLIYINDKLNNYDKVKT 66
QY 70 DLGSKDATNKYKGGKVDLYGAYGYOC-----AGTPNKTAACMYGGVTLHDNNRLTEE 122
DB 67 ELLNEDLANKYKDEVVDVYGSNYVNCYFSSKDNVGVKVTSGKTCMYGGITKHEGHPDNG 126
QY 123 --KKVFINLWIDGQTTVPIDKVKTSKEVTVELDLOARHYLHGKFLYNSDSFGKVKV 180
DB 127 NLQNVLRIV-ENKRNITISFE-VQTDKKSVAQELDIKARNFLINKNLYEFNS--SPYE 182
QY 181 RGLIVFHSBSGTVSYDLPDAQOQYD--TLLRIYRDNKTINSENLHIDLVLVT 232
DB 183 TGYIKTIESNGNFWIDMMPAPGDKFDQSKYLMYKDNKMKVDSKSVKIEVHLT 236

RESULT 59
US-09-144-776B-6
; Sequence 6, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
;           Mark A. Olson
;           Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
;                   Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US ATMY MVMC -504 Scott Street
;           MCMR-JA (Charles H. Harris-Patent
;           Acty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144, 776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-144-776B-6

Query Match      23.7%; Score 293.5; DB 2; Length 266;
Best Local Similarity 32.8%; Pred.No. 9.2e-22;
Matches 80; Conservative 45; Mismatches 100; Indels 19; Gaps 19;

```

QY 1 SEKSEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLPKGFFTG 60
Db 27 ASQDPKPEDELHKSKF--TGLMEDMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTK 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGYQC-----AGGTPNKTCMYGG 110
Db 85 LGDYDNVRVEFKNKDLADKYKVDVFGANGYCYFYSKKTNDINSHQTDKRTCMYGG 144
QY 111 VTLHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLY 170
Db 145 VTEHNGNQLDKYRSITVRVFEDEK-NLLSPD-VQTNKKKVTAGELDYLTRHYLVKNKKLY 202
QY 171 NDSFGGKVGQGLIVFHSSEGSTVSDLFDAQCG--YPTLLRIYRDNKTINSENHLIDL 228
Db 203 EFNW--SPYETGYIKFIENENS-FWYDMPAPGDKFAQSKYLMYNDNKNKVDKVKIEV 259
QY 229 YLYT 232
Db 260 YLTT 263

RESULT 60
US-08-882-431B-6
; Sequence 6, Application US/08882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431B-6

Query Match 23.7%; Score 293.5; DB 2; Length 266;
Best Local Similarity 32.8%; Pred. No. 9.2e-22;
Matches 80; Conservative 45; Mismatches 100; Indels 19; Gaps 7;

QY 1 SEKSEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLPKGFFTG 60

Db 27 ASQDPKPEDELHKSKF--TGLMEDMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTK 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGYQC-----AGGTPNKTCMYGG 110
Db 85 LGDYDNVRVEFKNKDLADKYKVDVFGANGYCYFYSKKTNDINSHQTDKRTCMYGG 144
QY 111 VTLHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLY 170
Db 145 VTEHNGNQLDKYRSITVRVFEDEK-NLLSPD-VQTNKKKVTAGELDYLTRHYLVKNKKLY 202
QY 171 NDSFGGKVGQGLIVFHSSEGSTVSDLFDAQCG--YPTLLRIYRDNKTINSENHLIDL 228
Db 203 EFNW--SPYETGYIKFIENENS-FWYDMPAPGDKFAQSKYLMYNDNKNKVDKVKIEV 259
QY 229 YLYT 232
Db 260 YLTT 263

RESULT 61
US-08-896-933-26
; Sequence 26, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-26

Query Match 23.6%; Score 292.5; DB 2; Length 239;
Best Local Similarity 34.0%; Pred. No. 1e-21;
Matches 82; Conservative 44; Mismatches 96; Indels 19; Gaps 8;

QY 2 EKSEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLPKGFFTG 61
Db 1 ESQDPKPEDELHKSKF-TGLMENMKVLYDDNHVSAL-NVKSIDQFLYFDLIYSIKDTKL 58
QY 62 PWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGYQC-----AGGTPNKTCMYGGV 111
Db 59 GNYDNVRVEFKNKDLADKYKVDVFGANGYCYFYSKKTNDINSHQTDKRTCMYGGV 118
QY 112 TLHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYN 171
Db 119 TEHNGNQLDKYRSITVRVFEDEK-NLLSPD-VQTNKKKVTAGELDYLTRHYLVKNKKLYE 176
QY 172 SDSFGGKVGQGLIVFHSSEGSTVSDLFDAQCGYDP--TLLRIYRDNKTINSENHLIDL 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDNKNKVDKVKIEV 233
QY 230 L 230
Db 234 L 234

RESULT 62
US-09-314-235-26
; Sequence 26, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,

Query Match 23.6%; Score 292.5; DB 2; Length 239;

RESULT 65
US-08-973-391C-14

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; Sequence 14, Application US/08973391C
; Patent No. 6632441
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggiani, Manuela
; APPLICANT: Stoehr, Jennifer
; APPLICANT: Orlendorf, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 600.311USWO
; CURRENT APPLICATION NUMBER: US/08/973,391C
; CURRENT FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 14
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-973-391C-14

Query Match      23.5%; Score 291.5; DB 2; Length 221;
Best Local Similarity 35.1%; Pred. No. 1.1e-21;
Matches 79; Conservative 42; Mismatches 85; Indels 19; Gaps 10;

Qy      16 SELQRNAL-SNLRLQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTGHPMYNDLLVLDLG 72
Db      7 SQLHRSSLVRLNQLNIYFEGDPVTHENVKSVDDLHLLIYN---VSGPNYDKLKTTELK 63

Qy      73 SKDATNKYKGGKVDLYGAYTYGYQC-AGGTPNKTACMYGGVTLHDNNRLTEEKVPINLWI 131
Db      64 NQEMATLFDKQNDVIYGEVYVHLYCYLCENAESACIYGGVTNHEGNHLEIPKKIIVKYSI 123

Qy      132 DKGQTTVPIDKVTSKSEVTVOELDLQARVHLHGKFGLYNSDSFGGKVQRLIIVFHSSEG 191
Db      124 DGQ-Q-SUSFD-IETNKKQWTAQELDYKVRKYLTDNKQLYNGP--SKYETGYIKFIPQNK 179

Qy      192 STVSYDLFD----AQGGYPTDLRIYRDNKTINSENHLIDLYLT 232
Db      180 ESFWDFPFPEPTOSKY-----LMIYKDNETLDSNTSOIEVLTT 220

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RESULT 66
US-10-625-221-14
; Sequence 14, Application US/10625221
; Patent No. 6870042
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggiani, Manuela
; APPLICANT: Stoehr, Jennifer
; APPLICANT: Orlendorf, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 600.311USWO
; CURRENT APPLICATION NUMBER: US/10/625,221
; CURRENT FILING DATE: 2003-07-22
; PRIOR APPLICATION NUMBER: US/08/973,391C
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-625-221-14

Query Match          23.5%; Score 291.5; DB 2; Length 221;
Best Local Similarity 35.1%; Pred. No. 1.1e-21;

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Matches	79;	Conservative	42;	Mismatches	85;	Indels	19;	Gaps	10;
Qy	16	SELORNAL-SNLRLQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFFTGHHPWYNDLLVDLG	72						
Db	7	SQLHRSSLVKNLQNIVFLYEGDPVTHENVKSVDPQLLSHLIYN---VSGPNYDKLKTELK	63						
Qy	73	SKDATNKYKKKVLDLYGAYGYQC-AGGTPTNKTACHMYGGVTTLHDNNRLETTEKKVPINLWI	131						
Db	64	NQEMATLFKDKNVDIVGEVYHLCYCLENASACTYGGVTNHGNHLETPKKIVVKVSI	123						
Qy	132	DGKOTTVIPIDKVTSSKEVTVQVELDLQARHYLHGKFCGLYNSDSFGGVQORGLIVFHSSEG	191						
Db	124	DGIQ-SUSFD-IETNKKQWTAQELDYKVRKILTDNKQLYTNGP--SKYETGYIKFIPXNK	179						
Qy	192	STVSYDLFD----AQGOYPDTLLRIYRDNKTTINSENLHIDLILYT	232						
Db	180	ESWFDFPFPEFTQSKY-----LMVIKDNETLSDNTSQIEVLTT	220						
RESULT 67									
US-09-308-830B-14									
; Sequence 14, Application US/09308830B									
; Patent No. 6913755									
; GENERAL INFORMATION:									
; APPLICANT: Schlievert, Patrick M.									
; APPLICANT: Roggiani, Manuela									
; APPLICANT: Auge, Jennifer Stoehr									
; APPLICANT: Ohlendorf, Douglas									
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE									
; FILE REFERENCE: 600.346USWO									
; CURRENT APPLICATION NUMBER: US/09/308,830B									
; CURRENT FILING DATE: 1999-08-04									
; PRIOR APPLICATION NUMBER: PCT/US97/22228									
; PRIOR FILING DATE: 1997-12-05									
; PRIOR APPLICATION NUMBER: US 60/032,930									
; PRIOR FILING DATE: 1996-12-06									
; NUMBER OF SEQ ID NOS: 14									
; SOFTWARE: PatentIn version 3.1									
; SEQ ID NO 14									
; LENGTH: 221									
; TYPE: PRF									
; ORGANISM: Streptococcus sp.									
US-09-308-830B-14									
Query Match 23.5%; Score 291.5; DB 2; Length 221;									
Best Local Similarity 35.1%; Pred. No. 1.1e-21;									
Matches	79;	Conservative	42;	Mismatches	85;	Indels	19;	Gaps	10;
Qy	16	SELORNAL-SNLRLQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFFTGHHPWYNDLLVDLG	72						
Db	7	SQLHRSSLVKNLQNIVFLYEGDPVTHENVKSVDPQLLSHLIYN---VSGPNYDKLKTELK	63						
Qy	73	SKDATNKYKKKVLDLYGAYGYQC-AGGTPTNKTACHMYGGVTTLHDNNRLETTEKKVPINLWI	131						
Db	64	NQEMATLFKDKNVDIVGEVYHLCYCLENASACTYGGVTNHGNHLETPKKIVVKVSI	123						
Qy	132	DGKOTTVIPIDKVTSSKEVTVQVELDLQARHYLHGKFCGLYNSDSFGGVQORGLIVFHSSEG	191						
Db	124	DGIQ-SUSFD-IETNKKQWTAQELDYKVRKILTDNKQLYTNGP--SKYETGYIKFIPXNK	179						
Qy	192	STVSYDLFD----AQGOYPDTLLRIYRDNKTTINSENLHIDLILYT	232						
Db	180	ESWFDFPFPEFTQSKY-----LMVIKDNETLSDNTSQIEVLTT	220						
RESULT 68									
US-09-144-776B-16									
; Sequence 16, Application US/09144776B									
; Patent No. 639332									
; GENERAL INFORMATION:									
; APPLICANT: Robert G. Ulrich,									
Mark A. Olson									
Sina Bavari									


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/ STATE: MARYLAND
/ COUNTRY: USA
/ ZIP: 21702-5012
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: Apple Macintosh
/ OPERATING SYSTEM: Macintosh 7.5
/ SOFTWARE: Microsoft Word 6.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/144,776B
/ FILING DATE: 01-Sep-1998
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/882,431
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Charles H. Harris
/ REGISTRATION NUMBER: 34,616
/ REFERENCE/DOCKET NUMBER: <Unknown>
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (301) 619-2065
/ TELEFAX: (301) 619-7714
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE DESCRIPTION: SEQ ID NO: 10:
/
/ US-09-144-776B-10
/
/ Query Match 23.3%; Score 288.5; DB 2; Length 239;
/ Best Local Similarity 33.9%; Pred. No. 2.6e-21;
/ Matches 80; Conservative 45; Mismatches 88; Indels 23; Gaps 8;
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/ QY 14 KKSELQRNA-----LSNLRQIYYVNEKAITENKESDDQFLENTLLFKGFFTGHWPWYNDLL 68
/ DB 7 KPDELHKSSKFTGLMENMKVLDHNVSAI-NVKSIDQRYFDLIYSIKDTKLGNYDNVR 65
/ QY 69 VDLGSKDATNKYKKVDLYGAYGYQCAGG-----TPNKTACMYGGVTLHDNNR 118
/ DB 66 VEFKNKDLADKYKVDVFGANAYVQCASFSSKKTNDINSHQTDKRKTCMYGGVTEHNGQ 125
/ QY 119 LTEKKVPINLWIDGQTVTPIDKVKTSKEVTVQELDLQABHYLHGKFLYNSDSFGGK 178
/ DB 126 LDKYRSITVRVFEDEGK-NLLSFD-VQTNKKKYTAQELDYLTRHYLVNKKLYEFNN--SP 181
/ QY 179 VORGLIVFHSSSGSTVSVDLFDAGQGYPD--TLRIYRDNKNTINSNLHIDLVLTY 232
/ DB 182 YETGVIKFIENENS-FWYDMPPAGDKFDQSKYLMYNDNKNVDSKDVKIEVLTT 236
/
/ RESULT 71
/ US-08-882-431B-10
/ Sequence 10, Application US/08882431B
/ Patent No. 6713284
/ GENERAL INFORMATION:
/ APPLICANT: Robert G. Ulrich,
/ APPLICANT: Mark A. Olson
/ APPLICANT: Sina Bavari
/ TITLE OF INVENTION: Bacterial Superantigen
/ NUMBER OF SEQUENCES: 25
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Charles H. Harris
/ STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
/ CITY: FORT DETRICK
/ STATE: MARYLAND
/ COUNTRY: USA
/ ZIP: 21702-5012
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
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/ COMPUTER: Apple Macintosh
/ OPERATING SYSTEM: Macintosh 7.5
/ SOFTWARE: Microsoft Word 6.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/882,431B
/ FILING DATE: June 25, 1997
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Charles H. Harris
/ REGISTRATION NUMBER: 34,616
/ REFERENCE/DOCKET NUMBER:
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (301) 619-2065
/ TELEFAX: (301) 619-7714
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 239
/ TYPE: Amino Acid
/ STRANDEDNESS: Unknown
/ TOPOLOGY: Unknown
/ MOLECULE TYPE: Peptide
/
/ US-08-882-431B-10
/
/ Query Match 23.3%; Score 288.5; DB 2; Length 239;
/ Best Local Similarity 33.9%; Pred. No. 2.6e-21;
/ Matches 80; Conservative 45; Mismatches 88; Indels 23; Gaps 8;
/
/ QY 14 KKSELQRNA-----LSNLRQIYYVNEKAITENKESDDQFLENTLLFKGFFTGHWPWYNDLL 68
/ DB 7 KPDELHKSSKFTGLMENMKVLDHNVSAI-NVKSIDQRYFDLIYSIKDTKLGNYDNVR 65
/ QY 69 VDLGSKDATNKYKKVDLYGAYGYQCAGG-----TPNKTACMYGGVTLHDNNR 118
/ DB 66 VEFKNKDLADKYKVDVFGANAYVQCASFSSKKTNDINSHQTDKRKTCMYGGVTEHNGQ 125
/ QY 119 LTEKKVPINLWIDGQTVTPIDKVKTSKEVTVQELDLQABHYLHGKFLYNSDSFGGK 178
/ DB 126 LDKYRSITVRVFEDEGK-NLLSFD-VQTNKKKYTAQELDYLTRHYLVNKKLYEFNN--SP 181
/ QY 179 VORGLIVFHSSSGSTVSVDLFDAGQGYPD--TLRIYRDNKNTINSNLHIDLVLTY 232
/ DB 182 YETGVIKFIENENS-FWYDMPPAGDKFDQSKYLMYNDNKNVDSKDVKIEVLTT 236
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/ RESULT 72
/ US-09-555-115A-3
/ Sequence 3, Application US/09555115A
/ Patent No. 6872394
/ GENERAL INFORMATION:
/ APPLICANT: Bohach, Gregory I.
/ TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
/ FILE REFERENCE: 12136.1USWO
/ CURRENT APPLICATION NUMBER: US/09/555,115A
/ CURRENT FILING DATE: 2000-08-01
/ PRIOR APPLICATION NUMBER: PCT/US98/25107
/ PRIOR FILING DATE: 1998-12-01
/ PRIOR APPLICATION NUMBER: US 60/067,357
/ PRIOR FILING DATE: 1997-12-02
/ NUMBER OF SEQ ID NOS: 66
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3
/ LENGTH: 240
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (240)..(240)
/ OTHER INFORMATION: Xaa is unknown.
/
/ US-09-555-115A-3
/
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Query Match 23.3%; Score 288.5; DB 2; Length 240;
Best Local Similarity 32.1%; Pred. No. 2.6e-21;
Matches 75; Conservative 49; Mismatches 91; Indels 19; Gaps 9;

QY 11 DLKKSSELRNLSNRQIYYNEKAITENK-ESDDQFLENTLLFKGFFTGHPWYNDLLV 69
DB 10 DLKKSSEF-TGTWGNMK--LYDDHYVSATKVKSVKFLAHDLIYNSDKKLNKYDKVKT 66
QY 70 DLGSKDATNKYKGGKVDLYGAYGYQC-----AGTGNKTKACMYGGVTLHDNRLTEE 122
DB 67 ELLNEDLAKYKDEVDVYGSNYVNCYFSSKDNVGVKVTGGKTCMYGGITKHGHNFDNG 126
QY 123 --KKVPINLWIDGKQTTVPIDKVKTSKVEYTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 127 NLQNLVLRVY-ENKRNITISPE-VQTDKKSVTQAELDIKARNFLINKNLYEFNS--SPYE 182
QY 181 RGLIVHSSGSGTVSVDLFAQCGQYD--TLRIYRDNKTINSENHLIDLTYT 232
DB 183 TGYIKFIENNGNTFYDMPAPGDKFQSKYLMYNDKNTVDSKVKIEVHLTT 236

RESULT 73
US-09-555-115A-6
; Sequence 6, Application US/09555115A
; Patent No. 6872394
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 6
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (240)..(240)
; OTHER INFORMATION: Xaa is unknown.
US-09-555-115A-6

Query Match 23.2%; Score 287.5; DB 2; Length 240;
Best Local Similarity 32.1%; Pred. No. 3.3e-21;
Matches 75; Conservative 48; Mismatches 92; Indels 19; Gaps 9;

QY 11 DLKKSSELRNLSNRQIYYNEKAITENK-ESDDQFLENTLLFKGFFTGHPWYNDLLV 69
DB 10 DLKKSSEF-TGTWGNMK--LYDDHYVSATKVKSVKFLAHDLIYNSDKRLNLYDKVKT 66
QY 70 DLGSKDATNKYKGGKVDLYGAYGYQC-----AGTGNKTKACMYGGVTLHDNRLTEE 122
DB 67 ELLNEDLAKYKDEVDVYGSNYVNCYFSSKDNVGVKVTGGKTCMYGGITKHGHNFDNG 126
QY 123 --KKVPINLWIDGKQTTVPIDKVKTSKVEYTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 127 NLQNLVLRVY-ENKRNITISPE-VQTDKKSVTQAELDIKARNFLINKNLYEFNS--SPYE 182
QY 181 RGLIVHSSGSGTVSVDLFAQCGQYD--TLRIYRDNKTINSENHLIDLTYT 232
DB 183 TGYIKFIENNGNTFYDMPAPGDKFQSKYLMYNDKNTVDSKVKIEVHLTT 236

RESULT 74
US-09-555-115A-5
; Sequence 5, Application US/09555115A
; Patent No. 6872394
; GENERAL INFORMATION:

; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 5
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (240)..(240)
; OTHER INFORMATION: Xaa is unknown.
US-09-555-115A-5

Query Match 23.1%; Score 285.5; DB 2; Length 240;
Best Local Similarity 31.3%; Pred. No. 5.2e-21;
Matches 76; Conservative 49; Mismatches 99; Indels 19; Gaps 9;

QY 2 EKSEIEINEXDLRKSSELRNLSNRQIYYNEKAITENK-ESDDQFLENTLLFKGFFTG 60
DB 1 ESQDPTPDELKHSSEF-TGTWGNMK--LYDDHYVSATKVKSVKFLAHDLIYNSDKK 57
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQC-----AGTGNKTKACMYGGVTL 113
DB 58 LKNYDKVKTLELLEDLAKYKDEVDVYGSNYVNCYFSSKDNVGVKVTGGKTCMYGGITK 117
QY 114 HDNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKVEYTVQELDLQARHYLHGKFGLYN 171
DB 118 HEGNFDNGNLQNLVLRVY-ENKRNITISPE-VQTDKKSVTQAELDIKARNFLINKNLYE 175
QY 172 SDSFGGKVGRLIVHSSGSGTVSVDLFAQCGQYD--TLRIYRDNKTINSENHLIDL 229
DB 176 FNS--SPYETGYIKFIENNGNTFYDMPAPGDKFQSKYLMYNDKNTVDSKVKIEVH 233
QY 230 LYT 232
DB 234 LTT 236

RESULT 75
US-09-555-115A-2
; Sequence 2, Application US/09555115A
; Patent No. 6872394
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/09/555,115A
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (240)..(240)
; OTHER INFORMATION: Xaa is unknown.
US-09-555-115A-2

Query Match 22.9%; Score 283.5; DB 2; Length 240;

Best Local Similarity 31.3%; Pred. No. 8 4e-21;
Matches 76; Conservative 49; Mismatches 99; Indels 19; Gaps 9;

Qy	2	EKSEINEKDLRKXSELQNALSNLRQIYYINEKAITENK-ESDDQFLENTLLFKGFFTG	60
Db	1	ESQPDPTPDELKXSEF-TGTGNMK--YLYDDHYVSATKVMVDKFLAHDLIYNISDKK	57
Qy	61	HPWYNDLLVDLGSKDATNICYKGGKVDLYGAYGYQC-----AGGTPNKTACMYGGVTL	113
Db	58	LKNYDKVKTELLNEDLAKKYKDEWVDVYGSNYVNCYFSSKDNVGVKVTGGKTCMYGGITK	117
Qy	114	HNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYN	171
Db	118	HGHNHFDNGNLQNLIRVY-ENKRNITISPE-VQTDKKSVTAGELDIKARNFLINKNLYE	175
Qy	172	SDSFGGKVORGLIVFHSSEGSTVSYDLFDAQQGYPD--TLLRIYRDNKNTINSENHLIDLY	229
Db	176	FNS--SPYETGYIKFTIENNGNTFYDMPAPGDKFDQSKYLMWYNDNKTVDKSVKIEVH	233
Qy	230	LYT	232
Db	234	LTT	236

Search completed: February 15, 2006, 20:20:17
Job time : 21.7646 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 15, 2006, 20:34:11 ; Search time 58.958 Seconds
(without alignments)
1651.247 Million cell updates/sec

Title: us-09-900-766-7

Perfect score: 1238

Sequence: 1 SEKSEINEKRLKRSSELQR.....RDNKTINSENHIDLYLTYT 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Published Applications AA_Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1238	100.0	233	3	US-09-900-766-7
2	1238	100.0	233	4	US-10-283-838-8
3	1238	100.0	257	4	US-10-267-682-112
4	1238	100.0	257	4	US-10-267-748-112
5	1238	100.0	257	4	US-10-428-817A-188
6	1210	97.7	233	3	US-09-900-766-3
7	1188	96.0	248	3	US-09-870-759-16
8	1188	96.0	248	3	US-09-751-708A-16
9	1188	96.0	248	5	US-10-428-817A-12
10	1188	96.0	248	5	US-10-937-758A-16
11	1107	89.4	233	3	US-09-900-766-2
12	1107	89.4	672	3	US-09-900-766-1
13	1023	82.6	233	3	US-09-900-766-4
14	1023	82.6	233	4	US-10-283-838-7
15	1023	82.6	257	4	US-10-267-682-113
16	1023	82.6	257	4	US-10-267-748-113
17	1023	82.6	257	5	US-10-951-225-5
18	1019	82.3	233	4	US-10-354-948-4
19	1013	81.8	257	3	US-09-870-759-8
20	1013	81.8	257	3	US-09-751-708A-8
21	1013	81.8	257	4	US-10-428-817A-4
22	1013	81.8	257	5	US-10-937-758A-8
23	1000	80.8	257	4	US-10-002-784A-2
24	1000	80.8	257	5	US-10-767-687-2
25	996	80.5	233	4	US-10-002-784A-4
26	996	80.5	233	5	US-10-767-687-4
27	991	80.0	231	4	US-10-428-817A-182

28	983	79.4	257	2	US-08-882-431-2	Sequence 2, Appli
29	978	79.0	233	2	US-08-882-431-4	Sequence 4, Appli
30	921	74.4	227	5	US-10-997-690-11	Sequence 11, Appl
31	830	67.0	268	4	US-10-428-817A-175	Sequence 175, App
32	663	53.6	258	3	US-09-870-759-14	Sequence 14, Appl
33	663	53.6	258	3	US-09-751-708A-14	Sequence 14, Appl
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35	663	53.6	258	4	US-10-428-817A-187	Sequence 187, App
36	663	53.6	258	5	US-10-937-758A-14	Sequence 14, Appl
37	523	42.2	203	3	US-09-900-766-5	Sequence 5, Appli
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42	366	29.6	217	3	US-09-900-766-6	Sequence 6, Appli
43	366	29.6	217	4	US-10-428-817A-173	Sequence 173, App
44	343	27.7	259	5	US-10-474-792-416	Sequence 416, App
45	339.5	27.4	242	4	US-10-428-817A-174	Sequence 174, App
46	337	27.2	240	4	US-10-428-817A-177	Sequence 177, App
47	320	25.8	239	4	US-10-428-817A-178	Sequence 178, App
48	319.5	25.8	242	4	US-10-428-817A-172	Sequence 172, App
49	310	25.0	242	4	US-10-428-817A-176	Sequence 176, App
50	300.5	24.3	266	3	US-09-870-759-10	Sequence 10, Appl
51	300.5	24.3	266	3	US-09-751-708A-10	Sequence 10, Appl
52	300.5	24.3	266	4	US-10-428-817A-6	Sequence 6, Appli
53	300.5	24.3	266	5	US-10-937-758A-10	Sequence 10, Appl
54	300	24.2	255	4	US-10-354-948-2	Sequence 2, Appli
55	299.5	24.2	238	4	US-10-428-817A-183	Sequence 183, App
56	299.5	24.2	239	3	US-09-150-947B-12	Sequence 12, Appl
57	299.5	24.2	239	4	US-10-172-425B-12	Sequence 12, Appl
58	299.5	24.2	239	5	US-10-525-113-1	Sequence 1, Appli
59	295.5	23.9	251	4	US-10-428-817A-163	Sequence 163, App
60	294.5	23.8	251	2	US-08-973-391A-13	Sequence 13, Appl
61	294.5	23.8	251	3	US-09-308-830-13	Sequence 13, Appl
62	293.5	23.7	240	5	US-10-923-324-4	Sequence 4, Appli
63	293.5	23.7	266	4	US-10-002-784A-6	Sequence 6, Appli
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75	285.5	23.1	240	5	US-10-923-324-5	Sequence 5, Appli
76	285.5	23.1	266	4	US-10-428-817A-186	Sequence 186, App
77	283.5	22.9	240	5	US-10-923-324-2	Sequence 2, Appli
78	282.5	22.8	266	4	US-10-002-784A-8	Sequence 8, Appli
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82	276.5	22.3	240	5	US-10-923-324-7	Sequence 7, Appli
83	276.5	22.3	240	5	US-10-923-324-8	Sequence 8, Appli
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86	266.5	21.5	266	3	US-09-870-759-12	Sequence 12, Appl
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88	266.5	21.5	266	4	US-10-428-817A-8	Sequence 8, Appli
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92	258.5	20.9	266	4	US-10-002-784A-14	Sequence 14, Appl
93	258.5	20.9	266	5	US-10-767-687-14	Sequence 14, Appl
94	256.5	20.7	220	4	US-10-002-784A-26	Sequence 26, Appl
95	256.5	20.7	468	4	US-10-002-784A-27	Sequence 27, Appl
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97	256	20.7	233	5	US-10-997-690-2	Sequence 2, Appli
98	245	19.8	250	3	US-09-870-759-20	Sequence 20, Appl
99	245	19.8	250	3	US-09-751-708A-20	Sequence 20, Appl
100	245	19.8	250	4	US-10-428-817A-16	Sequence 16, Appl

101	245	19.8	250	5	US-10-937-758A-20	Sequence 20, Appl	174	93	7.5	619	4	US-10-425-115-257344	Sequence 257344,
102	239	19.3	209	4	US-10-428-817A-169	Sequence 169, App	175	93	7.5	643	4	US-10-425-114-38468	Sequence 38468, A
103	220.5	17.8	240	4	US-10-428-817A-184	Sequence 184, App	176	93	7.5	653	4	US-10-425-114-62449	Sequence 62449, A
104	217	17.5	234	5	US-10-474-792-562	Sequence 562, App	177	93	7.5	847	4	US-10-282-122A-59134	Sequence 59134, A
105	217	17.5	234	5	US-10-997-690-4	Sequence 4, Appl	178	92.5	7.5	227	4	US-10-428-817A-193	Sequence 193, App
106	216	17.4	210	4	US-10-428-817A-166	Sequence 166, App	179	92	7.4	631	5	US-10-481-032A-634	Sequence 634, App
107	215	17.4	82	4	US-10-002-784A-33	Sequence 33, Appl	180	90	7.3	463	4	US-10-097-111-288	Sequence 288, App
108	215	17.4	82	5	US-10-767-687-18	Sequence 18, Appl	181	90	7.3	5005	4	US-10-282-122A-76871	Sequence 76871, A
109	197	15.9	204	5	US-10-997-690-22	Sequence 22, Appl	182	89.5	7.2	612	4	US-10-425-114-63660	Sequence 63660, A
110	197	15.9	236	4	US-10-428-817A-167	Sequence 167, App	183	89.5	7.2	612	4	US-10-425-115-246981	Sequence 246981, A
111	197	15.9	236	5	US-10-474-792-414	Sequence 414, App	184	89	7.2	171	4	US-10-282-122A-71154	Sequence 71154, A
112	197	15.9	236	5	US-10-997-690-6	Sequence 6, Appl	185	89	7.2	179	4	US-10-724-972A-6442	Sequence 6442, Ap
113	193	15.6	232	4	US-10-428-817A-168	Sequence 168, App	186	89	7.2	516	4	US-10-032-585-7147	Sequence 7147, Ap
114	185	14.9	234	4	US-10-428-817A-185	Sequence 165, App	187	89	7.2	631	4	US-10-043-344-115	Sequence 115, App
115	183.5	14.8	235	3	US-09-336-036-2	Sequence 2, Appl	188	89	7.2	941	4	US-10-369-493-19630	Sequence 19630, A
116	183.5	14.8	235	3	US-09-308-829-2	Sequence 2, Appl	189	89	7.2	1634	4	US-10-435-766-23	Sequence 23, Appl
117	183.5	14.8	235	5	US-10-914-417-2	Sequence 2, Appl	190	89	7.2	1634	5	US-10-734-563-96	Sequence 96, Appl
118	183.5	14.8	235	5	US-10-914-665-2	Sequence 2, Appl	191	89	7.2	1634	5	US-10-853-973A-23	Sequence 23, Appl
119	181.5	14.7	204	5	US-10-997-690-20	Sequence 20, Appl	192	88.5	7.1	308	5	US-10-470-048B-438	Sequence 438, App
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122	157	12.7	206	5	US-10-997-690-21	Sequence 21, Appl	195	88	7.1	611	4	US-10-424-599-173518	Sequence 173518, A
123	137.5	11.1	89	4	US-10-002-784A-35	Sequence 35, Appl	196	88	7.1	632	4	US-10-425-114-52842	Sequence 52842, A
124	137.5	11.1	89	5	US-10-767-687-20	Sequence 20, Appl	197	88	7.1	646	4	US-10-425-114-50103	Sequence 50103, A
125	121	9.8	79	4	US-10-002-784A-39	Sequence 39, Appl	198	88	7.1	646	4	US-10-425-114-57915	Sequence 57915, A
126	121	9.8	79	5	US-10-767-687-24	Sequence 24, Appl	199	87.5	7.1	556	4	US-10-282-122A-60731	Sequence 60731, A
127	121	9.8	203	5	US-10-997-690-10	Sequence 10, Appl	200	87.5	7.1	623	4	US-10-425-114-62505	Sequence 62505, A
128	116	9.4	231	4	US-10-428-817A-191	Sequence 191, App	201	87.5	7.1	1637	4	US-10-437-963-180397	Sequence 180397, A
129	114	9.2	231	4	US-10-428-817A-190	Sequence 190, App	202	87	7.0	286	4	US-10-724-972A-5172	Sequence 5172, Ap
130	113	9.1	232	4	US-10-282-122A-70242	Sequence 70242, A	203	87	7.0	361	4	US-10-425-114-51445	Sequence 51445, A
131	112.5	9.1	89	4	US-10-002-784A-37	Sequence 37, Appl	204	87	7.0	384	4	US-10-425-114-51527	Sequence 51527, A
132	112.5	9.1	89	4	US-10-002-784A-38	Sequence 38, Appl	205	87	7.0	617	4	US-10-424-599-173517	Sequence 173517, A
133	112.5	9.1	89	5	US-10-767-687-22	Sequence 22, Appl	206	87	7.0	636	4	US-10-425-114-44202	Sequence 44202, A
134	112.5	9.1	89	5	US-10-767-687-23	Sequence 23, Appl	207	87	7.0	1291	4	US-10-452-024-121	Sequence 121, App
135	110.5	8.9	444	4	US-10-724-972A-4705	Sequence 4705, Ap	208	86.5	7.0	460	4	US-10-425-114-38886	Sequence 38886, A
136	109	8.8	232	4	US-10-428-817A-194	Sequence 194, App	209	86.5	7.0	492	4	US-10-183-687-489	Sequence 489, App
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138	107.5	8.7	234	3	US-08-751-708A-18	Sequence 18, Appl	211	86.5	7.0	650	5	US-10-481-032A-182	Sequence 182, App
139	107.5	8.7	234	4	US-10-267-682-111	Sequence 111, App	212	86	6.9	399	4	US-10-374-780A-1313	Sequence 1313, Ap
140	107.5	8.7	234	4	US-10-267-748-111	Sequence 111, App	213	86	6.9	399	4	US-10-412-699B-1458	Sequence 1458, Ap
141	107.5	8.7	234	4	US-10-428-817A-14	Sequence 14, Appl	214	86	6.9	399	4	US-10-437-963-132822	Sequence 132822, A
142	107.5	8.7	234	4	US-10-428-817A-189	Sequence 189, App	215	85.5	6.9	228	4	US-10-425-115-248728	Sequence 248728, A
143	107.5	8.7	234	5	US-10-937-758A-18	Sequence 18, Appl	216	85.5	6.9	264	4	US-10-282-122A-71721	Sequence 71721, A
144	105.5	8.5	89	4	US-10-002-784A-36	Sequence 36, Appl	217	85.5	6.9	409	4	US-10-183-687-477	Sequence 477, App
145	105.5	8.5	89	5	US-10-767-687-21	Sequence 21, Appl	218	85.5	6.9	584	4	US-10-070-923-5	Sequence 5, Appl
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147	105.5	8.5	194	4	US-10-354-948-6	Sequence 6, Appl	220	85.5	6.9	618	4	US-10-767-701-46249	Sequence 46249, A
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149	105.5	8.5	234	4	US-10-282-122A-70390	Sequence 70390, A	222	85	6.9	17	5	US-10-923-324-34	Sequence 34, Appl
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151	105	8.5	226	3	US-09-815-242-5900	Sequence 5900, Ap	224	85	6.9	548	4	US-10-724-972A-7488	Sequence 7488, Ap
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155	104.5	8.4	234	5	US-10-767-687-12	Sequence 12, Appl	228	85	6.9	1500	4	US-10-437-963-154440	Sequence 154440, A
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159	98.5	8.0	621	4	US-10-424-599-264720	Sequence 264720, A	232	84.5	6.8	351	4	US-10-087-013-9	Sequence 9, Appl
160	98.5	8.0	628	4	US-10-425-114-57792	Sequence 57792, A	233	84.5	6.8	402	4	US-10-284-400-6	Sequence 6, Appl
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164	94	7.6	226	4	US-10-282-122A-43957	Sequence 43957, A	237	84	6.8	357	5	US-10-470-048B-555	Sequence 555, App
165	94	7.6	622	4	US-10-425-114-39433	Sequence 39433, A	238	84	6.8	366	4	US-10-724-972A-4827	Sequence 4827, Ap
166	94	7.6	622	4	US-10-425-114-60523	Sequence 60523, A	239	84	6.8	492	4	US-10-369-493-31	Sequence 31, Appl
167	93.5	7.6	631	4	US-10-043-344-111	Sequence 111, App	240	84	6.8	546	4	US-10-437-963-201874	Sequence 201874, A
168	93	7.5	16	4	US-10-283-838-20	Sequence 20, Appl	241	84	6.8	663	4	US-10-282-122A-52415	Sequence 52415, A
169	93	7.5	306	4	US-10-425-114-54166	Sequence 54166, A	242	84	6.8	675	4	US-10-724-972A-6913	Sequence 6913, Ap
170	93	7.5	335	4	US-10-425-115-257338	Sequence 257338, A	243	84	6.8	1014	4	US-10-654-416-2	Sequence 2, Appl
171	93	7.5	616	4	US-10-431-273-60	Sequence 60, Appl	244	84	6.8	1341	5	US-10-732-923-6898	Sequence 6898, Ap
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US-10-283-838-8

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RESULT 3
US-10-267-682-112
; Sequence 112, Application US/10267682
; Publication No. US2004003235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/267,682
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
;

;
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-267-682-112

Query Match      100.0%; Score 1238; DB 4; Length 257;
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QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPDTLRIYRDNKTINSENHLHIDLTYTT 233
DB 205 RGLIVFHSSEGSTVSVDLFDAGQGYPDTLRIYRDNKTINSENHLHIDLTYTT 257

RESULT 4
US-10-267-748-112
; Sequence 112, Application US/10267748
; Publication No. US20040052820A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/267,748
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
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```
;
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-267-748-112

Query Match      100.0%; Score 1238; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 8.1e-105;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSLOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKKSLOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HPWYNLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 204
QY 181 RGLIVFHSSEGSTSVSYDLFDAQQYPTLLRIYRDNKTINSENHLDLYLYTT 233
Db 205 RGLIVFHSSEGSTSVSYDLFDAQQYPTLLRIYRDNKTINSENHLDLYLYTT 257

RESULT 5
US-10-428-817A-188
; Sequence 188, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; PRIOR FILING DATE: 2003-05-05
; PRIOR FILING DATE: 2002-05-08
; PRIOR FILING DATE: 2002-05-08
; PRIOR FILING DATE: 2002-05-08
; PRIOR FILING DATE: 2002-06-15
; PRIOR FILING DATE: 2002-06-15
; PRIOR FILING DATE: 2002-06-15
; PRIOR FILING DATE: 2002-08-28
; PRIOR FILING DATE: 2002-08-28
; PRIOR FILING DATE: 2002-08-28
; PRIOR FILING DATE: 2002-08-29
; PRIOR FILING DATE: 2002-08-29
; PRIOR FILING DATE: 2002-10-01
; PRIOR FILING DATE: 2002-10-01
; PRIOR FILING DATE: 2002-10-01
; PRIOR FILING DATE: 2002-10-02
; PRIOR FILING DATE: 2002-10-02
; PRIOR FILING DATE: 2002-10-09
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 188
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-188

Query Match      100.0%; Score 1238; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 8.1e-105;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSLOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKKSLOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HPWYNLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 204
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QY 181 RGLIVFHSSEGSTSVSYDLFDAQQYPTLLRIYRDNKTINSENHLDLYLYTT 233
Db 205 RGLIVFHSSEGSTSVSYDLFDAQQYPTLLRIYRDNKTINSENHLDLYLYTT 257

RESULT 6
US-09-900-766-3
; Sequence 3, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(233)
; OTHER INFORMATION: Chimeric Protein
US-09-900-766-3

Query Match      97.7%; Score 1210; DB 3; Length 233;
Best Local Similarity 97.9%; Pred. No. 2.6e-102;
Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSLOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 1 SEKSEINEKDLRKKSLOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
QY 61 HPWYNLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 61 HPWYNLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
QY 181 RGLIVFHSSEGSTSVSYDLFDAQQYPTLLRIYRDNKTINSENHLDLYLYTT 233
Db 181 RGLIVFHSSEGSTSVSYDLFDAQQYPTLLRIYRDNKTINSENHLDLYLYTT 233

RESULT 7
US-09-870-759-16
; Sequence 16, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR FILING DATE: 2002-01-14
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 16
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-16

Query Match      96.0%; Score 1188; DB 3; Length 248;
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Best Local Similarity 100.0%; Pred. No. 2.9e-100;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204
QY 181 RGLIVFHSSEGSTVSVDLFDQAQQYPTDLLRIYRDNKTINSENL 224
Db 205 RGLIVFHSSEGSTVSVDLFDQAQQYPTDLLRIYRDNKTINSENL 248

RESULT 8
US-09-751-708A-16
; Sequence 16, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-16

Query Match 96.0%; Score 1188; DB 3; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.9e-100;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204
QY 181 RGLIVFHSSEGSTVSVDLFDQAQQYPTDLLRIYRDNKTINSENL 224
Db 205 RGLIVFHSSEGSTVSVDLFDQAQQYPTDLLRIYRDNKTINSENL 248

RESULT 9
US-10-428-817A-12
; Sequence 12, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
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; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-12

Query Match 96.0%; Score 1188; DB 4; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.9e-100;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204
QY 181 RGLIVFHSSEGSTVSVDLFDQAQQYPTDLLRIYRDNKTINSENL 224
Db 205 RGLIVFHSSEGSTVSVDLFDQAQQYPTDLLRIYRDNKTINSENL 248

RESULT 10
US-10-937-758A-16
; Sequence 16, Application US/10937758A
; Publication No. US20050112141A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: FILE REFERENCE 650884
; CURRENT APPLICATION NUMBER: US/10/937,758A
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: 09/650,884
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-937-758A-16

Query Match 96.0%; Score 1188; DB 5; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.9e-100;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
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QY 121 EEKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
Db 145 EEKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204
QY 181 RGLIVHSSSGSTVSVDLFAQOQYPTLLRIYRDKNKTINSENL 224
Db 205 RGLIVHSSSGSTVSVDLFAQOQYPTLLRIYRDKNKTINSENL 248

RESULT 11
US-09-900-766-2
; Sequence 2, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(233)
; OTHER INFORMATION: Chimeric Protein
US-09-900-766-2

Query Match 89.4%; Score 1107; DB 3; Length 233;
Best Local Similarity 89.7%; Pred. No. 6.8e-93;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOQNALSNLROIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 1 SEKSEINEKDLRKSELOQNALSNLROIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLLHDNNRLT 120
Db 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLLHDNNRLT 120
QY 121 EEKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
Db 121 EEKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
QY 181 RGLIVHSSSGSTVSVDLFAQOQYPTLLRIYRDKNKTINSENLHIDLILYTT 233
Db 181 RGLIVHSSSGSTVSVDLFAQOQYPTLLRIYRDKNKTINSENLHIDLILYTT 233

RESULT 12
US-09-900-766-1
; Sequence 1, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 672
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(672)
; OTHER INFORMATION: Conjugate protein
US-09-900-766-1
Query Match 89.4%; Score 1107; DB 3; Length 672;
Best Local Similarity 89.7%; Pred. No. 2.7e-92;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOQNALSNLROIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 226 SEKSEINEKDLRKSELOQNALSNLROIYYNEKAITENKESDDQFLENTLLFKGFFTG 285
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLLHDNNRLT 120
Db 286 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLLHDNNRLT 345
QY 121 EEKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
Db 346 EEKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 405
QY 181 RGLIVHSSSGSTVSVDLFAQOQYPTLLRIYRDKNKTINSENLHIDLILYTT 233
Db 406 RGLIVHSSSGSTVSVDLFAQOQYPTLLRIYRDKNKTINSENLHIDLILYTT 458

RESULT 13
US-09-900-766-4
; Sequence 4, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 4
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Staphylococcus sp.
US-09-900-766-4

Query Match 82.6%; Score 1023; DB 3; Length 233;
Best Local Similarity 82.0%; Pred. No. 3.3e-85;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOQNALSNLROIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 1 SEKSEINEKDLRKSELOQNALSNLROIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLLHDNNRLT 120
Db 61 HSWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLLHDNNRLT 120
QY 121 EEKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
Db 121 EEKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
QY 181 RGLIVHSSSGSTVSVDLFAQOQYPTLLRIYRDKNKTINSENLHIDLILYTT 233
Db 181 RGLIVHSSSGSTVSVDLFAQOQYPTLLRIYRDKNKTINSENLHIDLILYTT 233

RESULT 14
US-10-283-838-7
; Sequence 7, Application US/10283838

Publication No. US20030092894A1
GENERAL INFORMATION:
APPLICANT: Per Antonsson, Per Bjork, Mikael Dohltsten,
Johan Hansson, Terje Kalland, Lars
Abrahamson and Goran Foreberg
TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
AND THEIR USE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
STREET: 1177 West Loop South, 10th Floor
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77027-9095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,838
FILING DATE: 30-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/695,692
FILING DATE: August 12, 1996
APPLICATION NUMBER: 9601245-5
FILING DATE: March 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Krieger, Paul E.
REGISTRATION NUMBER: 25,886
REFERENCE/DOCKET NUMBER: 41986/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-283-838-7

Query Match 82.6%; Score 1023; DB 4; Length 233;
Best Local Similarity 82.0%; Pred. No. 3.3e-85;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFGFFTG 60
DB 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFGFFTD 60
QY 61 HPWYNLLVDLGSKATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 61 HSWYNLLVDLGSKATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
QY 121 EEKVPINLWDGKQTPIDVKYTKSKVTVQELDLQARHYLHGKFLYNSDSFGKQV 180
DB 121 EEKVPINLWDGKQNTVPLETVTKNKNVTVQELDLQARRYLQEKYLYNSDVDFGKQV 180
QY 181 RGLIVFHSSEGSTVSYDLFDAQGOYPTLLRIYRDNKTINSENHLDLYLT 233
DB 181 RGLIVFHTSTEPSVNYDLFGAQQOYNTLLRIYRDNKTINSENHLDIYLYTS 233

RESULT 15
US-10-267-682-113
Sequence 113, Application US/10267682
Publication No. US20040033235A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.

Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,682
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-10-267-682-113

Query Match 82.6%; Score 1023; DB 4; Length 257;
Best Local Similarity 82.0%; Pred. No. 3.7e-85;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFGFFTG 60
DB 25 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLQHTLLFGFFTD 84
QY 61 HPWYNLLVDLGSKATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNLLVDLGSKATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWDGKQTPIDVKYTKSKVTVQELDLQARHYLHGKFLYNSDSFGKQV 180
DB 145 EEKVPINLWDGKQNTVPLETVTKNKNVTVQELDLQARRYLQEKYLYNSDVDFGKQV 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGOYPTLLRIYRDNKTINSENHLDLYLT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQQOYNTLLRIYRDNKTINSENHLDIYLYTS 257

RESULT 16
US-10-267-748-113
Sequence 113, Application US/10267748
Publication No. US20040052820A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.

Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-10-267-748-113
Query Match 82.6%; Score 1023; DB 4; Length 257;
Best Local Similarity 82.0%; Pred. No. 3.7e-85;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKSSELQARNLSNLROIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKKSSELQALGNLQIYYNEKAKTENKESHDPLOHTILFKGFFTD 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKKVPINLWDGKQTTPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
Db 145 EEKKVPINLWDGKQNTVPLETVKTKNKNVTVOELDLQARRYLQEKYNYNSDVFDGKVQ 204
QY 181 RGLIVPHSSSGSTVSYDLFDAQOQYPTLRIYRDNKTINSENHLDLYLTT 233
Db 205 RGLIVFHTSTEPSVNYDLFQAQOQSYNTLLRIYRDNKTINSENHLDIYLYTS 257
RESULT 17
US-10-951-225-5
; Sequence 5, Application US/10951225
; Publication No. US2005023345A1
; GENERAL INFORMATION:
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-10-267-748-113
Query Match 82.6%; Score 1023; DB 4; Length 257;
Best Local Similarity 82.0%; Pred. No. 3.7e-85;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKSSELQARNLSNLROIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKKSSELQALGNLQIYYNEKAKTENKESHDPLOHTILFKGFFTD 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKKVPINLWDGKQTTPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
Db 145 EEKKVPINLWDGKQNTVPLETVKTKNKNVTVOELDLQARRYLQEKYNYNSDVFDGKVQ 204
QY 181 RGLIVPHSSSGSTVSYDLFDAQOQYPTLRIYRDNKTINSENHLDLYLTT 233
Db 205 RGLIVFHTSTEPSVNYDLFQAQOQSYNTLLRIYRDNKTINSENHLDIYLYTS 257
RESULT 18
US-10-354-948-4
; Sequence 4, Application US/10354948
; Publication No. US20030202962A1
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; Elmellie, Robyn E.
; Potex, Terence A.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/354,948
; FILING DATE: 29-Jan-2003
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,806
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-29-C1

APPLICANT: PADMAPRIYA, BANDA PADMANABHA
APPLICANT: RAMESH, AIYAGARI
APPLICANT: CHANDRASHEKAR, ARUN
APPLICANT: CHAKRAVARTHY, MANDYAM
TITLE OF INVENTION: PRIMERS FOR DETECTING FOOD POISONING BACTERIA AND A USE
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 501303-2002
CURRENT APPLICATION NUMBER: US/10/951,225
CURRENT FILING DATE: 2004-09-27
PRIOR APPLICATION NUMBER: PCT/IB02/01150
PRIOR FILING DATE: 2002-03-26
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 5
LENGTH: 257
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-951-225-5
Query Match 82.6%; Score 1023; DB 5; Length 257;
Best Local Similarity 82.0%; Pred. No. 3.7e-85;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKSSELQARNLSNLROIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKKSSELQALGNLQIYYNEKAKTENKESHDPLOHTILFKGFFTD 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKKVPINLWDGKQTTPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
Db 145 EEKKVPINLWDGKQNTVPLETVKTKNKNVTVOELDLQARRYLQEKYNYNSDVFDGKVQ 204
QY 181 RGLIVPHSSSGSTVSYDLFDAQOQYPTLRIYRDNKTINSENHLDLYLTT 233
Db 205 RGLIVFHTSTEPSVNYDLFQAQOQSYNTLLRIYRDNKTINSENHLDIYLYTS 257
RESULT 18
US-10-354-948-4
; Sequence 4, Application US/10354948
; Publication No. US20030202962A1
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; Elmellie, Robyn E.
; Potex, Terence A.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/354,948
; FILING DATE: 29-Jan-2003
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,806
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-29-C1

```

;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-354-948-4

Query Match
Best Local Similarity 82.3%; Score 1019; DB 4; Length 233;
Matches 190; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 61
DB 2 EKSEINEKDLRKSELQNALGNLQIYYNEKAKTENKESHQDQLQHTILFKGFFTDH 61

QY 62 PWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
DB 62 SWYNDLLVDFDSKDIVDKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121

QY 122 EKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGKVOR 181
DB 122 EKKVPINLWLDGKQNTVPLETVTNKKNVTVOELDQARHYLQEKYLNLYNSDVFDGKVOR 181

QY 182 GLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHLDLYLYTT 233
DB 182 GLIVFHTSTEPSVNYDLFGAQGQSNLTLLRIYRDNKTINSENHLDIYLYTS 233

RESULT 19
US-09-870-759-8
; Sequence 8, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-8

Query Match
Best Local Similarity 81.8%; Score 1013; DB 3; Length 257;
Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELQNALGNLQIYYNEKAKTENKESHQDQLQHTILFKGFFTN 84

QY 61 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDIVDKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 121 EKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGKVQ 180
DB 145 EKKVPINLWLDGKQNTVPLETVTNKKNVTVOELDQARHYLQEKYLNLYNSDVFDGKVQ 204

QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHLDLYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQGQSNLTLLRIYRDNKTINSENHLDIYLYTS 257

RESULT 20
US-09-751-708A-8
; Sequence 8, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-8

Query Match
Best Local Similarity 81.5%; Score 1013; DB 3; Length 257;
Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELQNALGNLQIYYNEKAKTENKESHQDQLQHTILFKGFFTN 84

QY 61 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDIVDKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 121 EKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGKVQ 180
DB 145 EKKVPINLWLDGKQNTVPLETVTNKKNVTVOELDQARHYLQEKYLNLYNSDVFDGKVQ 204

QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHLDLYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQGQSNLTLLRIYRDNKTINSENHLDIYLYTS 257

RESULT 21
US-10-428-817A-4
; Sequence 4, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-4
```

Query Match 81.8%; Score 1013; DB 4; Length 257;
Best Local Similarity 81.5%; Pred. No. 3.1e-84;
Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSELOALNLSRLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKSELOALNLSRLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVQ 204
QY 181 RGLIVHSSGSGTVSDVLDFAQOQYPTLLRIYRDKNKTINSENHLDLYLTT 233
DB 205 RGLIVHSTSTPSVNYDLFGAQQNSNTLLRIYRDKNKTINSENHLDLYLTS 257

RESULT 22
US-10-937-758A-8
; Sequence 8, Application US/10937758A
; Publication No. US20050112141A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: FILE REFERENCE 650884
; CURRENT APPLICATION NUMBER: US/10/937,758A
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: 09/650,884
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-937-758A-8

Query Match 81.8%; Score 1013; DB 5; Length 257;
Best Local Similarity 81.5%; Pred. No. 3.1e-84;
Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSELOALNLSRLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKSELOALNLSRLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVQ 204
QY 181 RGLIVHSSGSGTVSDVLDFAQOQYPTLLRIYRDKNKTINSENHLDLYLTT 233
DB 205 RGLIVHSTSTPSVNYDLFGAQQNSNTLLRIYRDKNKTINSENHLDLYLTS 257

RESULT 23
US-10-002-784A-2
; Sequence 2, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A

; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 2
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant staphylococcal enterotoxin A periplasmic
US-10-002-784A-2

Query Match 80.8%; Score 1000; DB 4; Length 257;
Best Local Similarity 80.7%; Pred. No. 4.7e-83;
Matches 188; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSELOALNLSRLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKSELOALNLSRLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVQ 204
QY 181 RGLIVHSSGSGTVSDVLDFAQOQYPTLLRIYRDKNKTINSENHLDLYLTT 233
DB 205 RGLIVHSTSTPSVNYDLFGAQQNSNTLLRIYRDKNKTINSENHLDLYLTS 257

RESULT 24
US-10-767-687-2
; Sequence 2, Application US/10767687
; Publication No. US20050064526A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent A
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/767,687
; FILING DATE: 29-Jan-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

```

;
; LENGTH: 257
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-767-687-2

Query Match      80.8%; Score 1000; DB 5; Length 257;
Best Local Similarity 80.7%; Pred. No. 4.7e-83;
Matches 188; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKSELOQNALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELOQNALSNLRQIYYNEKAITENKESDDQPROHTILFKGFTH 84
Qy 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTAQMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVRFDSKOIVDKYKGGKVDLYGAYAGYQCAGGTPNKTAQMYGGVTLHDNNRLT 144
Qy 121 EKKVPINLWIDGKQTTPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EKKVPINLWLDGKQNTVPLETVKTKNKNVTVOELDLQARRYLQEKYKLYNSDVFQKVQ 204
Qy 181 RGLIVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDNKTINSENHLHIDLILYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFQAQGYSNLTLLRIYRDNKTINSENMHIDIYLYTS 257
```

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RESULT 25
US-10-002-784A-4
; Sequence 4, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 4
; LENGTH: 233
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant staphylococcal enterotoxin A cytoplasmic
US-10-002-784A-4
```

```

Query Match      80.5%; Score 996; DB 4; Length 233;
Best Local Similarity 80.6%; Pred. No. 9.7e-83;
Matches 187; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

Qy 2 EKSEINEKDLRKSELOQNALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFFTGH 61
Db 2 EKSEINEKDLRKSELOQNALSNLRQIYYNEKAITENKESDDQPROHTILFKGFTH 61
Qy 62 PWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTAQMYGGVTLHDNNRLTE 121
Db 62 SWYNDLLVRFDSKOIVDKYKGGKVDLYGAYAGYQCAGGTPNKTAQMYGGVTLHDNNRLTE 121
Qy 122 EKKVPINLWIDGKQTTPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 181
Db 122 EKKVPINLWLDGKQNTVPLETVKTKNKNVTVOELDLQARRYLQEKYKLYNSDVFQKVQ 181
Qy 182 GLIVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDNKTINSENHLHIDLILYTT 233
Db 182 GLIVFHTSTEPSVNYDLFQAQGYSNLTLLRIYRDNKTINSENMHIDIYLYTS 233
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RESULT 26
US-10-767-687-4
; Sequence 4, Application US/10767687
; Publication No. US20050064526A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent A
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/767,687
; FILING DATE: 29-Jan-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-767-687-4
```

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Query Match      80.5%; Score 996; DB 5; Length 233;
Best Local Similarity 80.6%; Pred. No. 9.7e-83;
Matches 187; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

Qy 2 EKSEINEKDLRKSELOQNALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFFTGH 61
Db 2 EKSEINEKDLRKSELOQNALSNLRQIYYNEKAITENKESDDQPROHTILFKGFTH 61
Qy 62 PWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTAQMYGGVTLHDNNRLTE 121
Db 62 SWYNDLLVRFDSKOIVDKYKGGKVDLYGAYAGYQCAGGTPNKTAQMYGGVTLHDNNRLTE 121
Qy 122 EKKVPINLWIDGKQTTPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 181
Db 122 EKKVPINLWLDGKQNTVPLETVKTKNKNVTVOELDLQARRYLQEKYKLYNSDVFQKVQ 181
Qy 182 GLIVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDNKTINSENHLHIDLILYTT 233
Db 182 GLIVFHTSTEPSVNYDLFQAQGYSNLTLLRIYRDNKTINSENMHIDIYLYTS 233
```

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RESULT 27
US-10-428-817A-182
; Sequence 182, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
```

APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 38373-189118
CURRENT APPLICATION NUMBER: US/10/428,817A
CURRENT FILING DATE: 2003-05-05
PRIOR APPLICATION NUMBER: US 60/378,988
PRIOR FILING DATE: 2002-05-08
PRIOR APPLICATION NUMBER: US 60/389,366
PRIOR FILING DATE: 2002-06-15
PRIOR APPLICATION NUMBER: US 60/406,697
PRIOR FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: US 60/406,750
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/415,310
PRIOR FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: US 60/415,400
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: US 60/438,686
PRIOR FILING DATE: 2003-01-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn version 3.2
SEQ ID NO 182
LENGTH: 231
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-428-817A-182

Query Match 80.0%; Score 991; DB 4; Length 231;
Best Local Similarity 80.3%; Pred. No. 2.7e-82;
Matches 187; Conservative 18; Mismatches 26; Indels 2; Gaps 1;

QY 1 SEKSEINEKDLRKSELOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKSELOQTA--GNKQIYYNEKAKTENKESHQDQFLOHTILFKGFFTD 58
QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 59 HSWYNLLVDFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 118
QY 121 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 119 EEKVPINLWDGKQNTVPLETKNKNVTVOELDLQARHYLHGKFGLYNSDSFGKQV 178
QY 181 RGLIVFHSSEGSTSVSYDLFDAQOQYPTLLRIYRDNKTINSENHIDLYLYTT 233
DB 179 RGLIVFHTSTEPSVNYDLFGAQOQYSNTLLRIYRDNKSINSENHIDLYLYTS 231

RESULT 28
US-08-882-431-2
Sequence 2, Application US/08882431
Publication No. US20030009015A1
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: John Moran
STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431

FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Moran, John
REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 257
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431-2

Query Match 79.4%; Score 983; DB 2; Length 257;
Best Local Similarity 79.8%; Pred. No. 1.7e-81;
Matches 186; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSEKQCTALGNLKQIYYNEKAKTENKESHQDQFROHTILFKGFFTD 84
QY 61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNLLVDFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 145 EEKVPINLWDGKQNTVPLETKNKNVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204
QY 181 RGLIVFHSSEGSTSVSYDLFDAQOQYPTLLRIYRDNKTINSENHIDLYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQOQYSNTLLRIYRDNKTINSENHIDLYLYTS 257

RESULT 29
US-08-882-431-4
Sequence 4, Application US/08882431
Publication No. US20030009015A1
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: John Moran
STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Moran, John
REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 233
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431-4

Query Match 79.0%; Score 978; DB 2; Length 233;
Best Local Similarity 79.3%; Pred. No. 4.3e-81;
Matches 184; Conservative 17; Mismatches 31; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKSELRNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGH 61
DB 2 EKSEINEKDLRKSELRNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGH 61

QY 62 PWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLTE 121
DB 62 SWYNDLLVDFDSKDIQVVKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLTE 121

QY 122 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQR 181
DB 122 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQR 181

QY 182 GLIVHSSSGSTVSVDLFDAGQYPTLLRIYRDNKTINSENHLDLYLTT 233
DB 182 GLIVFHTSTEPSVNYDLFGAQGSNTLLRIYRDNKTINSENHLDLYLTS 233

RESULT 30
US-10-997-690-11
; Sequence 11, Application US/10997690
; Publication No. US20050153376A1
; GENERAL INFORMATION:
; APPLICANT: FRASER, JOHN DAVID
; APPLICANT: PROF. THOMAS
; TITLE OF INVENTION: SUPERANTIGENS
; FILE REFERENCE: 12669-004001
; CURRENT APPLICATION NUMBER: US/10/997,690
; PRIOR FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: 09/869,136
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: PCT/NZ99/00228
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: NZ 333589
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Streptococcus aureus
US-10-997-690-11

Query Match 74.4%; Score 921; DB 5; Length 227;
Best Local Similarity 79.4%; Pred. No. 6.8e-76;
Matches 185; Conservative 17; Mismatches 25; Indels 6; Gaps 6;

QY 1 SEKSEINEKDLRKSELRNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKSELRNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTN 59

QY 61 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 120
DB 60 HSWYNDLLVDFDSKDIQVVKYKGVLDLYGAYGYQCAGGTPNKTACMY-GVTLHNNRLT 118

QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 119 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 175

QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDNKTINSENHLDLYLTT 233
DB 176 RGLIVFHTSTEPSVNYDLFGAQGSNTLLRIYRDNKTINSENHLDLYLTS 227

RESULT 31
US-10-428-817A-175
; Sequence 175, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 175
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-175

Query Match 67.0%; Score 830; DB 4; Length 268;
Best Local Similarity 64.9%; Pred. No. 1.8e-67;
Matches 150; Conservative 38; Mismatches 43; Indels 0; Gaps 0;

QY 3 KSEINEKDLRKSELRNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGH 62
DB 27 KNETIKEKNLHKKSELSSITLNNLRHIYFPNEKIGSEKIMTEDQFLDYTLFLKSPFISHS 86

QY 63 WYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLTEE 122
DB 87 QYNDLLVDFDSKETVNFKQGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLTYD 146

QY 123 KKVPIINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQRG 182
DB 147 KKVPIINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQRG 206

QY 183 LIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDNKTINSENHLDLYLTT 233
DB 207 LIVFHTSKEPLSVYDLFNVIGQYDPKLLKIYQDNKIISENHLDLYLTS 257

RESULT 32
US-09-870-759-14
; Sequence 14, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128

; Sequence 10, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-10

Query Match 53.6%; Score 663; DB 4; Length 258;
Best Local Similarity 54.5%; Pred. No. 3.2e-52;
Matches 126; Conservative 35; Mismatches 70; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLKKSELQARNLSNRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 26 NENIDSVKELHKKSELSTALNNMKHSYADKNPIIGENKSTGDOFLENTLLYKKFFTD 85
Qy 61 HPWYNLDLVDSKDATNKYKGKVDLYGYAYGYQCAGTGNPKTKACMYGGVTLHDNRLT 120
Db 86 LINFEDLLINFSKEMAQHFKSKNDVYPYRISYCYGEIDRTACTYGGVTPEHGKCLK 145
Qy 121 EEKVPINLWDGQTTPIDIKVTSKEVTVOQLDQARHYLHGKFGLYNSDSFGKVKQ 180
Db 146 ERKKIPINLWINGVQEVSLDKVQTDKNVTVOQLDAQARRYLOKDLKLYNNDTLGGKI 205
Qy 181 RGLIVFSSSEGTVSYDLFDAQQYPTDLLRIYRDKNKTINSENHLIDLILY 231
Db 206 RGKIEFDSDSGSVYDLDFVKGDPPEKQLRIYSNDKNTLSTEHLHIDIYL 256

RESULT 35
US-10-428-817A-187
; Sequence 187, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02


```

; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 173
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-173

Query Match      29.6%; Score 366; DB 4; Length 217;
Best Local Similarity 37.9%; Pred. No. 3.7e-25;
Matches 85; Conservative 46; Mismatches 81; Indels 12; Gaps 7;

QY      10 KDLRKSELQNALNLRQIYYNEKAITENKESDDOFLNTLLFKGFTGHPWYNDLLV 69
Db      1 EDLHDKSELTDLALAN--AYGOYNHPFIKENIKSDEISGEKDLIFRN--QGDSG-NDLRV 55

QY      70 DLGSKDATNKYKGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINL 129
Db      56 KPATADLAQKFNKNVDIYGASFYKCEKISENSECLYGGTTL-NSEKLAQERVIGANV 114

QY      130 WIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQORGLIYVHSS 189
Db      115 WVDGIQKETEL--IRTNKNVTQLQELDIKIRKILSDKYKIYYKDS---EISKGLIEFDMK 169

QY      190 EGSTVSYDLFDAQGOVPTDLLRIYRDNKTINSENL-HIDLXYLT 232
Db      170 TPRDYSFDIYDLKGENDYEIDKIYEDNKTILKSDDISHDVNLVT 213

RESULT 42
US-09-900-766-6
; Sequence 6, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0:10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Staphylococcus sp.
US-09-900-766-6

Query Match      29.6%; Score 366; DB 3; Length 217;
Best Local Similarity 37.9%; Pred. No. 3.7e-25;
Matches 85; Conservative 46; Mismatches 81; Indels 12; Gaps 7;

QY      10 KDLRKSELQNALNLRQIYYNEKAITENKESDDOFLNTLLFKGFTGHPWYNDLLV 69
Db      1 EDLHDKSELTDLALAN--AYGOYNHPFIKENIKSDEISGEKDLIFRN--QGDSG-NDLRV 55

QY      70 DLGSKDATNKYKGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINL 129
Db      56 KPATADLAQKFNKNVDIYGASFYKCEKISENSECLYGGTTL-NSEKLAQERVIGANV 114

QY      130 WIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQORGLIYVHSS 189
Db      115 WVDGIQKETEL--IRTNKNVTQLQELDIKIRKILSDKYKIYYKDS---EISKGLIEFDMK 169

QY      190 EGSTVSYDLFDAQGOVPTDLLRIYRDNKTINSENL-HIDLXYLT 232
Db      170 TPRDYSFDIYDLKGENDYEIDKIYEDNKTILKSDDISHDVNLVT 213

RESULT 43
US-10-428-817A-173
; Sequence 173, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
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; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 173
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-173

Query Match      29.6%; Score 366; DB 4; Length 217;
Best Local Similarity 37.9%; Pred. No. 3.7e-25;
Matches 85; Conservative 46; Mismatches 81; Indels 12; Gaps 7;

QY      10 KDLRKSELQNALNLRQIYYNEKAITENKESDDOFLNTLLFKGFTGHPWYNDLLV 69
Db      1 EDLHDKSELTDLALAN--AYGOYNHPFIKENIKSDEISGEKDLIFRN--QGDSG-NDLRV 55

QY      70 DLGSKDATNKYKGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINL 129
Db      56 KPATADLAQKFNKNVDIYGASFYKCEKISENSECLYGGTTL-NSEKLAQERVIGANV 114

QY      130 WIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQORGLIYVHSS 189
Db      115 WVDGIQKETEL--IRTNKNVTQLQELDIKIRKILSDKYKIYYKDS---EISKGLIEFDMK 169

QY      190 EGSTVSYDLFDAQGOVPTDLLRIYRDNKTINSENL-HIDLXYLT 232
Db      170 TPRDYSFDIYDLKGENDYEIDKIYEDNKTILKSDDISHDVNLVT 213

RESULT 44
US-10-474-792-416
; Sequence 416, Application US/10474792
; Publication No. US20040236072A1
; GENERAL INFORMATION:
; APPLICANT: Olmsted, Stephen
; APPLICANT: Zagursky, Robert
; APPLICANT: Nickbarg, Elliot
; APPLICANT: Winter, Lourie
; TITLE OF INVENTION: SURFACE PROTEINS OF STREPTOCOCCUS PYOGENES
; FILE REFERENCE: AM 100399
; CURRENT APPLICATION NUMBER: US/10/474,792
; CURRENT FILING DATE: 2003-10-14
; NUMBER OF SEQ ID NOS: 674
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 416
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-474-792-416

Query Match      27.7%; Score 343.5; DB 5; Length 259;
Best Local Similarity 34.1%; Pred. No. 5.3e-23;
Matches 78; Conservative 44; Mismatches 84; Indels 23; Gaps 6;

QY      17 ELQNALNLRQIYYNEKAITENKESDDOFLNTLLFKGFTGHPWYN---DLLYDLGS 73
Db      34 EMSGVGVINLRNLVSTYDTEVKGKINEGPPFSGSLFYKNI-----PYGNSSIELKVELNS 89

QY      74 KDATNKYKGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDG 133
Db      90 VEKANPFSGKRVDFITLTPSPCNSNIKNKS---YGGITLSDGNRI-DKKNIPVNFIDG 145

QY      134 ---KQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLY-----NSDSFGGKVOR 181
Db      146 VOOKYSYTDISTVSTDKKEVTQELDVKSKRYLQKHFNIFYGFGDKDFGRSSRFQSGFEE 205
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QY 25 NLRQIYYNEKAITENK--ESDDQFLENTLLFKGFTGHPWYNDDLVLVLDGSKDATNKYKG 82
Db 28 NLRN--YGSYPTEDHQSPENPNHLSHQLVFS-----MDNSTVTAEFKNVDDVKKFKN 79
QY 83 KKVLDLYGAYGYQACAGTGNKTAACMYGGVTLHDNNRLTEBKVPINLWIDGKQTTPIDK 142
Db 80 HAVDVVGLSYGVCL-----KNKYIYGGVTL-AGDYLEKSRRIPIPINLWNGEHOQTISTDK 133
QY 143 VYTSKKEVTVOELDLQARHYLHGKFGLY-----NSDSFGKQVQORGLIVPHSSE 190
Db 134 VSTNKKLVTAQEIDTKLRRYLOBEVNIYGFNDTKGRNYGNKSKFSSGFGNAGKILPHLD 193
QY 191 GSTVSVDLDAQGOYPTDLLRIYRDNKTINSENHLIDL 228
Db 194 GGSFSYDLPTGTGQAESFLKIYNDKNKTETEFKFLDV 231

RESULT 48
US-10-428-817A-172
; Sequence 172, Application US/104288917A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US 10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2003-05-05
; CURRENT APPLICATION NUMBER: US 10/428,817A
; FILE REFERENCE: 38373-189118
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; APPLICANT: TERMAN, David S
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US 10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 172
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-172

Query Match 25.8%; Score 319.5; DB 4; Length 242;
Best Local Similarity 33.8%; Pred. No. 7.6e-21;
Matches 76; Conservative 35; Mismatches 71; Indels 43; Gaps 8;

QY 25 NLRQIY--YNEK--AITENKESDDQFLENTLLFKGFTGHPWYNDDLVLVLDGSKDATNKY 80
Db 32 NLRFNFAVYQPEKLQGVSSGNFSTSHLE---YIDKYLTSQFH-----NEY 76
QY 81 KGK-----KVDLYGAYGYQACAGTGNKTAACMYGGVTLHDNNRLTEBKVPINLWIDGKQ 135
Db 77 EAKRLKDHKVDIFGISYGLC-----NTKMYGGITLANQN-LDKPRNIPINLWVNGKQ 129
QY 136 TVVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYN-----SDSFGKQVQORGL 183
Db 130 NVISTDKVTSQKKEVTAQEIDIKRLYQNEVNIYGFNFKTKGQEGYKSKFNSGPNKKG 189
QY 184 IVFHSSEGSTVSVDLDAQGOYPTDLLRIYRDNKTINSENHLIDL 228
Db 190 IYFHLNNEPSFYDLYFTGTGQAESFLKIYNDKNKTIDAENFHLDV 234

RESULT 49
US-10-428-817A-176
```

```
; Sequence 176, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US 10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 176
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-176

Query Match 25.0%; Score 310; DB 4; Length 242;
Best Local Similarity 33.2%; Pred. No. 5.6e-20;
Matches 74; Conservative 39; Mismatches 76; Indels 34; Gaps 9;

QY 23 LSNLRQIY----YNEKAITENKESDDQFLENTLLFKGFTGHPWYNDDLVLVLDGSKDATN 78
Db 29 IDNLRFNFTKDFINLKDVKDN---DTPIANQLQF-----SNESY-DLISESKDFNKFS 78
QY 79 KYGKGVLDLYGAYGYQACAGTGNKTAACMYGGVTLHDNNRLTEBKVPINLWIDGKQTTV 138
Db 79 NFKGKKLDVFGISYNGQC-----NTKIYGGITA-TNEYLDKPRNIPINIWINGNHKTI 131
QY 139 PIDKVKTSKKEVTVOELDLQARHYLHGKFGLY-----NSDSFGKQ-----VQORGLIV 186
Db 132 STNKYSTNKKFVTAQEIDIKRLRYLQEEVNIYGHNGTKKGEEYGHKSKFYSGFNICKVTF 191
QY 187 HSSEGSTVSVDLP-DAQGOYPTDLLRIYRDNKTINSENHLIDL 228
Db 192 HLNNNDTFSYDLFTYTGDDGLPKSFLKIYEDNKTVESEKPHLDV 234

RESULT 50
US-09-870-759-10
; Sequence 10, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US 09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-10

Query Match 24.3%; Score 300.5; DB 3; Length 266;
Best Local Similarity 33.6%; Pred. No. 4.7e-19;
```



```
Qy 230 LYT 232
Db 234 LYT 236

RESULT 56
US-09-150-947B-12
; Sequence 12, Application US/09150947B
; Patent No. US2002028211A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Arad, Gila
; TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS
; FILE OF INVENTION: ANTAGONISTS AND VACCINES
; FILE REFERENCE: A31967-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/150,947B
; CURRENT FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/IL97/00438
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: ISRAEL 119938
; PRIOR FILING DATE: 1996-12-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-150-947B-12

Query Match 24.2%; Score 299.5; DB 3; Length 239;
Best Local Similarity 33.7%; Pred. No. 5e-19;
Matches 82; Conservative 46; Mismatches 96; Indels 19; Gaps 8;

Qy 2 EKSEINEKDLRKKSQELQNALSNLROIYYNEKAITENKESDDQFLNTLLPKGPFTH 61
Db 1 ESQDPKPDELHKSSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
Qy 62 PWYNDLLVLGSKDATNKYKGGKVDLYGAYGYQC-----AGTPNKTAACMYGGV 111
Db 59 GNYDNVRVEPKNLDADKYDKYDVFEGANYYYQCYFSKKTNDINSHETDKRKTCTMYGGV 118
Qy 112 TLHDNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYN 171
Db 119 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHYLVKNKKLYE 176
Qy 172 SDSFGGKVORGLIVFHSSEGSTVSVDLFDAGQGYPD--TLLRIYRDNKTINSENHLDLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMMPAGDKFDQSKYLMYNDNKNVDSKDKVIEVY 233
Qy 230 LYT 232
Db 234 LYT 236

RESULT 57
US-10-172-425B-12
; Sequence 12, Application US/10172425B
; Publication No. US20030147908A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Arad, Gila
; TITLE OF INVENTION: BROAD SPECTRUM ANTAGONISTS AND VACCINES
; FILE OF INVENTION: DIRECTED AGAINST PYROGENIC EXOTOXINS
; FILE REFERENCE: A31967-PCT-USA-A 066031.0164
; CURRENT APPLICATION NUMBER: US/10/172,425B
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: 09/150,947
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/IL97/00438
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: ISRAEL 119938
; PRIOR FILING DATE: 1996-12-30
; NUMBER OF SEQ ID NOS: 57

Qy 2 EKSEINEKDLRKKSQELQNALSNLROIYYNEKAITENKESDDQFLNTLLPKGPFTH 61
Db 1 ESQDPKPDELHKSSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
Qy 62 PWYNDLLVLGSKDATNKYKGGKVDLYGAYGYQC-----AGTPNKTAACMYGGV 111
Db 59 GNYDNVRVEPKNLDADKYDKYDVFEGANYYYQCYFSKKTNDINSHETDKRKTCTMYGGV 118
Qy 112 TLHDNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYN 171
Db 119 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHYLVKNKKLYE 176
Qy 172 SDSFGGKVORGLIVFHSSEGSTVSVDLFDAGQGYPD--TLLRIYRDNKTINSENHLDLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMMPAGDKFDQSKYLMYNDNKNVDSKDKVIEVY 233
Qy 230 LYT 232
Db 234 LYT 236

RESULT 58
US-10-525-113-1
; Sequence 1, Application US/10525113
; Publication No. US2005024009A1
; GENERAL INFORMATION:
; APPLICANT: MERCK PATENT GMBH
; APPLICANT: CARR, Francis J.
; APPLICANT: BAKER, Matthew
; APPLICANT: CARTER, Graham
; TITLE OF INVENTION: T-CELL EPITOPES IN STAPHYLOCOCCAL
; FILE OF INVENTION: ENTEROTOXIN B
; FILE REFERENCE: MER-138
; CURRENT APPLICATION NUMBER: US/10/525,113
; PRIOR FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: PCT/EP2003/009116
; PRIOR FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: EP 02018229.1
; PRIOR FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-525-113-1

Query Match 24.2%; Score 299.5; DB 5; Length 239;
Best Local Similarity 33.7%; Pred. No. 5e-19;
Matches 82; Conservative 46; Mismatches 96; Indels 19; Gaps 8;

Qy 2 EKSEINEKDLRKKSQELQNALSNLROIYYNEKAITENKESDDQFLNTLLPKGPFTH 61
Db 1 ESQDPKPDELHKSSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
Qy 62 PWYNDLLVLGSKDATNKYKGGKVDLYGAYGYQC-----AGTPNKTAACMYGGV 111
Db 59 GNYDNVRVEPKNLDADKYDKYDVFEGANYYYQCYFSKKTNDINSHETDKRKTCTMYGGV 118
Qy 112 TLHDNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYN 171
Db 119 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHYLVKNKKLYE 176
Qy 172 SDSFGGKVORGLIVFHSSEGSTVSVDLFDAGQGYPD--TLLRIYRDNKTINSENHLDLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMMPAGDKFDQSKYLMYNDNKNVDSKDKVIEVY 233
Qy 230 LYT 232
Db 234 LYT 236
```

Qy	172	SDSFGKVGORGLIVFHSSGEGSTVSDLPDAQGPDP--TLRLIYRDNKTINSENHLIDLY	229
		:: :: :: :: :: :: ::	
Db	177	FNN--SPYETGYIKFTENENS-FWYDMPAPGDKPFDQSKYLLMMYNDNRKWDSDKDVLEVY	233
Qy	230	LYT	232
Db	234	LTT	236

RESULT 59
 US-10-428-817A-163
 ; Sequence 163, Application US/10428817A
 ; Publication No. US20040214783A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TERMAN, David S
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
 ; FILE REFERENCE: 38373-189118
 ; CURRENT APPLICATION NUMBER: US/10/428,817A
 ; CURRENT FILING DATE: 2003-05-05
 ; PRIOR APPLICATION NUMBER: US 60/378,988
 ; PRIOR FILING DATE: 2002-05-08
 ; PRIOR APPLICATION NUMBER: US 60/389,366
 ; PRIOR FILING DATE: 2002-06-15
 ; PRIOR APPLICATION NUMBER: US 60/406,697
 ; PRIOR FILING DATE: 2002-08-28
 ; PRIOR APPLICATION NUMBER: US 60/406,750
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/415,310
 ; PRIOR FILING DATE: 2002-10-01
 ; PRIOR APPLICATION NUMBER: US 60/415,400
 ; PRIOR FILING DATE: 2002-10-02
 ; PRIOR APPLICATION NUMBER: US 60/438,686
 ; PRIOR FILING DATE: 2003-01-09
 ; NUMBER OF SEQ ID NOS: 224
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 163
 ; LENGTH: 251
 ; TYPE: PR1
 ; ORGANISM: Streptococcus pyogenes
 US-10-428-817A-163

Query Match	23.9%	Score 295.5;	DB 4;	Length 251;
Best Local Similarity	34.2%;	Pred. No. 1.2e-18;		
Matches 81;	Conservative 45;	Mismatches 92;	Indels 19;	Gaps 10;
Qy	4	SEETNEKDLRKSLSQNAL--SNLRQIYY-VNERAIT-ENKESDDQFLENTLLFKGFFTG	60	
Db	25	SQEVFAQDDPPSQLRHSSLVKNLNIYFLYEGDPVTHENVKSDQLLSHDLIYN--VS	81	
Qy	61	HPWYNDLLVLGSKDAKNYKGGKVDLYGAYGYQC-AGGTPNKTACWGGVTLHDNNRL	119	
Db	82	GPNYDKLKTENQEMATLFDKDKNDVIYGVVEYHLCYLCENASRACIYGGVTNHEGNHL	141	
Qy	120	TEEKVPINLWIDCKQTTPVTDVKYTSKKEVTVCQELDQARHYLHGKFLGYNDSDFGKV	179	
Db	142	EIPKIVVKSIDIGQ-SLSFD-IETNKKWTAQELDKVKRYLTDNKKQLYTNP--SKY	197	
Qy	180	QRGLIVFHSSEGSTVSYDLFD- ---AQQYPTDTLLRIYRNKNTINSNLHIDLXYLT	232	
Db	198	ETGYIKFIPKNKESFWDFPEPEFTOSKY- ---LMYKNETLDSNTSQIEVLVLT	250	

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RESULT 60
US-08-973-391A-13
; Sequence 13, Application US/08973391A
; Publication No. US20020054897A1
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggianni, Manuela
; APPLICANT: Stoeck, Jennifer
; APPLICANT: Ohlendorf, Douglas
; TITLE OF INVENTION: MUTANTS OF USE

```

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; FILE REFERENCE: 600.311USWO
; CURRENT APPLICATION NUMBER: US/08/973.391A
; CURRENT FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 251
; TYPE: ERT
; ORGANISM: Streptococcus pyogenes
US-08-973-391A-13

Query Match      23.8%; Score 294.5; DB 2; Length 251;
Best Local Similarity 34.2%; Pred.No.1.5e-18;
Matches 81; Conservative 45; Mismatches 92; Indels 19; Gaps 10

Qy    4 SEEINEKDLRKSELRNAL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG 60
Db    25 SQEYFAQQDPSPQLHRSSLVKNLQNIFYEGDVPVTHENVKSVDQLLSHHLIYN--VS 81

Qy    61 HPWYNDLLVLGSKDAKNKYKKVLDLYGAYGYQC-AGGTPNKTCACYGVTUHDNNRL 119
Db    82 GPNYDKLKTELKNGEMATFLKDKNVDIYGVVEYHLCYLCAERASACTYGGVTNHEGNHL 141

Qy    120 TEKKVPINLWDCKOTTVPIDVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKV 179
Db    142 EIPKKIVVKVISIDIG-QSLSFD-IETNKKMWTAEGLDYKVRKYLTUDNKKQLTNGP--SKY 197

Qy    180 QRGLIVFHSSSEGSTSVSYDLFD---AQOQPDTLLRIYRDNKTINSNLHIDLXYLT 232
Db    198 ETGYIKPIPKNKSEFWDFPEPEFTOSKY----LMYKONETLSDNTSQIEVLTT 250

RESULT 61
US-09-308-830-13
; Sequence 13, Application US/09308830
; Publication No. US20020086813A1
; GENERAL INFORMATION:
; APPLICANT: Regents of the University of Minnesota
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould P.C.
; STREET: P.O. Box 2903
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402-0903
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-SEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/308,830
; FILING DATE: 04-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/22228
; FILING DATE: 05-DEC-1997
; APPLICATION NUMBER: 60/032,930
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Skoog, Mark T
; REGISTRATION NUMBER: 40,178
; REFERENCE/DOCKET NUMBER: 600.346USWO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081

```



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; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431-16

Query Match      23.4%; Score 289.5; DB 2; Length 251;
Best Local Similarity 33.8%; Pred. No. 4.4e-18;
Matches 80; Conservative 45; Mismatches 93; Indels 19; Gaps 10;

QY 4 SEINEKDLRKSELOARNL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG 60
Db 25 SQEVFAQQDPDPQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYN---VS 81
QY 61 HPWNDDLVDLGSKDATNKYKGKVDLYGAYGYQC-AGGTPNKTCACMYGGVTLHNNRL 119
Db 82 GPNYDKLKTTELKQEMATLFDKKNVDIYGVYYHLCYLCENASACIYGGVTNHEGNHL 141
QY 120 TEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKV 179
Db 142 EIPKIVVKVSDIGIQ-SLSFD-IETNKMVTAQELDYKVKRYLTDNKQLYTNGP--SKY 197
QY 180 ORGLIVFHSSEGSTVSVDLFD----AQGYPTDLLRIYRDNKTINSNLHIDLVLVT 232
Db 198 ETGVKIPKPKESFWDFPFPEFTQSKY----LMIYKDNETLDSNTSQIEVLVLT 250

RESULT 67
US-10-002-784A-16
; Sequence 16, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 16
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: streptococcal pyrogenic exotoxin-A mutant
US-10-002-784A-16

Query Match      23.4%; Score 289.5; DB 4; Length 251;
Best Local Similarity 33.8%; Pred. No. 4.4e-18;
Matches 80; Conservative 45; Mismatches 93; Indels 19; Gaps 10;

QY 4 SEINEKDLRKSELOARNL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG 60
Db 25 SQEVFAQQDPDPQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYN---VS 81
QY 61 HPWNDDLVDLGSKDATNKYKGKVDLYGAYGYQC-AGGTPNKTCACMYGGVTLHNNRL 119
Db 82 GPNYDKLKTTELKQEMATLFDKKNVDIYGVYYHLCYLCENASACIYGGVTNHEGNHL 141
QY 120 TEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKV 179
Db 142 EIPKIVVKVSDIGIQ-SLSFD-IETNKMVTAQELDYKVKRYLTDNKQLYTNGP--SKY 197
QY 180 ORGLIVFHSSEGSTVSVDLFD----AQGYPTDLLRIYRDNKTINSNLHIDLVLVT 232
Db 198 ETGVKIPKPKESFWDFPFPEFTQSKY----LMIYKDNETLDSNTSQIEVLVLT 250

RESULT 68
US-10-767-687-16
; Sequence 16, Application US/10767687
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; Publication No. US20050064526A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavazi
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US ATMY MMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent A
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/767,687
; FILING DATE: 29-Jan-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-767-687-16

Query Match      23.4%; Score 289.5; DB 5; Length 251;
Best Local Similarity 33.8%; Pred. No. 4.4e-18;
Matches 80; Conservative 45; Mismatches 93; Indels 19; Gaps 10;

QY 4 SEINEKDLRKSELOARNL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG 60
Db 25 SQEVFAQQDPDPQLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYN---VS 81
QY 61 HPWNDDLVDLGSKDATNKYKGKVDLYGAYGYQC-AGGTPNKTCACMYGGVTLHNNRL 119
Db 82 GPNYDKLKTTELKQEMATLFDKKNVDIYGVYYHLCYLCENASACIYGGVTNHEGNHL 141
QY 120 TEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKV 179
Db 142 EIPKIVVKVSDIGIQ-SLSFD-IETNKMVTAQELDYKVKRYLTDNKQLYTNGP--SKY 197
QY 180 ORGLIVFHSSEGSTVSVDLFD----AQGYPTDLLRIYRDNKTINSNLHIDLVLVT 232
Db 198 ETGVKIPKPKESFWDFPFPEFTQSKY----LMIYKDNETLDSNTSQIEVLVLT 250

RESULT 69
US-10-002-784A-10
; Sequence 10, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
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; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 10
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant staphylococcal enterotoxin B cytoplasmic
US-10-002-784A-10

Query Match                23.3%; Score 288.5; DB 4; Length 239;
Best Local Similarity      33.9%; Pred.No. 5.1e-18;
Matches 80; Conservative 45; Mismatches 88; Indels 23; Gaps 8;

Qy 14 KXSELQRNA-----LSNLRIQIYYNEKAITENKESDDQPLENTLLPKGFPTHGHPWYNDLL 68
Db 7 KPDELHKKSSFTGLMKNKNKVLVDDNHVSAL-NVKSIDQFRYFDLIYSIKDTKLGINDVR 65

Qy 69 VDLGSKDANKYKGGKVDLYGAYGYQCAGS-----TPNKTCAMYGGVTLHDNNR 118
Db 66 VEFKGNKDLADKYDKYVDVDFGANAYYQCAFSKKTNDINSHTDKRKTMYGGVTEHNGQ 125

Qy 119 LTEKKVPINLWDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGK 178
Db 126 LDKYRSITVAVFEDGK-NLLSFD-VQTNKKKVTQAELDYLTRHYLVKNKKLYEFNN--SP 181

Qy 179 VORGLIVFHSESGSTVSYDLFDAGQGYD--TLLRIYRDNKTINSENHLIDLYLT 232
Db 182 YETGYIKFIEINENS-FYDMMWPAQDFDQSKYLMYNDKNWVDSKDVKEIVLTT 236

RESULT 70
US-10-767-687-10
; Sequence 10, Application US/10767687
; Publication No. US20050064526A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent A
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/767,687
; FILING DATE: 29-Jan-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714

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Db 127 NLQNLVRVY-ENKRNITSEF-VQTDKSVTAQELDIKARNFLINKKNLYEFNS--SPYE 182

Qy 181 RGLIVFHSSEGSTVSYDLFDAQGYPD--TLRLRYRDNKTINSENHLIDLVLVT 232

Db 183 TGYIKFIENNGNTFYQDMMAPAGDKFDQSKYLMYNDNKTVDKSVKIEVHLTT 236

RESULT 72

US-08-882-431-10

Sequence 10, Application US/08882431

Publication No. US20030009015A1

GENERAL INFORMATION:

APPLICANT: Robert G. Ulrich,

APPLICANT: Mark A. Olson

APPLICANT: Sina Bavari

TITLE OF INVENTION: Bacterial Superantigen

TITLE OF INVENTION: Vaccines

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: John Moran

STREET: US Army MPMC -504 Scott Street MCMR-JA (John Moran-Patent Atty)

CITY: FORT DETRICK

STATE: MARYLAND

COUNTRY: USA

ZIP: 21702-5012

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.5

SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/882,431

FILING DATE: June 25, 1997

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Moran, John

REGISTRATION NUMBER: 26,313

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 619-2065

TELEFAX: (301) 619-7714

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 239

TYPE: Amino Acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

MOLECULE TYPE: Peptide

US-08-882-431-10

Query Match 23.2%; Score 287.5; DB 2; Length 239;

Best Local Similarity 33.9%; Pred. No. 6.3e-18;

Matches 80; Conservative 45; Mismatches 88; Indels 23; Gaps 8;

Qy 14 KXSELORNA-----LSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLL 68

Db 7 KPDELHSSKFTGKMNKMYLDNHNVSAT-NVKSIDQFRFYDLIYSIKDTKLGNDNVR 65

Qy 69 VDLGSKDATNKYKGGKVDLYGAYGYQAGG-----TPNKTACMYGGVTLHDNNR 118

Db 66 VEFKNKDLADKYDKYVDVFGANAYQCAF-SKKTNDINSHTDKRKTQWYGGVTEHNGNQ 125

Qy 119 LTBEEKVPINLWDGKQTTVPIDKVTSKKEVTQVELDLQARHYLHGKFGLYNSDSFGGK 178

Db 126 LDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTAEQLDYLTRHYLVKDKKLYEFNN--SP 181

Qy 179 VQGLIVFHSSEGSTVSYDLFDAQGYPD--TLRLRYRDNKTINSENHLIDLVLVT 232

Db 182 YETGYIKFIENENS-FWYDMMAPAGDKFDQSKYLMYNDNKMVDSKDVKIEVHLTT 236

RESULT 73

US-10-923-324-6

Sequence 6, Application US/10923324

Publication No. US20050026272A1

GENERAL INFORMATION:

APPLICANT: Bohach, Gregory I.

TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS

FILE REFERENCE: 12136.1USMO

CURRENT APPLICATION NUMBER: US/10/923,324

CURRENT FILING DATE: 2004-08-20

PRIOR APPLICATION NUMBER: US/09/555,115

PRIOR FILING DATE: 2000-08-01

PRIOR APPLICATION NUMBER: PCT/US98/25107

PRIOR FILING DATE: 1998-12-01

PRIOR APPLICATION NUMBER: US 60/067,357

PRIOR FILING DATE: 1997-12-02

NUMBER OF SEQ ID NOS: 66

SOFTWARE: Patent in version 3.1

SEQ ID NO 6

TYPE: PRT

LENGTH: 240

ORGANISM: Staphylococcus aureus

FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (240)..(240)

OTHER INFORMATION: Xaa is unknown.

US-10-923-324-6

Query Match 23.2%; Score 287.5; DB 5; Length 240;

Best Local Similarity 32.1%; Pred. No. 6.3e-18;

Matches 75; Conservative 48; Mismatches 92; Indels 19; Gaps 9;

Qy 11 DLRKSELQORNALSRLRQIYYNEKAITENK-ESDDQFLENTLLFKGFFTGHPWYNDLLV 69

Db 10 DLHKSFP-TGTGNMK--YLDDHYVSATKVSVDKFLAHLDIYINISDKRLKNYKVT 66

Qy 70 DLGSKDATNKYKGGKVDLYGAYGYQ-----AGTTPNKTACMYGGVTLHDNNRLEE 122

Db 67 ELLNEDLAKKYKDEVVDVYGSNYVNCYFSSKDNVCKVTGGKTCMYGGITKHGHNPDNG 126

Qy 123 --KKVPINLWDGKQTTVPIDKVTSKKEVTQVELDLQARHYLHGKFGLYNSDSFGGKVQ 180

Db 127 NLQNLVRVY-ENKRNITSEF-VQTDKSVTAQELDIKARNFLINKKNLYEFNS--SPYE 182

Qy 181 RGLIVFHSSEGSTVSYDLFDAQGYPD--TLRLRYRDNKTINSENHLIDLVLVT 232

Db 183 TGYIKFIENNGNTFYQDMMAPAGDKFDQSKYLMYNDNKTVDKSVKIEVHLTT 236

RESULT 74

US-10-525-113-5

Sequence 5, Application US/10525113

Publication No. US20050240009A1

GENERAL INFORMATION:

APPLICANT: MERCK PATENT GMBH

APPLICANT: CARR, Francis J.

APPLICANT: BAKER, Matthew

APPLICANT: CARTER, Graham

TITLE OF INVENTION: T-CELL EPITOPES IN STAPHYLOCOCCAL

TITLE OF INVENTION: ENTEROTOXIN B

FILE REFERENCE: MER-138

CURRENT APPLICATION NUMBER: US/10/525,113

CURRENT FILING DATE: 2005-02-18

PRIOR APPLICATION NUMBER: PCT/EP2003/009116

PRIOR FILING DATE: 2003-08-18

PRIOR APPLICATION NUMBER: EP 02018229.1

PRIOR FILING DATE: 2002-08-21

NUMBER OF SEQ ID NOS: 84

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5

LENGTH: 239

TYPE: PRT

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Modified enterotoxin protein
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 21, 24, 28
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, or Met
; OTHER INFORMATION: Xaa=Ala, Gly, Pro, or Met
; OTHER INFORMATION: Xaa=Thr, Ala, Asp, Glu, Gly, His, Lys, Asn, Pro,
; OTHER INFORMATION: Gln, Arg, Ser, or Tyr
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 53, 58
; OTHER INFORMATION: Xaa=Ala or Ile
; OTHER INFORMATION: Xaa=His or Leu
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 81
; OTHER INFORMATION: Xaa=Thr, Ala, Asp, Glu, Gly, His, Lys, Asn, Pro,
; OTHER INFORMATION: Gln, Arg, Ser, or Tyr
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 82, 84, 85
; OTHER INFORMATION: Xaa=His or Val
; OTHER INFORMATION: Xaa=Ala, Pro, Gly, or Val
; OTHER INFORMATION: Xaa=Thr, His, or Phe
; US-10-525-113-5

Query Match      23.1%; Score 285.5; DB 5; Length 239;
Best Local Similarity 33.5%; Pred. No. 9.6e-18;
Matches 80; Conservative 43; Mismatches 87; Indels 29; Gaps 9;

QY 14 KKSELORNA-LSNLRQIYYNEKAITE-----NKESDDQFLENTLLFKGFTGHPWYN 65
Db 7 KPDELHKSKFTGLXE---NKKVLXDDNHVSAINVKSIDQFLYFDLIYSXXKDTKXGNYD 62

QY 66 DLLVDLGSKDATNKYKGKKVDLYGAYGYQC-----AGGTENKTACMYGGVTLHD 115
Db 63 NVRVEFNKDLADKYDKKXXDXGANYYYQCYPFSKKTNDINSHQTDKRTKTCMYGGVTEHN 122

QY 116 NNRLTEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSF 175
Db 123 GNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTQAELDYLTRHYLVKNKKLYEFNN- 179

QY 176 GGVQVQGLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNKTINSENHLIDLTYT 232
Db 180 -SPYETGYIKFIENENS-FWYDMMPPAGDKFDQSKYLMYNDNMVDSKDVKIEVYLT 236
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RESULT 75
US-10-923-324-5
; Sequence 5, Application US/10923324
; Publication No. US20050026272A1
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.USWO
; CURRENT APPLICATION NUMBER: US/10/923,324
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/555,115
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC_FEATURE
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; LOCATION: (240)..(240)
; OTHER INFORMATION: Xaa is unknown.
; US-10-923-324-5

Query Match      23.1%; Score 285.5; DB 5; Length 240;
Best Local Similarity 31.3%; Pred. No. 9.6e-18;
Matches 76; Conservative 49; Mismatches 99; Indels 19; Gaps 9;

QY 2 EKSEINEKDLRKKSELQORNALSNLRQIYYNEKAITENK-BSDDOFLENTLLFKGFFTG 60
Db 1 ESQPDPTPDELHKSSEF-TGTWGNMK--LYDDHYVSATKVKSVSKFLAHDLLIYNSDKK 57

QY 61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYGYQC-----AGGTENKTACMYGGVTL 113
Db 58 LKNYDKVKTELLNEDLAKYKDEVVDVYGSNYVNCYFSSKONVGVKVTGKTCMYGKITK 117

QY 114 HDNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLYN 171
Db 118 HEGNHFDNGNLQNLIRVY-ENKRNITISPE-VQTDKKSVTQAELDIKARNFLINKKNLYE 175

QY 172 SDSFGKVQVQGLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNKTINSENHLIDL 229
Db 176 FNS--SPYETGYIKFIENNGNTFYDMMPPAGDKFDQSKYLMYNDNMVDSKRVKIEVH 233

QY 230 LYT 232
Db 234 LIT 236
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Search completed: February 15, 2006, 20:38:35
Job time : 63.958 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 15, 2006, 20:34:56 ; Search time 5.66409 Seconds
(without alignments)
584.618 Million cell updates/sec

Title: US-09-900-766-7

Perfect score: 1238

Sequence: 1 SERSEINEKURKSELOR.....RDNKTINSENHLIDLYTT 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 107799 seqs, 14211699 residues

Total number of hits satisfying chosen parameters: 107799

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications AA_New.*

1: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB pep.*

2: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB pep.*

3: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB pep.*

4: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB pep.*

5: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB pep.*

6: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB pep.*

7: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB pep.*

8: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1019	82.3	233	7	US-11-022-562-226
2	111.5	9.0	443	6	US-10-793-626-1860
3	94.5	7.6	402	6	US-10-485-517-422
4	89	7.2	171	6	US-10-793-626-1074
5	84.5	6.8	228	6	US-10-793-626-1166
6	84.5	6.8	579	7	US-11-045-802-33
7	83.5	6.7	752	6	US-10-793-626-1138
8	82.5	6.7	361	6	US-10-485-517-125
9	82.5	6.7	361	6	US-10-485-517-295
10	82	6.6	584	7	US-11-045-802-31
11	81.5	6.6	313	6	US-10-485-517-123
12	81.5	6.6	313	6	US-10-485-517-293
13	81.5	6.6	579	7	US-11-045-802-32
14	81.5	6.6	1017	7	US-11-072-512-2312
15	81	6.5	1562	7	US-11-052-554A-211
16	80	6.5	573	7	US-11-196-475-112
17	79	6.4	1208	7	US-11-115-639-46
18	79	6.4	1208	7	US-11-115-639-47
19	79	6.4	1208	7	US-11-115-639-48
20	78	6.3	332	6	US-10-793-626-2494
21	78	6.3	585	6	US-10-510-386-20
22	78	6.3	594	6	US-10-510-386-38
23	77.5	6.3	581	7	US-11-045-802-30
24	76.5	6.2	1604	7	US-11-037-243-73
25	76	6.1	182	7	US-11-065-943-55
					Sequence 226, App
					Sequence 1860, App
					Sequence 422, App
					Sequence 1074, App
					Sequence 1166, App
					Sequence 33, Appl
					Sequence 1138, App
					Sequence 125, App
					Sequence 295, App
					Sequence 31, Appl
					Sequence 123, App
					Sequence 293, App
					Sequence 32, Appl
					Sequence 2312, App
					Sequence 211, App
					Sequence 112, App
					Sequence 46, Appl
					Sequence 47, Appl
					Sequence 48, Appl
					Sequence 2494, App
					Sequence 20, Appl
					Sequence 38, Appl
					Sequence 30, Appl
					Sequence 73, Appl
					Sequence 55, Appl

26	76	6.1	303	6	US-10-517-939-214	Sequence 214, App
27	76	6.1	805	6	US-10-485-517-198	Sequence 198, App
28	76	6.1	1006	6	US-10-467-657-8400	Sequence 8400, App
29	76	6.1	2233	6	US-10-873-528-2	Sequence 2, Appl
30	75.5	6.1	457	6	US-10-995-561-797	Sequence 797, App
31	75.5	6.1	627	6	US-10-873-528-191	Sequence 191, App
32	75	6.1	646	6	US-10-793-626-676	Sequence 676, App
33	74.5	6.0	120	6	US-10-501-039-14	Sequence 14, Appl
34	74.5	6.0	423	6	US-10-641-678-48	Sequence 48, Appl
35	74.5	6.0	836	7	US-11-052-554A-27	Sequence 27, Appl
36	74	6.0	518	6	US-10-793-626-506	Sequence 506, App
37	74	6.0	531	7	US-11-060-914-4	Sequence 4, Appl
38	73.5	5.9	345	6	US-10-467-657-252	Sequence 252, App
39	73.5	5.9	345	6	US-10-467-657-3086	Sequence 3086, App
40	73.5	5.9	583	7	US-11-080-991-64	Sequence 64, Appl
41	73.5	5.9	708	7	US-11-196-475-76	Sequence 76, Appl
42	73.5	5.9	900	6	US-10-909-769-20	Sequence 20, Appl
43	73	5.9	352	6	US-10-793-626-216	Sequence 216, App
44	73	5.9	693	7	US-11-196-475-72	Sequence 72, Appl
45	73	5.9	744	6	US-10-873-528-184	Sequence 184, App
46	72.5	5.9	251	6	US-10-485-517-126	Sequence 126, App
47	72.5	5.9	539	6	US-10-793-626-340	Sequence 340, App
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49	72	5.8	407	6	US-10-517-939-12	Sequence 12, Appl
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51	71.5	5.8	1992	7	US-11-013-759-3	Sequence 3, Appl
52	71.5	5.8	1992	7	US-11-013-759-13	Sequence 13, Appl
53	71.5	5.8	2047	7	US-11-013-759-4	Sequence 4, Appl
54	71.5	5.8	2047	7	US-11-013-759-7	Sequence 7, Appl
55	71	5.7	621	6	US-10-632-150-28	Sequence 28, Appl
56	71	5.7	621	7	US-11-073-457-28	Sequence 28, Appl
57	71	5.7	621	7	US-11-073-460-28	Sequence 28, Appl
58	71	5.7	3610	6	US-10-995-561-1016	Sequence 1016, App
59	71	5.7	3714	6	US-10-995-561-1015	Sequence 1015, App
60	71	5.7	3717	6	US-10-821-234-1076	Sequence 1076, App
61	70.5	5.7	269	6	US-10-793-626-880	Sequence 880, App
62	70.5	5.7	459	6	US-10-467-657-2368	Sequence 2368, App
63	70.5	5.7	792	7	US-11-088-686-29	Sequence 29, Appl
64	70.5	5.7	1070	7	US/11/062	Sequence 4, Appl
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66	70.5	5.7	1169	7	US-11-077-550-20	Sequence 20, Appl
67	70	5.7	266	7	US-11-082-544-10	Sequence 10, Appl
68	70	5.7	281	6	US-10-821-234-1288	Sequence 1288, App
69	70	5.7	281	7	US-11-077-272-2	Sequence 2, Appl
70	70	5.7	281	7	US-11-136-842-1	Sequence 1, Appl
71	70	5.7	281	7	US-11-136-079-5	Sequence 5, Appl
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73	70	5.7	459	7	US-11-098-686-11240	Sequence 11240, A
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83	69	5.6	311	6	US-10-793-626-3080	Sequence 3080, App
84	69	5.6	407	6	US-10-517-939-68	Sequence 68, Appl
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87	69	5.6	784	6	US-10-517-939-324	Sequence 324, App
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90	69	5.6	2333	6	US-10-453-372-114	Sequence 114, App
91	69	5.6	2662	6	US-10-453-372-114	Sequence 114, App
92	69	5.6	2724	6	US-10-453-372-148	Sequence 148, App
93	69	5.6	2733	6	US-10-453-372-136	Sequence 136, App
94	69	5.6	2733	6	US-10-453-372-142	Sequence 142, App
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96	69	5.6	2733	6	US-10-453-372-150	Sequence 150, App
97	69	5.6	2733	6	US-10-453-372-154	Sequence 154, App
98	69	5.6	2759	6	US-10-453-372-168	Sequence 168, App

99	69	5.6	2765	6	US-10-453-372-116	Sequence 116, App	172	65	5.3	177	6	US-10-467-657-882	Sequence 882, App
100	68.5	5.5	335	7	US-11-072-512-2943	Sequence 2943, Ap	173	65	5.3	214	6	US-10-793-626-896	Sequence 896, App
101	68.5	5.5	374	6	US-10-995-561-668	Sequence 668, App	174	65	5.3	365	6	US-10-453-372-560	Sequence 560, App
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103	68.5	5.5	428	7	US-11-156-084-329	Sequence 329, App	176	65	5.3	433	6	US-10-131-826A-334	Sequence 334, App
104	68.5	5.5	491	6	US-10-793-626-2808	Sequence 2808, Ap	177	65	5.3	503	7	US-11-074-176-350	Sequence 350, App
105	68.5	5.5	533	7	US-11-072-512-3224	Sequence 3224, Ap	178	65	5.3	506	7	US-11-074-176-176	Sequence 176, App
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107	68	5.5	178	6	US-10-453-372-56	Sequence 56, Appl	180	65	5.3	2871	7	US-11-124-367A-264	Sequence 264, App
108	68	5.5	321	6	US-10-467-657-216	Sequence 216, App	181	64.5	5.2	272	6	US-10-793-626-2290	Sequence 2290, Ap
109	68	5.5	321	6	US-10-467-657-7912	Sequence 7912, Ap	182	64.5	5.2	373	6	US-10-498-026-99	Sequence 99, Appl
110	68	5.5	404	6	US-10-793-626-1130	Sequence 1130, Ap	183	64.5	5.2	374	6	US-10-498-026-96	Sequence 96, Appl
111	68	5.5	522	6	US-11-072-512-2264	Sequence 2264, Ap	184	64.5	5.2	698	6	US-10-793-626-2388	Sequence 2388, Ap
112	68	5.5	535	6	US-10-793-626-1084	Sequence 1024, Ap	185	64.5	5.2	826	6	US-10-873-528-194	Sequence 194, App
113	68	5.5	551	6	US-10-793-626-1668	Sequence 1668, Ap	186	64.5	5.2	1022	7	US-11-186-284-163	Sequence 163, App
114	68	5.5	572	7	US-11-072-512-3907	Sequence 3907, Ap	187	64.5	5.2	1022	7	US-11-072-175-244	Sequence 244, App
115	68	5.5	1031	6	US-10-857-780-27	Sequence 22, Appl	188	64.5	5.2	1122	7	US-11-191-374-3	Sequence 3, Appli
116	68	5.5	1114	6	US-10-857-780-27	Sequence 27, Appl	189	64.5	5.2	1122	7	US-11-191-375-3	Sequence 3, Appli
117	68	5.5	1484	6	US-10-517-939-74	Sequence 74, Appl	190	64.5	5.2	1122	7	US-11-191-588-3	Sequence 3, Appli
118	68	5.5	8746	7	US-11-098-686-10232	Sequence 10232, A	191	64.5	5.2	1332	7	US-11-091-643-18	Sequence 18, Appl
119	67.5	5.5	170	6	US-10-793-626-2518	Sequence 2518, Ap	192	64.5	5.2	2015	7	US-11-052-554A-374	Sequence 374, App
120	67.5	5.5	189	6	US-10-793-626-1998	Sequence 1998, Ap	193	64	5.2	266	6	US-10-793-626-212	Sequence 212, App
121	67.5	5.5	370	6	US-10-793-626-1064	Sequence 1064, Ap	194	64	5.2	316	7	US-11-156-084-184	Sequence 184, App
122	67.5	5.5	456	6	US-10-793-626-1190	Sequence 1190, Ap	195	64	5.2	352	6	US-10-517-939-226	Sequence 226, App
123	67.5	5.5	711	6	US-10-510-386-10	Sequence 10, Appl	196	64	5.2	503	6	US-10-793-626-1810	Sequence 1810, Ap
124	67.5	5.5	897	6	US-10-517-939-258	Sequence 258, App	197	64	5.2	515	7	US-11-052-554A-255	Sequence 255, App
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126	67.5	5.5	1036	7	US-11-072-512-2812	Sequence 2812, Ap	199	64	5.2	1206	6	US-10-467-657-72	Sequence 72, Appl
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128	67	5.4	227	6	US-10-793-626-2396	Sequence 2396, Ap	201	63.5	5.1	167	6	US-10-967-457-79	Sequence 79, Appl
129	67	5.4	302	6	US-10-510-386-94	Sequence 94, Appl	202	63.5	5.1	211	6	US-10-493-864A-1	Sequence 1, Appli
130	67	5.4	320	6	US-10-793-626-2988	Sequence 2988, Ap	203	63.5	5.1	211	6	US-10-493-864A-2	Sequence 2, Appli
131	67	5.4	489	6	US-10-793-626-3068	Sequence 3068, Ap	204	63.5	5.1	218	7	US-11-060-920-2	Sequence 2, Appli
132	67	5.4	489	6	US-10-793-626-3178	Sequence 3178, Ap	205	63.5	5.1	296	7	US-11-196-475-22	Sequence 22, Appl
133	67	5.4	552	6	US-10-131-826A-332	Sequence 332, App	206	63.5	5.1	380	7	US-11-196-475-118	Sequence 118, App
134	67	5.4	655	7	US-11-045-802-29	Sequence 29, Appl	207	63.5	5.1	393	7	US-11-196-475-114	Sequence 114, App
135	67	5.4	710	7	US-11-045-802-2	Sequence 2, Appli	208	63.5	5.1	422	6	US-10-873-528-77	Sequence 77, Appl
136	67	5.4	710	7	US-11-045-802-19	Sequence 19, Appl	209	63.5	5.1	441	7	US-11-196-475-120	Sequence 120, App
137	67	5.4	710	7	US-11-045-802-20	Sequence 20, Appl	210	63.5	5.1	454	7	US-11-196-475-116	Sequence 116, App
138	67	5.4	710	7	US-11-045-802-21	Sequence 21, Appl	211	63.5	5.1	484	7	US-11-052-554A-177	Sequence 177, App
139	67	5.4	710	7	US-11-045-802-22	Sequence 22, Appl	212	63.5	5.1	547	7	US-11-052-554A-285	Sequence 285, App
140	67	5.4	710	7	US-11-045-802-23	Sequence 23, Appl	213	63.5	5.1	554	5	US-09-978-360A-410	Sequence 410, App
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143	67	5.4	1363	6	US-10-877-346-43	Sequence 43, Appl	216	63.5	5.1	685	7	US-11-089-554A-2	Sequence 2, Appli
144	67	5.4	5034	6	US-10-793-626-2964	Sequence 2964, Ap	217	63.5	5.1	696	6	US-10-131-826A-354	Sequence 354, App
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146	66.5	5.4	459	6	US-10-935-494-5	Sequence 5, Appli	219	63.5	5.1	775	6	US-10-795-201-1	Sequence 1, Appli
147	66.5	5.4	491	6	US-10-793-626-406	Sequence 406, App	220	63.5	5.1	955	7	US-11-052-554A-179	Sequence 179, App
148	66.5	5.4	491	6	US-10-793-626-2104	Sequence 2104, Ap	221	63.5	5.1	1194	7	US-11-098-686-10270	Sequence 10270, A
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155	66	5.3	430	6	US-10-525-710-30	Sequence 30, Appl	228	63	5.1	438	7	US-11-024-959-342	Sequence 342, App
156	66	5.3	612	7	US-11-098-686-10390	Sequence 10390, A	229	63	5.1	540	7	US-11-072-512-3747	Sequence 3747, Ap
157	66	5.3	657	6	US-10-873-528-57	Sequence 57, Appl	230	63	5.1	623	6	US-10-878-556A-62	Sequence 62, Appl
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160	66	5.3	1299	6	US-10-821-234-1145	Sequence 1145, Ap	233	63	5.1	1515	7	US-11-124-367A-402	Sequence 402, App
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162	66	5.3	2902	7	US-11-052-554A-91	Sequence 91, Appl	235	63	5.1	1518	7	US-11-124-367A-406	Sequence 406, App
163	66	5.3	3333	6	US-10-766-317-4	Sequence 4, Appli	236	63	5.1	1532	7	US-11-124-367A-403	Sequence 403, App
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167	65.5	5.3	333	6	US-10-978-556A-48	Sequence 48, Appl	240	63	5.1	1535	7	US-11-124-367A-408	Sequence 408, App
168	65.5	5.3	443	7	US-11-196-475-166	Sequence 166, App	241	63	5.1	1713	6	US-10-766-317-2	Sequence 2, Appli
169	65.5	5.3	478	6	US-10-793-626-768	Sequence 768, App	242	63	5.1	1724	6	US-10-766-317-6	Sequence 6, Appli
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171	65.5	5.3	1449	7	US-11-052-554A-237	Sequence 237, App	244	63	5.1	1730	7	US-11-193-715-4	Sequence 4, Appli

Db 236 FKGAITIDMSESDSIAYESFKQKRFNVDTGGYILDNVKIYANGKEI 282

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RESULT 3
US-10-485-517-422
; Sequence 422, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629WO
; CURRENT APPLICATION NUMBER: US/10/485.517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 422
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-485-517-422

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RESULT 4
US-10-793-626-1074
; Sequence 1074, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUJ480US
; CURRENT APPLICATION NUMBER: US/10793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1074
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

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; GENERAL INFORMATION:
; APPLICANT: Gordon-Kamm, William
; APPLICANT: Helentjaris, Tim
; APPLICANT: Lowe, Keith
; APPLICANT: Shen, Bo
; APPLICANT: Tarczynski, Mitchell
; APPLICANT: Zheng, Peizhong
; TITLE OF INVENTION: AP2 Domain Transcription Factor ODP2 (Ovule Development Protein 2)
; TITLE OF INVENTION: and Methods of Use
; FILE REFERENCE: 035718/286074
; CURRENT APPLICATION NUMBER: US/11/045,802
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: 60/541,122
; PRIOR FILING DATE: 2004-02-02
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Brassica napus
US-11-045-802-33

Query Match 6.8%; Score 84.5; DB 7; Length 579;
Best Local Similarity 21.0%; Pred. No. 4.1;
Matches 46; Conservative 32; Mismatches 84; Indels 57; Gaps 8;

QY 14 KKSELQNALSNLRQIYYVNEKAITENKESDD-----QFLENTLLPKGFFTGHP 62
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QY 120 TEEKVPIINLWDGKQTTVPIDKVTSKKEVTVOELDLQA-----RHYLHG 165
Db 278 SEYEK-----EIEEMKMTQREYVASLRKSSGFSRGSAGIYRGVTRHHQHG 323

QY 166 KFLGY-----NSDSFGGKQVORGLIVFHSSEGSTVSVDL 198
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RESULT 7
US-10-793-626-1138
; Sequence 1138, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1138
; LENGTH: 752
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1138

Query Match 6.7%; Score 83.5; DB 6; Length 752;
Best Local Similarity 23.1%; Pred. No. 7.1;
Matches 56; Conservative 33; Mismatches 88; Indels 65; Gaps 12;

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QY 103 -----KTACMYGGVTLHDNNRLTE-----EKKVPINLWDG-----KQTTV 138
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Db 610 FFDKNDIKSK--LQSVSKTGLNYM--SLGQPLSTLSGSGEIQRVKLGQHLDBEIKNSIFI 665

QY 199 FD 200
Db 666 FD 667

RESULT 8
US-10-485-517-125
; Sequence 125, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629WO
; CURRENT APPLICATION NUMBER: US/10/485,517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 125
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-125

Query Match 6.7%; Score 82.5; DB 6; Length 361;
Best Local Similarity 20.7%; Pred. No. 3.4;
Matches 28; Conservative 30; Mismatches 48; Indels 29; Gaps 3;

QY 64 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTTPNKTACMYGGVTLHDNNRLTEEK 123
Db 230 YDNIDVFIVLED--NKYQLKKYSV-----GGITKNTSKKVNHKV 266

QY 124 KVPINLWDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKQVORGL 183
Db 267 ELSITKQNGQMSIRDVSEYMITKEISLKELDFKLKQLIEKHNLV-----GNMGSQT 320

QY 184 IVFHSSEGSTVSVDL 198
Db 321 IVIKMKNGGKYTFEL 335

RESULT 9
US-10-485-517-295
; Sequence 295, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629WO
; CURRENT APPLICATION NUMBER: US/10/485,517
; CURRENT FILING DATE: 2004-02-02
```



```

Db 478 EDEQASIKAALEKHEKNEGNLTSPSAQNLVYDLEPNANLSLTDTGKFLKASAVDDAF 537
QY 58 --FTGHPWYNDLLVDSKADATNKKYKGVK--DLYGAYYVQCAGGT--PNKTACMYG 109
Db 538 SKSTSKAKYDQKILQLDLDITNLEQSNVASSMELYG-NFGDKAGWSTTVSNNSQVKWG 596
QY 110 GYTLHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKF-- 167
Db 597 SVLLERGQATATYTNLQNSYNGKISKIVKYTVDPKS-----KFOGQKWLIGIFTD 650
QY 168 ---GLYNSDSFGKQVORGLIVFHSSEGSTVSVDLFDAGQ---YPTLLRIYRDNKTINS 221
Db 651 PTLGVFAS-AYTQVEKNTSIFIKNE-----FTFYDEGDKPINFONALLSV----ASLNR 700
QY 222 ENLHIDL 228
Db 701 ENNSIEM 707

RESULT 16
US-11-196-475-112
; Sequence 112, Application US/11196475
; Publication No. US20050271682A1
; GENERAL INFORMATION:
; APPLICANT: Dattwyler, Raymond J.
; APPLICANT: Gomes Solecki, Maria J. C.
; APPLICANT: Luft, Benjamin J.
; TITLE OF INVENTION: Recombinant Constructs of Borrelia
; FILE REFERENCE: 2631.1001-011
; CURRENT APPLICATION NUMBER: US/11/196,475
; PRIOR FILING DATE: 2005-08-03
; PRIOR APPLICATION NUMBER: US 08/148,191
; PRIOR FILING DATE: 1993-11-01
; PRIOR APPLICATION NUMBER: US 08/235,836
; PRIOR FILING DATE: 1994-04-29
; PRIOR APPLICATION NUMBER: US 09/666,017
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: US 60/226,484
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: PCT/US01/24736
; PRIOR FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 112
; LENGTH: 573
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric Protein
; US-11-196-475-112

Query Match 6.5%; Score 80; DB 7; Length 573;
Best Local Similarity 22.4%; Pred. No. 10;
Matches 44; Conservative 27; Mismatches 71; Indels 54; Gaps 8;

QY 2 EKSEENKED---LRKKSLEQNALSNL-----ROIYYNEKAIT-ENKESDDQFL 48
Db 179 EVSVELNDTSSAATKKAWSNGTSLTITVNSKKTDLVFTKENTITVQQVDSNGTKL 238
QY 49 ENTLL-----PKGFTHPWYNDLLV---DLGSKD-----ATNKYKCK 83
Db 239 EGSAVEITKLDEIKNALKHPWDEKLLSKDKKADKSGKALDLDRELNSKASKEKSKAK 298
QY 84 KVDLYGAYYVQCAGGTGNKTCMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDKV 143
Db 299 EBEI-----TKGSKQSLGLDNNDENLWMPEDQKLPVVKKLSKKEFPVSEV 346
QY 144 ----KTSKKEVTVQEL 155
Db 347 EKLDKIFKGNNVGEL 362

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RESULT 17
US-11-115-639-46
; Sequence 46, Application US/11115639
; Publication No. US20050282242A1
; GENERAL INFORMATION:
; APPLICANT: Rothstein, David
; APPLICANT: Murphy, Christopher
; APPLICANT: MacNeil, Ian
; TITLE OF INVENTION: SCREENING ASSAYS FOR ANTIMICROBIAL
; FILE REFERENCE: 50150/075003
; CURRENT APPLICATION NUMBER: US/11/115,639
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/566,858
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 60/565,679
; PRIOR FILING DATE: 2004-04-27
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 1208
; TYPE: PRT
; ORGANISM: E. faecium
; US-11-115-639-46

Query Match 6.4%; Score 79; DB 7; Length 1208;
Best Local Similarity 24.8%; Pred. No. 33;
Matches 33; Conservative 17; Mismatches 65; Indels 18; Gaps 3;

QY 111 VTLHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFLY 170
Db 97 VTLRLTNRETGEIKAEQVFFGDFPLMTEGQTIIINGAERVIVSQLVRSQVYFHGKVDKN 156
QY 171 NSDSFGKGV--QRLIVFHSSEGSTVSVDLFDAGQGYP-----DTLLRIYRD 215
Db 157 GKEGFGSTVIPNRGAWLEMETSAKDYSVVRIDTRKIPLTLVLRALGFGSDDTIPEIFGD 216
QY 216 NKTINS---ENLH 225
Db 217 SETLRNTVEKDLH 229

RESULT 18
US-11-115-639-47
; Sequence 47, Application US/11115639
; Publication No. US20050282242A1
; GENERAL INFORMATION:
; APPLICANT: Rothstein, David
; APPLICANT: Murphy, Christopher
; APPLICANT: MacNeil, Ian
; TITLE OF INVENTION: SCREENING ASSAYS FOR ANTIMICROBIAL
; FILE REFERENCE: 50150/075003
; CURRENT APPLICATION NUMBER: US/11/115,639
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/566,858
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 60/565,679
; PRIOR FILING DATE: 2004-04-27
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 1208
; TYPE: PRT
; ORGANISM: E. faecium
; US-11-115-639-47

Query Match 6.4%; Score 79; DB 7; Length 1208;
Best Local Similarity 24.8%; Pred. No. 33;
Matches 33; Conservative 17; Mismatches 65; Indels 18; Gaps 3;

QY 111 VTLHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFLY 170

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Db 97 VTLLRLNRETGETKAQEVFFGDFPLPMTQGTFTIINGAERVIVSQLVRSPGVYFHGKVDKN 156
QY 171 NSDSFGGKV--ORGLIVFHSSEGSTVSVDLFDAGQGYV-----DTLLRIYRD 215
Db 157 GKEGFSTVIPNKGAWLEMETSAKDISYVRIDRTRKIPILTVLVRALFGSDDTIFEIIGD 216
QY 216 NKTINS---ENLH 225
Db 217 SETLRNTVEKDLH 229

RESULT 19
US-11-115-639-48
; Sequence 48, Application US/11115639
; Publication No. US20050282242A1
; GENERAL INFORMATION:
; APPLICANT: Rothstein, David
; APPLICANT: Murphy, Christopher
; APPLICANT: MacNeill, Ian
; TITLE OF INVENTION: SCREENING ASSAYS FOR ANTIMICROBIAL
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 50150/075003
; CURRENT APPLICATION NUMBER: US/11/115,639
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/566,858
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 60/565,679
; PRIOR FILING DATE: 2004-04-27
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 1208
; TYPE: PRT
; ORGANISM: E. faecium
US-11-115-639-48

Query Match 6.4%; Score 79; DB 7; Length 1208;
Best Local Similarity 24.8%; Pred. No. 33;
Matches 33; Conservative 17; Mismatches 65; Indels 18; Gaps 3;

QY 111 VTLLHNNRLTEKKVPINLWIDGKQTVIPDKVTSKKEVTVOELDLQARHYLHGKFLY 170
Db 97 VTLLRLNRETGETKAQEVFFGDFPLPMTQGTFTIINGAERVIVSQLVRSPGVYFHGKVDKN 156
QY 171 NSDSFGGKV--ORGLIVFHSSEGSTVSVDLFDAGQGYV-----DTLLRIYRD 215
Db 157 GKEGFSTVIPNKGAWLEMETSAKDISYVRIDRTRKIPILTVLVRALFGSDDTIFEIIGD 216
QY 216 NKTINS---ENLH 225
Db 217 SETLRNTVEKDLH 229

RESULT 20
US-10-793-626-2494
; Sequence 2494, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2494
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

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; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2494

Query Match 6.3%; Score 78; DB 6; Length 392;
Best Local Similarity 23.2%; Pred. No. 9.6;
Matches 42; Conservative 30; Mismatches 71; Indels 38; Gaps 9;

QY 40 NKESDDQFLENTLLFK-----GFTTGHPPWYNLDLLGSKDATNKYKKGKVDLYGAY 91
Db 115 SKKGDDFLKNGGILREKGTGPSAAGFRIDTGYVNDPLDKIQKQAGQGYRG-----YGTG 169
QY 92 YGQCAG-----GTPNKTACMYGGVTLHD--NNRLTEKKVPINLWIDGKQ---TTVPI 140
Db 170 VKNDSQGNSTKVGSGTPTDFTLNYADNTTNDLDGKFHGQKJANNVNLKYNASNQTFATYA 229
QY 141 DKVTSKKEVTVOELDL---QARHYL--HGKFLYNSDSFGGKVORGLIVFHSSEGSTVS 195
Db 230 GKTWTA---TLSELGLSPTDSYNFLVTSQYGNNGSGTYASGVMA-----DLDGATLT 280
QY 196 Y 196
Db 281 Y 281

RESULT 21
US-10-510-386-20
; Sequence 20, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-20

Query Match 6.3%; Score 78; DB 6; Length 585;
Best Local Similarity 26.0%; Pred. No. 16;
Matches 45; Conservative 27; Mismatches 73; Indels 28; Gaps 9;

QY 56 GFTTGHPPWYNLDLLGSKDATNKYKKGK-KVDLYGAYGYQCAGGT-----PNKTA 105
Db 421 GFHTADRWENDI---SGTCKLTKKGTGALKLEGDNITY-----SGGTRIDGTLEGGSETA 472
QY 106 CMYGGVTLHDNNRLTEKKVPINLWIDG--KQTVIPDKVTSKKEVTVOELDLQARHYL 163
Db 473 FGRGDVAL--NGGILKE-DAPGKLIIEGDYKQSAKGILEQLSGKK---DQLKIKGKARL 526
QY 164 HGKFLYNSDSFGGKVORGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRD 216
Db 527 KGTLRLNFTDNYVPADGSAIITFRKRHGSFSSVETSGLPSPKVKYKTI--IYKSN 577

RESULT 22
US-10-510-386-38
; Sequence 38, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
```

APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-38

Query Match 6.3%; Score 78; DB 6; Length 594;

Best Local Similarity 26.0%; Pred. No. 16;
Matches 45; Conservative 27; Mismatches 73; Indels 28; Gaps 9;

QY 56 GFTTGHWPYNDLLVDLGSKDATNKYKGK-KVDLYGAYGYQCAGGT-----PNKTA 105
DB 426 GFHTADRWNDI---SGTKLTKKGTGALKLEGDNTY-----SGGTRIDQGTLEGGSETA 477
QY 106 CMYGGVTLHDNNRLTBEKKVPINLWIDG--KQTTVPIDKVKTSKKEVTVQELDQARHYL 163
DB 478 FGRGDVAL--NGGILKE-DAPGKLIIEGDYKQSAKGILEQLSGKK---DQLKIKGKARL 531
QY 164 HKKFGLYNSDSFGGKVQRLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDN 216
DB 532 KGTLRINFDTNYPADGSAIITFRKRHGSFSSVETSGLPSKYKVKI--IYKSN 582

RESULT 23

US-11-045-802-30

; Sequence 30, Application US/11045802

; Publication No. US20050257289A1

; GENERAL INFORMATION:

; APPLICANT: Gordon-Kamm, William

; APPLICANT: Helentjaris, Tim

; APPLICANT: Lowe, Keith

; APPLICANT: Shen, Bo

; APPLICANT: Tarczynski, Mitchell

; APPLICANT: Zheng, Peizhong

; TITLE OF INVENTION: AP2 Domain Transcription Factor ODP2 (Ovule Development Protein 2

; FILE REFERENCE: 035718/286074

; CURRENT APPLICATION NUMBER: US/11/045,802

; PRIOR FILING DATE: 2005-01-28

; PRIOR FILING DATE: 2004-02-02

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 30

; LENGTH: 581

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

US-11-045-802-30

Query Match 6.3%; Score 77.5; DB 7; Length 581;

Best Local Similarity 20.1%; Pred. No. 18;

Matches 43; Conservative 34; Mismatches 78; Indels 59; Gaps 8;

QY 18 LQNALSNLRQIYYNEKAITEN-----KESDDQFLENTLLFKGFTGHPW---Y 64
DB 165 LSNMSTSSNNYNNDDVVQKTIIVDVVETTPKKTIESFGORTSIYRG-VTRHRWTGY 223
QY 65 NDLLVDLGSKDATNKYKKKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLTEERK 124
DB 224 EAHLDWNSCKREQQTRKGRQ---GGYDKEEKAARAYDLAALKYGTGTTTTTFPLSEYEK 279
QY 125 VPINLWIDGKQTTVPIDKVKTSKKEVTVQELDQA-----RHYLHGKFGLY 170
DB 280 -----EVEEMKHMTRQBYVASLRRKSSGFRGASIVRGVTRHHQGRQWAR 325
QY 171 -----NSDSFGGKVQRLIVFHSSEGSTVSVDL 198

DB 326 IGRVAGNKDLYLG-----TFGTQEEAAEAYDI 352

RESULT 24

US-11-037-243-73

; Sequence 73, Application US/11037243

; Publication No. US20050287546A1

; GENERAL INFORMATION:

; APPLICANT: PLOWMAN, GREGORY

; APPLICANT: WHYTE, DAVID

; APPLICANT: CAENEPEEL, SEAN

; APPLICANT: CHARYDCZAK, GLEN

; APPLICANT: MANNING, GERARD

; APPLICANT: SUDARSANAM, SUCHA

; TITLE OF INVENTION: NOVEL PROTEASES

; FILE REFERENCE: 038602/1214

; CURRENT APPLICATION NUMBER: US/11/037,243

; CURRENT FILING DATE: 2005-05-26

; PRIOR FILING DATE: 2001-08-26

; PRIOR FILING DATE: 2000-06-26

; NUMBER OF SEQ ID NOS: 150

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 73

; LENGTH: 1604

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-037-243-73

Query Match 6.2%; Score 76.5; DB 7; Length 1604;

Best Local Similarity 24.3%; Pred. No. 81;

Matches 41; Conservative 18; Mismatches 53; Indels 57; Gaps 9;

QY 74 KDATNKYKKKVDLYGAYGYQC-----AGGTPNKTA---CMYGGVT--LHDNNRLTE 121
DB 29 KDAFKRTCG-----LSYYMGQHCFFIREVLGDGVPKVAEVIYCSFGTSGKLHFNLI-- 81
QY 122 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDQARHYLHGKFGLYNSDSFGGKVOR 181
DB 82 ---VGLVLLTRGK-----DEEKAKYI---FSLFSSS-GNYVIR 113
QY 182 GLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKNTINSENLDLYL 230
DB 114 -----EEMERMLHVVDGKVDPDTLTKCFSEGEKVNVEKFRNWLFL 152

RESULT 25

US-11-065-943-55

; Sequence 55, Application US/11065943

; Publication No. US20050250131A1

; GENERAL INFORMATION:

; APPLICANT: JESTIN, JEAN-LUC

; APPLICANT: VICHIER-GUERRE, SOPHIE

; APPLICANT: FERRIS, STEPHANE

; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I

; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,

; FILE REFERENCE: 266426US0XCIP

; CURRENT APPLICATION NUMBER: US/11/065,943

; CURRENT FILING DATE: 2005-02-25

; PRIOR FILING DATE: 2004-02-27

; NUMBER OF SEQ ID NOS: 106

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 55

; LENGTH: 182

; TYPE: PRT

; ORGANISM: Bacillus subtilis

US-11-065-943-55

Query Match 6.1%; Score 76; DB 7; Length 182;


```
QY 74 -----KDATNKYKGVLDYGYGYQCAGGTPNKACMYGGVTLHDNNRLTEEEKVPIN 128
Db 241 DKTQIKDIT---QGTVDLGLTKPRIELSKGWKNRLDRFLG-----NWTLSDKGKVSYN 292
QY 129 LWIDGQTTVPIDK-----VKTSSKEVTVQELDLQARHYLHGKFGLYNSDFGKGKVRQG 182
Db 293 LGLPQVKGACRINKPNNNTKAPSLTAPAL-----WFGPVQNG 333
QY 183 LIVFHSSEGSTVSYDLFDAQGYPD-TLLRIYRDNTKINSEN 223
Db 334 KVMYSASVST-----YPDSSSRIVLQNLKRKTES 364

RESULT 29
US-10-873-528-2
; Sequence 2, Application US/10873528
; Publication No. US20050276814A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129WO
; CURRENT APPLICATION NUMBER: US/10/873,528
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: US/09/769,787
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-873-528-2

Query Match 6.1%; Score 76; DB 6; Length 2233;
Best Local Similarity 20.3%; Pred. No. 1.4e+02;
Matches 55; Conservative 35; Mismatches 77; Indels 104; Gaps 16;

QY 3 KSEENEKDLRKSELOALNLRIRIYYNEKAITENKESDDQFLENTLLPKGFTGH- 61
Db 216 KTFKLDKDLK-----NVLTF-----DGVYMDSQVYNGQLVGHY 252
QY 62 -PWYNDLLVLDGSKDATNKYKGVLDYGYGYQCAGGTPNKACMYGGVTLHDNNRLT 120
Db 253 PNGYNQFSYDI-----TKYLQK-----DGENV-----IAVHAVN--- 282
QY 121 BEKKVPINLWDG-----KQTTVPI-DKVKTSKEVTVQELDLQARHYLHGKF-----GL 169
Db 283 ---KQPSRWYSGGIYRDVTLQVTDKVVKXNGTTLTPKLEBQO--HGKVEHTVTSKI 337
QY 170 YNSD-----SFGKVQVGLIYVHS---SEGSTVSYD-----LFD 200
Db 338 VNTDDKDHVLAQYQIVERGHAHTGLVRTASRTLKAHESSTLDAITAEVERPKLMTVLND 397
QY 201 AQOQYPTDLLRIYRDNTKINSENHLIDLVL 231
Db 398 KPALY-ELITRYRDQQLVDAKK---DLFGY 424

RESULT 30
US-10-995-561-797
; Sequence 757, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
```

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; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 797
; LENGTH: 457
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-797

Query Match 6.1%; Score 75.5; DB 6; Length 457;
Best Local Similarity 26.2%; Pred. No. 20;
Matches 27; Conservative 23; Mismatches 38; Indels 15; Gaps 5;

QY 116 NNRLTEEEKVPINLWIDGQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSF 175
Db 209 NFRDTEEAKEQINNYVEKRTGRKVVLDLVKHLKDTSLALVDVIS---FHGKW----KDKF 261
QY 176 GGVQVGLIV-FHSSEGSTVSYDLFDAQGYPTDLLRIYRDNK 217
Db 262 --KAERIMVEGFHVDKTIIRVPMINHLGRFD-----IHRDRE 297

RESULT 31
US-10-873-528-191
; Sequence 191, Application US/10873528
; Publication No. US20050276814A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129WO
; CURRENT APPLICATION NUMBER: US/10/873,528
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: US/09/769,787
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 191
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-873-528-191

Query Match 6.1%; Score 75.5; DB 6; Length 627;
Best Local Similarity 21.1%; Pred. No. 30;
Matches 42; Conservative 21; Mismatches 67; Indels 69; Gaps 8;

QY 51 TLLFGKFTGHWPYNDLLVLDGSKDATNKYKGVLDYGYGYQCAGGTPNKACMYGG 110
Db 7 SLALVAGFLGLSWYGNVQAQESS-----GNKTHFINVQEGSDA----- 45
QY 111 VTLHDNNRLT-----BEKKVPINLWIDGQTT---VPIDKVKTSKEVTVQE 154
Db 46 IILESNGHFAMVDTGDEDVDFPDGSDSRYP---WREGIETSYKHVLTDRVFRRLKELGVQK 102
QY 155 LDQARHYLHGKFGLYNSDSFGKVGQVGLIYVHSSEGSTVSYDLFDAQGYPD---DTLLRI 212
Db 103 LDFILVLTHTH-----SDHIG-----NVDELLSTYPVDRLVYLKK 135
QY 213 YRDNKTINSENHLIDLVL 231
Db 136 YSDSRITNSERLWDNLGY 154

RESULT 32
US-10-793-626-676
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```
; Sequence 676, Application US/10793626
; Publication No. US2005025478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR FILING DATE: 2004-164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 676
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-676

Query Match          6.1%; Score 75; DB 6; Length 646;
Best Local Similarity 21.2%; Pred. No. 34;
Matches 36; Conservative 24; Mismatches 58; Indels 52; Gaps 6;

QY 71 LGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLW 130
Db 202 IGRDRTVKQPSSKVKIGN-----TKTDKTKTKNQ----- 233

QY 131 IDSKQITVPTDKVTSKKEVTVELDLQARH-----YLHGKFGLYNSDFGKVGORGL 183
Db 234 ---KOTSLTSPRVKSKQTHINQLTAQAQYKQYVPVVFHGFVLGDSDFS----- 283

QY 184 IVFHSSEGSVSYDLFDAQGYPTDLRLR1YRDKNKTINSENLH--IDLVL 231
Db 284 -MYPNWTGGT-----KYNVKQELIKLGYRVHEANVGAFSSNYDRAVELYY 328

RESULT 33
US-10-501-039-14
; Sequence 14, Application US/10501039
; Publication No. US2005024482A1
; GENERAL INFORMATION:
; APPLICANT: Tetsuro Kokubo, Masahiro Shirakawa, and Jeremy Robin Howard Tame
; TITLE OF INVENTION: Method of monitoring gene expression
; FILE REFERENCE: 4439-4023
; CURRENT APPLICATION NUMBER: US/10/501,039
; CURRENT FILING DATE: 2004-07-08
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-501-039-14

Query Match          6.0%; Score 74.5; DB 6; Length 120;
Best Local Similarity 21.5%; Pred. No. 4.4;
Matches 32; Conservative 27; Mismatches 43; Indels 47; Gaps 6;

QY 28 QIYYNEKAITENKES-----DQOFLNTLLFKGFFTGHPWYNDLLVLDLGSKDATNKYK 82
Db 3 KVSYSQVAEHNGPENFIIDDKYD-----VSQFKDEHGGDEIMDLGGQATSP-- 56

QY 83 KKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDK 142
Db 57 --VDI-----GHSDEALRLKGLVIGVDKTSR-----VSVEK 88

QY 143 VKTSKKE-----VTVQELDLQARHL 163
Db 89 VSTSENQSGSGTLVLVILAILMLGVAYYL 117
```

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RESULT 34
US-10-641-678-48
; Sequence 48, Application US/10641678
; Publication No. US20050277172A1
; GENERAL INFORMATION:
; APPLICANT: Day, Anthony, G.
; APPLICANT: Goedegebuur, Frits
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Neefe, Paulien
; APPLICANT: Sandgren, Mats
; APPLICANT: Stahlberg, Jerry
; TITLE OF INVENTION: Novel Variant Hypocrea jecorina CBH1
; FILE REFERENCE: GC772-3
; CURRENT APPLICATION NUMBER: US/10/641,678
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/458,853
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/458,696
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/456,368
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US 60/404,063
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Alternaria alternata
US-10-641-678-48

Query Match          6.0%; Score 74.5; DB 6; Length 423;
Best Local Similarity 24.8%; Pred. No. 22;
Matches 30; Conservative 20; Mismatches 36; Indels 35; Gaps 7;

QY 77 TNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTL-----HDNNRLTEKKVPINL 129
Db 317 TTRFCQQKRAVGDYTYTFKDGGMANMAKALANGMLVMSLWDDHYSNM-----L 366

QY 130 WIDGKQTTVPIDK-----VKTSKKEVTVQ-----LDLQARH-----YLHGKFGLYNSDSF 175
Db 367 WLD---STYPTDKNPDTDLGTGRGECETSSGVPADVESQHADATVYVYSNLIKFGPLNS-TF 422

QY 176 G 176
Db 423 G 423

RESULT 35
US-11-052-554A-27
; Sequence 27, Application US/11052554A
; Publication No. US2005028866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 836
; TYPE: PRT
```



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;
;
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-216

Query Match          5.9%; Score 73; DB 6; Length 352;
Best Local Similarity 24.1%; Pred. No. 24;
Matches 27; Conservative 13; Mismatches 34; Indels 38; Gaps 3;

Db 434 KSRASLGLDNLNKNLMLPEQKLPBKLDK-----LOGKEFKVPSEVKLD----- 482
Qy 163 LHGKFGLYNSDFGGKQVQRGLIVFHSSEGSTVSYDLFDAQQGYPDYLLRIYRDNKNTINSE 222
Db 483 ---KISKSNNEVG-----KLSPLDKPSYDDIDSKEEV-----DNKAINLQ 520
Qy 223 NL 224
Db 521 KI 522

RESULT 42
US-10-909-769-20
; Sequence 20, Application US/10909769
; Publication No. US20060024331A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Lin, Wei-Jen
; APPLICANT: Aoki, Kei Roger
; APPLICANT: Sachs, George
; TITLE OF INVENTION: Toxin Compounds with Enhanced Membrane Translocation Characteristic
; FILE REFERENCE: ALL0010-100 (ROI2003-146)
; CURRENT APPLICATION NUMBER: US/10/909,769
; CURRENT FILING DATE: 2004-08-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 20
; LENGTH: 900
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of HC
US-10-909-769-20

Query Match          5.9%; Score 73.5; DB 6; Length 900;
Best Local Similarity 19.4%; Pred. No. 72;
Matches 42; Conservative 44; Mismatches 65; Indels 65; Gaps 12;

Qy 18 LORNALSNLRQIYYNEKAITENKESDDQFLEN-----TLFPKGFFT-GHPWY 64
Db 411 LKKNLLNYDENKNLYLIGSVEDESKVDKYLTIIPFDLSTYSNIBILIKIFKNYNSEIL 470
Qy 65 NDLVLVDSKDATNKYKGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNN----- 117
Db 471 NNIIILNRYD-----NNLIDLSG--YGAKVE-----VYDGVKLNDRKNQFKLTS 513
Qy 118 ----RLTEKKVPIN-LWID-GKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLY 170
Db 514 ADSKIRVTQNIIFNSMFLDFSFSWIRIPKYRND-----DIQ--NYIHNEYTII 562
Qy 171 N--SDSFGGKQVQRGLIVFHSSEGSTVSYDLFDAQQG 204
Db 563 NCMKNNSGNKI-----SIRGNRIIWTLIDINGK 590

RESULT 43
US-10-793-626-216
; Sequence 216, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 216
; LENGTH: 352
```

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;
;
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-216

Query Match          5.9%; Score 73; DB 6; Length 352;
Best Local Similarity 24.1%; Pred. No. 24;
Matches 27; Conservative 13; Mismatches 34; Indels 38; Gaps 3;

Qy 71 LGSKDATNKYKGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLW 130
Db 202 IGDRLTKVPQSSKVHKIGN-----TKTDKTVKTNQK----- 233
Qy 131 IDGKQTTVPIDKVKTSKEVTVQELDLQARH-----YLHGKFGLYNSDSF 175
Db 234 ---KQTSLTSPRVKSKQTKHINQLTAQAKYKNQYVWVHGVFVGLVGEDSF 282

RESULT 44
US-11-196-475-72
; Sequence 72, Application US/11196475
; Publication No. US20050271682A1
; GENERAL INFORMATION:
; APPLICANT: Dattwyler, Raymond J.
; APPLICANT: Gomes Solecki, Maria J. C.
; APPLICANT: Luft, Benjamin J.
; APPLICANT: Dunn, John J.
; TITLE OF INVENTION: Recombinant Constructs of Borrelia
; FILE REFERENCE: 2631.1001-011
; CURRENT APPLICATION NUMBER: US/11/196,475
; CURRENT FILING DATE: 2005-08-03
; PRIOR APPLICATION NUMBER: US 08/148,191
; PRIOR FILING DATE: 1993-11-01
; PRIOR APPLICATION NUMBER: US 08/235,836
; PRIOR FILING DATE: 1994-04-29
; PRIOR APPLICATION NUMBER: US 09/666,017
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: US 60/226,484
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: PCT/US01/24736
; PRIOR FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 693
; TYPE: PRT
; ORGANISM: Borrelia burgdorferi
US-11-196-475-72

Query Match          5.9%; Score 73; DB 7; Length 693;
Best Local Similarity 24.6%; Pred. No. 57;
Matches 47; Conservative 26; Mismatches 42; Indels 76; Gaps 12;

Qy 2 EKSEIN-EKDLRKXSELQ-----RNALSNL-----RQIYYNEKAI 37
Db 329 EDINEINKEKNLPKPGDVSSPKVDKQLQIKESLELQEQKETSNDENQKREI-----EKQI 384
Qy 38 TENKESDDQFLENTLLFKGFFTGHPWYNDDLVDLGSK-DATNKYKGK-----KVDL 87
Db 385 -EIKSDELLKSK-----DPKALDLNRDLNSKASSKEKIKGKEIVKEKSVSL 434
Qy 88 YGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDKY----- 143
Db 435 -----GDLNDETILM-----TPDQKLSEDKK-----LDSKQNLKPVSEIERN 473
Qy 144 ---KTSKKEVT 151
Db 474 EISKSNNEVS 484
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 2053
; TYPE: PRT
; ORGANISM: Moraxella catarrhalis
US-11-013-759-9

Query Match      5.8%; Score 72.5; DB 7; Length 2053;
Best Local Similarity 21.8%; Pred. No. 2.5e+02;
Matches 45; Conservative 20; Mismatches 78; Indels 63; Gaps 7;

QY 68 LVDLGSKDATNKYKGGKVDLYGAYGYQCAGGPNKTCACMYGGVTLHDNNRLTEKKVPI 127
DB 1273 IVDVLSAGNLOQNGAVDFVSTYDVPFANG--NTTAK---VTYDDTSKTS---KVY 1324

QY 128 NLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKVGQGLIVPH 187
DB 1325 DVNVD--DTTIEVKDKKLGKVTTLTSTGTGA-----NKFALSNQATGDALVKASDIVAH 1377

QY 188 -----SSEGSTVSVDLFD----- 200
DB 1378 LNTLSGDIQTAKGASQANNSAGYVDADGNKVIYDSTDNKYQAKNDGTVDKTKEVAOKL 1437

QY 201 -AQGOVPPDTLRIYRDNKNTINSENLH 225
DB 1438 VAQAQTPDGTGLAQMNVKSVINKEQVN 1463

RESULT 49
US-10-517-939-12
; Sequence 12, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghalalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; PRIOR FILING DATE: 2004-12-13
; PRIOR FILING DATE: 2003-06-16
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 407
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(28)
US-10-517-939-12

Query Match      5.8%; Score 72; DB 6; Length 407;
Best Local Similarity 21.3%; Pred. No. 35;
Matches 37; Conservative 27; Mismatches 72; Indels 38; Gaps 7;

QY 7 INEKLRKSEQLRQNALSNLRQIYYNEKAITENKESDDQF---LENTLLFKGFFFTGHPW 63
DB 145 VNEDTPVKEQNQLLLKLELET-----HIKTIYERYKDDIKYWDVNEVVGDDGKLNSPW 200

QY 64 YNDLLVDL--GSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
DB 201 YQIAGIDYIKVAFQARKYGGGNIKLY-----NNDYNTVEVE 236
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QY 122 EKKVPI-NLWIDGKQTTVPIDKVKTSKEVTV---QELDLQARHYLHGKFLYN 171
DB 237 PKRTALYNLVKQLKEGVPIDGI-GHQSHIQIOWPSEAEIEKTINMPAAGLDN 289

RESULT 50
US-11-196-475-68
; Sequence 68, Application US/11196475
; Publication No. US20050271682A1
; GENERAL INFORMATION:
; APPLICANT: Dattwyler, Raymond J.
; APPLICANT: Gomez Solecki, Maria J. C.
; APPLICANT: Luft, Benjamin J.
; APPLICANT: Dunn, John J.
; TITLE OF INVENTION: Recombinant Constructs of Borrelia
; FILE REFERENCE: 2631.1001-011
; CURRENT APPLICATION NUMBER: US/11/196,475
; CURRENT FILING DATE: 2005-08-03
; PRIOR APPLICATION NUMBER: US 08/148,191
; PRIOR FILING DATE: 1993-11-01
; PRIOR APPLICATION NUMBER: US 08/235,836
; PRIOR FILING DATE: 1994-04-29
; PRIOR APPLICATION NUMBER: US 09/666,017
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: US 60/226,484
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: PCT/US01/24736
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 693
; TYPE: PRT
; ORGANISM: Borrelia burgdorferi
US-11-196-475-68

Query Match      5.8%; Score 71.5; DB 7; Length 693;
Best Local Similarity 21.8%; Pred. No. 78;
Matches 45; Conservative 37; Mismatches 63; Indels 61; Gaps 11;

QY 2 EKSEIN-EKDLRKSELQ-----RNALSNL-----RQIYYVNEKAI 37
DB 329 EDIDEINKEKLPKPGDVSSPKVDQLQIKESLEDLQEQLKETSDENQKEI---EKQI 384

QY 38 TENKESDDQFLENTLLFKGFFFTGHPWYNDLLVDLGSK-DATNKYKGGKVDLYGAYGYQC 96
DB 385 -BIKKSDELLKSK-----DPKALDLNGDLNSKVSSKEKIKGEGEI----- 425

QY 97 AGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDKV-----KTSKKE 149
DB 426 ---VKEESKASLADLNNDENLRPDDQKLSDDKLDKSNLKPVSIEIRVNEISKSNNE 482

QY 150 VTQVQELDLQARHY--LHGKFLYNSD 173
DB 483 IS-ESSPLYKPSYSDMDSKEGIDNKD 507

RESULT 51
US-11-013-759-3
; Sequence 3, Application US/11013759
; Publication No. US20050249747A1
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M.
; APPLICANT: Sasaki, Ken
; APPLICANT: Yang, Yan Ping
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
; FILE REFERENCE: 1038-921MIS:jb
; CURRENT APPLICATION NUMBER: US/11/013,759
; CURRENT FILING DATE: 2004-12-16
```


Best Local Similarity 21.8%; Pred. No. 3.1e+02;
Matches 45; Conservative 20; Mismatches 78; Indels 63; Gaps 7;
QY 68 LVDLGSKDATNKKYKKKVDLYGAYGYQACGTPNKTACMYGGVTLHDNNRLTEKKVPI 127
Db 1264 IVDVLSAGFNLOQNGEAVDFSVTYDTWNPADG--NATTAK---VTYDDTSTKTS---KVYV 1315
QY 128 NWDIGKQTTVPIDKVKTSKKEVTVCQELDLQARHYLHGKFGLYNSDSFGGKVQVQGLIVFH 187
Db 1316 DVNVD--DTTIEVKDKLGVKTTLTSTGTGA-----NKPALSNQATGALVKASDIVAH 1368
QY 188 -----SSEGSTVSVDLFD----- 200
Db 1369 LNTLSGDIQTAKGASQANNSAGVVDADGNKVIYDSTDNKYVQAQKNDGTVDTKTEVAKDKL 1428
QY 201 -AQGYPTDLLRIYRNKNTINSENH 225
Db 1429 VAQAQTPDGTGLAQMNVKSVINKEQVN 1454

RESULT 55

US-10-632-150-28
; Sequence 28, Application US/10632150
; Publication No. US20050251871A1
; GENERAL INFORMATION:
; APPLICANT: Chiaux, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/10/632,150
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/385,219
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-632-150-28

Query Match 5.7%; Score 71; DB 6; Length 621;
Best Local Similarity 20.6%; Pred. No. 75;
Matches 55; Conservative 39; Mismatches 75; Indels 98; Gaps 17;
QY 27 ROIYY-----NEKAITENKESDDQPLENTL----- 52
Db 167 KKILYLRQOKILNNLKAFLOQPDYSEYLEGAVIDQYCNPLDSLKDIAQAIDSIVE 226
QY 53 ----LPGKFTGHP-----WYNDLL--VDLGSK--DATN-----KYGKKVDLYGA- 90
Db 227 LVCKTLRGINSRHPSLAFKAGESSMIELOSQVLDAMNVYLDQLKFGKGRMDYNNAL 286
QY 91 -YGYQC---AGTPTNKTACMYGGVTLHDNNRLTEKKV-----PINL-----WIDGK 134
Db 287 NLYMHQVLIIRRTGIPISMSLLY-----LTIAQLGVPLEPVNPFSHFLLRWCQGA 336
QY 135 Q-TTVPID-KVKTSK----KEVTVOELD-IQARHYLHGKFGLYNSDSFGGKVQVQGLIVFH 187
Db 337 EGATLDIFDYIIDAFGKGKQLTVKECEYLIGQHVTAALYGVNVKVLQRMVGNLLSLG 396
QY 188 SSEGSTVS-----DLFDAQGGQYPD 207
Db 397 KREGIDQSYQLLRDSLDLYLA--MYPD 421

RESULT 56

US-11-073-457-28
; Sequence 28, Application US/11073457
; Publication No. US20050260556A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,457
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-457-28

Query Match 5.7%; Score 71; DB 7; Length 621;
Best Local Similarity 20.6%; Pred. No. 75;
Matches 55; Conservative 39; Mismatches 75; Indels 98; Gaps 17;
QY 27 ROIYY-----NEKAITENKESDDQPLENTL----- 52
Db 167 KKILYLRQOKILNNLKAFLOQPDYSEYLEGAVIDQYCNPLDSLKDIAQAIDSIVE 226
QY 53 ----LPGKFTGHP-----WYNDLL--VDLGSK--DATN-----KYGKKVDLYGA- 90
Db 227 LVCKTLRGINSRHPSLAFKAGESSMIELOSQVLDAMNVYLDQLKFGKGRMDYNNAL 286
QY 91 -YGYQC---AGTPTNKTACMYGGVTLHDNNRLTEKKV-----PINL-----WIDGK 134
Db 287 NLYMHQVLIIRRTGIPISMSLLY-----LTIAQLGVPLEPVNPFSHFLLRWCQGA 336
QY 135 Q-TTVPID-KVKTSK----KEVTVOELD-IQARHYLHGKFGLYNSDSFGGKVQVQGLIVFH 187
Db 337 EGATLDIFDYIIDAFGKGKQLTVKECEYLIGQHVTAALYGVNVKVLQRMVGNLLSLG 396
QY 188 SSEGSTVS-----DLFDAQGGQYPD 207
Db 397 KREGIDQSYQLLRDSLDLYLA--MYPD 421

RESULT 57

US-11-073-460-28
; Sequence 28, Application US/11073460
; Publication No. US2005027066A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,460
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-460-28

Query Match 5.7%; Score 71; DB 7; Length 621;
Best Local Similarity 20.6%; Pred. No. 75;

```
Matches 55; Conservative 39; Mismatches 75; Indels 98; Gaps 17;
QY 27 RQIYY-----NEKAITENKESDDQFLENTL----- 52
Db 167 KKILYLROQKILNNLKAFLQPPDDYSYLEGAVYIDQYCNPLSDISLKDIQAQDSIVE 226
QY 53 -----LFKGFTHP-----WYNDLL--VDLGSK--DATN-----KYGKKVDLYGA- 90
Db 227 LVCKTLRGINSRHPSLAFKAGESSMIMEIELQSQVLDAMNYVLYDQLKFKGNRMYYNAL 286
QY 91 -YGYQC--AGGTPNKTCMYGGVTLHDNNRLTEKKV-----PINL-----WIDGK 134
Db 287 NLYHQVLIRRTGIPISMSLY-----LTIAQLGVLEPVNPPHFLRWQCGA 336
QY 135 Q-TTVPI-DKVTSK-----KEVTVQELD-LQARHYLHGKFLYNSDSFGGKVQGLIVFH 187
Db 337 EGATLDFDIYIDAFGKQLTVKECEYLIGHVHTAALYGVNVKVLQRMVGNLLSIG 396
QY 188 SSGSTVSY-----DLFDAQOQYPD 207
Db 397 KREGIDQSYQLLRDSL DLYLA--MYPD 421

RESULT 58
US-10-995-561-1016
; Sequence 1016, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCES: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1016
; LENGTH: 3690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1016

Query Match 5.7%; Score 71; DB 6; Length 3690;
Best Local Similarity 28.8%; Pred. No. 7.4e+02;
Matches 55; Conservative 23; Mismatches 69; Indels 44; Gaps 13;
QY 56 GFTGHPWYNDLLVDLGSKDATNKYKGV-----DLYGAYGYQCAGTGNKT- 104
Db 41 GGFSLHPPYPNLAE--GARTASATCGEAPARGSPRPRTEDLYCKLVGGPVAGGDPNQTI 98
QY 105 ACMYGGVTLHDNNRLTEKKVPINLWIDGKQ---TTVPIDK-VKTSKKEVTVQELDL-QA 159
Db 99 RGQYCDICTAANS-----NKAHPASNAIDGTERWQSPPLSRGLEYNVNT---LDLGQV 151
QY 160 RH--YLHGKFG-----LYNSDSFGGKVQGLIVFHSSEGSTVSYDLFDAQOQYPT 208
Db 152 FHVAYVLIKFANSPRDLWLERSMDFGRTYQPMQF-FASSK-----RDCLERFG--PQT 203
QY 209 LLRIYRDNKTI 219
Db 204 LERITRDAAI 214

RESULT 59
US-10-995-561-1015
; Sequence 1015, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCES: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1015
; LENGTH: 3714
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1015

Query Match 5.7%; Score 71; DB 6; Length 3714;
Best Local Similarity 28.8%; Pred. No. 7.5e+02;
Matches 55; Conservative 23; Mismatches 69; Indels 44; Gaps 13;
QY 56 GFTGHPWYNDLLVDLGSKDATNKYKGV-----DLYGAYGYQCAGTGNKT- 104
Db 63 GGFSLHPPYPNLAE--GARTASATCGEAPARGSPRPRTEDLYCKLVGGPVAGGDPNQTI 120
QY 105 ACMYGGVTLHDNNRLTEKKVPINLWIDGKQ---TTVPIDK-VKTSKKEVTVQELDL-QA 159
Db 121 RGQYCDICTAANS-----NKAHPASNAIDGTERWQSPPLSRGLEYNVNT---LDLGQV 173
QY 160 RH--YLHGKFG-----LYNSDSFGGKVQGLIVFHSSEGSTVSYDLFDAQOQYPT 208
Db 174 FHVAYVLIKFANSPRDLWLERSMDFGRTYQPMQF-FASSK-----RDCLERFG--PQT 225
QY 209 LLRIYRDNKTI 219
Db 204 LERITRDAAI 214
```

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; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1015
; LENGTH: 3714
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-1015

Query Match 5.7%; Score 71; DB 6; Length 3714;
Best Local Similarity 28.8%; Pred. No. 7.5e+02;
Matches 55; Conservative 23; Mismatches 69; Indels 44; Gaps 13;
QY 56 GFTGHPWYNDLLVDLGSKDATNKYKGV-----DLYGAYGYQCAGTGNKT- 104
Db 41 GGFSLHPPYPNLAE--GARTASATCGEAPARGSPRPRTEDLYCKLVGGPVAGGDPNQTI 98
QY 105 ACMYGGVTLHDNNRLTEKKVPINLWIDGKQ---TTVPIDK-VKTSKKEVTVQELDL-QA 159
Db 99 RGQYCDICTAANS-----NKAHPASNAIDGTERWQSPPLSRGLEYNVNT---LDLGQV 151
QY 160 RH--YLHGKFG-----LYNSDSFGGKVQGLIVFHSSEGSTVSYDLFDAQOQYPT 208
Db 152 FHVAYVLIKFANSPRDLWLERSMDFGRTYQPMQF-FASSK-----RDCLERFG--PQT 203
QY 209 LLRIYRDNKTI 219
Db 204 LERITRDAAI 214

RESULT 60
US-10-821-234-1076
; Sequence 1076, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Grain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1076
; LENGTH: 3717
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1076

Query Match 5.7%; Score 71; DB 6; Length 3717;
Best Local Similarity 28.8%; Pred. No. 7.5e+02;
Matches 55; Conservative 23; Mismatches 69; Indels 44; Gaps 13;
QY 56 GFTGHPWYNDLLVDLGSKDATNKYKGV-----DLYGAYGYQCAGTGNKT- 104
Db 63 GGFSLHPPYPNLAE--GARTASATCGEAPARGSPRPRTEDLYCKLVGGPVAGGDPNQTI 120
QY 105 ACMYGGVTLHDNNRLTEKKVPINLWIDGKQ---TTVPIDK-VKTSKKEVTVQELDL-QA 159
Db 121 RGQYCDICTAANS-----NKAHPASNAIDGTERWQSPPLSRGLEYNVNT---LDLGQV 173
QY 160 RH--YLHGKFG-----LYNSDSFGGKVQGLIVFHSSEGSTVSYDLFDAQOQYPT 208
Db 174 FHVAYVLIKFANSPRDLWLERSMDFGRTYQPMQF-FASSK-----RDCLERFG--PQT 225
QY 209 LLRIYRDNKTI 219
Db 204 LERITRDAAI 214
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; PRIOR APPLICATION NUMBER: 09/831,050
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: PCT/GB99/03699
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: GB 9824282.9
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1070
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Construct comprising Mn-SOD from B. stearothermophilus, a linker.
US/11/062,471A-4

Query Match          5.7%; Score 70.5; DB 7; Length 1070;
Best Local Similarity 19.9%; Pred. No. 1.7e+02;
Matches 46; Conservative 43; Mismatches 65; Indels 77; Gaps 14;

QY 9 EKDLRKSELRQNALSLRQIYYNEKAITENKESDDQFLENTLLFK-GFFTGHWPYND- 66
Db 572 EKLLDFDNTLKKNLNVIDENKLYLSAEYKSKVKNYKLTIMPDLISIY-----NDT 626

QY 67 LLVDLGSK-----DATN-----KYGKK-VDLYGAYGYQCAGTTPNKTCACMYGGVTLHDN 116
Db 627 ILIEMFNKYNSEILNLIILNRYKNNLIDLSG--YGAKVE-----VYDGVELNDK 675

QY 117 N-----RLTEKKV-----PINLWDGKQTTVPIDKVKTSKKEVTVOEL 155
Db 676 NQPKLTSSANSKIRVTQNNIIFNSVFLDPSVFWI-----RIPKYKND----- 719

QY 156 DLQARHYLHGKFGLYN--SDSFGKQVORGLIVFHSSEGSTVSYDLFDAQGQ 204
Db 720 --GIQNYIHNEYTIINCMKNNSGSKI-----SIRGNRIIWLIDINGK 760

RESULT 65
US/11/062
; Sequence 7, Application US/11062471A
; Publication No. US20050255093A1
; GENERAL INFORMATION:
; APPLICANT: SHONE, Clifford Charles
; APPLICANT: SUTTON, John Mark
; APPLICANT: HALLIS, Bassem
; APPLICANT: SILMAN, Nigel
; TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
; FILE REFERENCE: 1581.0800001
; CURRENT APPLICATION NUMBER: US/11/062,471A
; PRIOR FILING DATE: 2005-02-22
; PRIOR FILING DATE: 09/831,050
; PRIOR APPLICATION NUMBER: PCT/GB99/03699
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: GB 9824282.9
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Construct comprising a mitochondrial leader sequence from Human M
US/11/062,471A-7

Query Match          5.7%; Score 70.5; DB 7; Length 1095;
Best Local Similarity 19.9%; Pred. No. 1.7e+02;
Matches 46; Conservative 43; Mismatches 65; Indels 77; Gaps 14;

QY 9 EKDLRKSELRQNALSLRQIYYNEKAITENKESDDQFLENTLLFK-GFFTGHWPYND- 66
Db 597 EKLLDFDNTLKKNLNVIDENKLYLSAEYKSKVKNYKLTIMPDLISIY-----NDT 651
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QY 67 LLVDLGSK-----DATN-----KYGKK-VDLYGAYGYQCAGTTPNKTCACMYGGVTLHDN 116
Db 652 ILIEMFNKYNSEILNLIILNRYKNNLIDLSG--YGAKVE-----VYDGVELNDK 700

QY 117 N-----RLTEKKV-----PINLWDGKQTTVPIDKVKTSKKEVTVOEL 155
Db 701 NQPKLTSSANSKIRVTQNNIIFNSVFLDPSVFWI-----RIPKYKND----- 744

QY 156 DLQARHYLHGKFGLYN--SDSFGKQVORGLIVFHSSEGSTVSYDLFDAQGQ 204
Db 745 --GIQNYIHNEYTIINCMKNNSGSKI-----SIRGNRIIWLIDINGK 785
```

RESULT 66

```
US-11-077-550-20
; Sequence 20, Application US/11077550
; Publication No. US2005024435A1
; GENERAL INFORMATION:
; APPLICANT: SHONE, Clifford Charles
; APPLICANT: Quinn, Conrad Padraig
; APPLICANT: Foster, Keith Alan
; APPLICANT: Chaddock, John
; APPLICANT: Marks, Philip
; APPLICANT: Sutton, J. Mark
; APPLICANT: Stancombe, Patrick
; APPLICANT: Wayne, Jonathan
; TITLE OF INVENTION: Recombinant Toxin Fragments
; FILE REFERENCE: 1581.0130004
; CURRENT APPLICATION NUMBER: US/11/077,550
; CURRENT FILING DATE: 2005-03-11
; PRIOR FILING DATE: 10/241,596
; PRIOR APPLICATION NUMBER: 09/255,829
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: PCT/GB97/02273
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/782,893
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: GB9625996.5
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: GB9617671.4
; PRIOR FILING DATE: 1996-08-23
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 20
; LENGTH: 1169
; TYPE: PRT
; ORGANISM: Clostridium botulinum
; OTHER INFORMATION:
US-11-077-550-20
```

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Query Match          5.7%; Score 70.5; DB 7; Length 1169;
Best Local Similarity 19.9%; Pred. No. 1.9e+02;
Matches 46; Conservative 43; Mismatches 65; Indels 77; Gaps 14;
```

```
QY 9 EKDLRKSELRQNALSLRQIYYNEKAITENKESDDQFLENTLLFK-GFFTGHWPYND- 66
Db 793 EKLLDFDNTLKKNLNVIDENKLYLSAEYKSKVKNYKLTIMPDLISIY-----NDT 847

QY 67 LLVDLGSK-----DATN-----KYGKK-VDLYGAYGYQCAGTTPNKTCACMYGGVTLHDN 116
Db 848 ILIEMFNKYNSEILNLIILNRYKNNLIDLSG--YGAKVE-----VYDGVELNDK 896

QY 117 N-----RLTEKKV-----PINLWDGKQTTVPIDKVKTSKKEVTVOEL 155
Db 897 NQPKLTSSANSKIRVTQNNIIFNSVFLDPSVFWI-----RIPKYKND----- 940

QY 156 DLQARHYLHGKFGLYN--SDSFGKQVORGLIVFHSSEGSTVSYDLFDAQGQ 204
Db 941 --GIQNYIHNEYTIINCMKNNSGSKI-----SIRGNRIIWLIDINGK 981
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RESULT 67

```
US-11-082-544-10
; Sequence 10, Application US/11082544
; Publication No. US20050249706A1
; GENERAL INFORMATION:
; APPLICANT: Bermudes, G.
; APPLICANT: King, I.
; APPLICANT: Clairmont, C.
; APPLICANT: Lin, S.
; APPLICANT: Belcourt, M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES
; FILE REFERENCE: 8002-059
; CURRENT APPLICATION NUMBER: US/11/082,544
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US/09/645,415
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/157,581
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: 60/157,637
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fuslon construct
US-11-082-544-10

Query Match          5.7%; Score 70; DB 7; Length 266;
Best Local Similarity 25.5%; Pred. No. 31;
Matches 35; Conservative 21; Mismatches 33; Indels 48; Gaps 9;

QY 8 NEKDLRKK-----SELQNALSNLR-----QIYYNEKAITENKES 43
DB 128 NEKALGRKINSWESSRSGHSFLSNLHRLNGELVHKGFFYYISQTYFRFQBEIKENTKN 187
QY 44 DQOFLNTLLFKGFTGHPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNK 103
DB 188 DKQMVQ--YIYK--YTSYP--DPILL---MKSARNCSWSKDAE-YGLYSIQ-----229
QY 104 TACMGYGV-TLHDNNRL 119
DB 230 -----GGIFELKENDRI 241

RESULT 68
US-10-821-234-1288
; Sequence 1288, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Suesan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1288
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1288

Query Match          5.7%; Score 70; DB 6; Length 281;
Best Local Similarity 25.5%; Pred. No. 33;
Matches 35; Conservative 21; Mismatches 33; Indels 48; Gaps 9;

US-11-082-544-10
; Sequence 10, Application US/11082544
; Publication No. US20050249706A1
; GENERAL INFORMATION:
; APPLICANT: Bermudes, G.
; APPLICANT: King, I.
; APPLICANT: Clairmont, C.
; APPLICANT: Lin, S.
; APPLICANT: Belcourt, M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES
; FILE REFERENCE: 8002-059
; CURRENT APPLICATION NUMBER: US/11/082,544
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: US/09/645,415
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/157,581
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: 60/157,637
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fuslon construct
US-11-082-544-10

Query Match          5.7%; Score 70; DB 7; Length 266;
Best Local Similarity 25.5%; Pred. No. 31;
Matches 35; Conservative 21; Mismatches 33; Indels 48; Gaps 9;

QY 8 NEKDLRKK-----SELQNALSNLR-----QIYYNEKAITENKES 43
DB 128 NEKALGRKINSWESSRSGHSFLSNLHRLNGELVHKGFFYYISQTYFRFQBEIKENTKN 187
QY 44 DQOFLNTLLFKGFTGHPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNK 103
DB 188 DKQMVQ--YIYK--YTSYP--DPILL---MKSARNCSWSKDAE-YGLYSIQ-----229
QY 104 TACMGYGV-TLHDNNRL 119
DB 230 -----GGIFELKENDRI 241

RESULT 68
US-10-821-234-1288
; Sequence 1288, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Suesan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1288
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1288

Query Match          5.7%; Score 70; DB 6; Length 281;
Best Local Similarity 25.5%; Pred. No. 33;
Matches 35; Conservative 21; Mismatches 33; Indels 48; Gaps 9;

US-11-077-272-2
; Sequence 2, Application US/11077272
; Publication No. US20050244927A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, MOON-LAM SUSAN
; APPLICANT: SWARTZ, JAMES R.
; TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDES
; FILE REFERENCE: P2019R1
; CURRENT APPLICATION NUMBER: US/11/077,272
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: US 60/552,678
; PRIOR FILING DATE: 2004-03-11
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-077-272-2

Query Match          5.7%; Score 70; DB 7; Length 281;
Best Local Similarity 25.5%; Pred. No. 33;
Matches 35; Conservative 21; Mismatches 33; Indels 48; Gaps 9;

QY 8 NEKDLRKK-----SELQNALSNLR-----QIYYNEKAITENKES 43
DB 143 NEKALGRKINSWESSRSGHSFLSNLHRLNGELVHKGFFYYISQTYFRFQBEIKENTKN 202
QY 44 DQOFLNTLLFKGFTGHPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNK 103
DB 203 DKQMVQ--YIYK--YTSYP--DPILL---MKSARNCSWSKDAE-YGLYSIQ-----244
QY 104 TACMGYGV-TLHDNNRL 119
DB 245 -----GGIFELKENDRI 256

RESULT 69
US-11-077-272-2
; Sequence 2, Application US/11077272
; Publication No. US20050244927A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, MOON-LAM SUSAN
; APPLICANT: SWARTZ, JAMES R.
; TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDES
; FILE REFERENCE: P2019R1
; CURRENT APPLICATION NUMBER: US/11/077,272
; CURRENT FILING DATE: 2005-03-10
; PRIOR APPLICATION NUMBER: US 60/552,678
; PRIOR FILING DATE: 2004-03-11
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-077-272-2

Query Match          5.7%; Score 70; DB 7; Length 281;
Best Local Similarity 25.5%; Pred. No. 33;
Matches 35; Conservative 21; Mismatches 33; Indels 48; Gaps 9;

QY 8 NEKDLRKK-----SELQNALSNLR-----QIYYNEKAITENKES 43
DB 143 NEKALGRKINSWESSRSGHSFLSNLHRLNGELVHKGFFYYISQTYFRFQBEIKENTKN 202
QY 44 DQOFLNTLLFKGFTGHPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNK 103
DB 203 DKQMVQ--YIYK--YTSYP--DPILL---MKSARNCSWSKDAE-YGLYSIQ-----244
QY 104 TACMGYGV-TLHDNNRL 119
DB 245 -----GGIFELKENDRI 256

RESULT 70
US-11-136-842-1
; Sequence 1, Application US/11136842
; Publication No. US20060009387A1
; GENERAL INFORMATION:
; APPLICANT: Flores, Heather
; APPLICANT: Lin, Tanya P.
; APPLICANT: Matthews, Timothy C.
; APPLICANT: Pai, Roger
; APPLICANT: Shahrokh, Zahra
; TITLE OF INVENTION: APO-2 LIGAND/TRAIL FORMULATIONS
; FILE REFERENCE: 39766-0174A
; CURRENT APPLICATION NUMBER: US/11/136,842
; CURRENT FILING DATE: 2005-05-24
; PRIOR APPLICATION NUMBER: US 10/771,254
; PRIOR FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: PCT/US02/36251
; PRIOR FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 281
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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-136-842-1

Query Match      5.7%; Score 70; DB 7; Length 281;
Best Local Similarity 25.5%; Pred. No. 33;
Matches 35; Conservative 21; Mismatches 33; Indels 48; Gaps 9;

QY      8 NEKDLRKK-----SELQRNALSNLR-----QIYYNEKAITENKES 43
DB      143 NEKALGRKINSWESSRSGHSFLSNLHNLNGELVIHEKGFYIYSQTYFRFQBEIKENTKN 202
QY      44 DQOFLNTLLFKGFFTHGHPWYNDDLVLGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNK 103
DB      203 DKQMVQ--YIYK--YTSYP--DPILL---MKSARNCSWCKDAE-YGLYSIQ----- 244
QY      104 TACMYGGV-TLHDNNRL 119
DB      245 -----GGIFELKENDRI 256

RESULT 71
US-11-136-079-5
; Sequence 5, Application US/11136079
; Publication No. US20060014248A1
; GENERAL INFORMATION:
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Moore, Gregory L.
; APPLICANT: Chirino, Arthur J.
; APPLICANT: Desjarlais, John R.
; TITLE OF INVENTION: TNF SUPER FAMILY MEMBERS WITH ALTERED IMMUNOGENICITY
; FILE REFERENCE: A-72175-4
; CURRENT APPLICATION NUMBER: US/11/136,079
; CURRENT FILING DATE: 2005-05-23
; PRIOR APPLICATION NUMBER: US 60/573,206
; PRIOR FILING DATE: 2004-05-21
; PRIOR APPLICATION NUMBER: US 60/573,301
; PRIOR FILING DATE: 2004-05-21
; PRIOR APPLICATION NUMBER: US 60/573,395
; PRIOR FILING DATE: 2004-05-21
; PRIOR APPLICATION NUMBER: US 60/588,314
; PRIOR FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/607,396
; PRIOR FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/607,397
; PRIOR FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 10/794,751
; PRIOR FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: US 60/452,707
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: US 60/482,081
; PRIOR FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: US 10/338,785
; PRIOR FILING DATE: 2003-01-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 772
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-136-079-5

Query Match      5.7%; Score 70; DB 7; Length 281;
Best Local Similarity 25.5%; Pred. No. 33;
Matches 35; Conservative 21; Mismatches 33; Indels 48; Gaps 9;

QY      8 NEKDLRKK-----SELQRNALSNLR-----QIYYNEKAITENKES 43
DB      143 NEKALGRKINSWESSRSGHSFLSNLHNLNGELVIHEKGFYIYSQTYFRFQBEIKENTKN 202
QY      44 DQOFLNTLLFKGFFTHGHPWYNDDLVLGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNK 103
DB      203 DKQMVQ--YIYK--YTSYP--DPILL---MKSARNCSWCKDAE-YGLYSIQ----- 244
QY      104 TACMYGGV-TLHDNNRL 119
DB      245 -----GGIFELKENDRI 256

RESULT 72
US-11-105-172-4
; Sequence 4, Application US/11105172
; Publication No. US20050244370A1
; GENERAL INFORMATION:
; APPLICANT: Pfizenmaier, Klaus
; APPLICANT: Wajant, Harald
; TITLE OF INVENTION: Selective local activation of members of the TNF
; TITLE OF INVENTION: receptor family by systemically inactive
; TITLE OF INVENTION: non-antibody TNF ligand fusion proteins
; FILE REFERENCE: 2910-1-001
; CURRENT APPLICATION NUMBER: US/11/105,172
; CURRENT FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: DE 102 47 755.8
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: Coding
; OTHER INFORMATION: sequence and/or translated amino acid sequence
; OTHER INFORMATION: of the fusion protein CD40ex-Flag-TRAIL
; OTHER INFORMATION: (construct B) according to the invention.
US-11-105-172-4

Query Match      5.7%; Score 70; DB 7; Length 391;
Best Local Similarity 25.5%; Pred. No. 51;
Matches 35; Conservative 21; Mismatches 33; Indels 48; Gaps 9;

QY      8 NEKDLRKK-----SELQRNALSNLR-----QIYYNEKAITENKES 43
DB      253 NEKALGRKINSWESSRSGHSFLSNLHNLNGELVIHEKGFYIYSQTYFRFQBEIKENTKN 312
QY      44 DQOFLNTLLFKGFFTHGHPWYNDDLVLGSKDATNKYKGGKVDLYGAYYGYQCAGGTPNK 103
DB      313 DKQMVQ--YIYK--YTSYP--DPILL---MKSARNCSWCKDAE-YGLYSIQ----- 354
QY      104 TACMYGGV-TLHDNNRL 119
DB      355 -----GGIFELKENDRI 366

RESULT 73
US-11-098-686-11240
; Sequence 11240, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11240
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
```

US-11-098-686-11240

```
Query Match          5.7%; Score 70; DB 7; Length 459;
Best Local Similarity 21.1%; Pred. No. 62;
Matches 56; Conservative 39; Mismatches 74; Indels 96; Gaps 15;

QY  7 INEKDL-RKSELO--RNALSRLRQIYYNEKAITENKES-----DDQFLENTLLFK 55
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 204 INKLDLTRAKEVETARTAL-----YQKRIAQENAEATLSVLLGRSPRLIMDTAIR 255
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
QY  56 GFFTGHWPYNLLVDLGSKDAT-----NKYKGKVDLYGAY-----GYQC 96
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 256 G-----VSMKDCIPVPGQIPSELLERRPDIRQAEBYTLKATSANIGVAR 301
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
QY  97 AGTPTN-KTACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDIKVTSKKEVTVQEL 155
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 302 AAWLPSISITGLFGVSPH-----LSDLLKNPLKTSYGETGVPI-----L 343
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
QY  156 DLQARHYLHGKFG--LYNSDSFGGKVQRGILIVFHSSEGSTVSVDLPDAQGQYPTLLRIY 213
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 344 D-----FGQVYINVEAAQAKREALANYEKTVQNAFK-DIHDA-----LIRY 385
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
QY  214 RDNKTISS-----ENLHIDLILYTT 233
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 386 ESKNIVNSLERNVWVKELRIAVHLART 410
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
```

```
RESULT 74
US-10-453-372-42
; Sequence 42, Application US/10453372
; Publication No. US20060003323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 42
; LENGTH: 3130
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-42
```

```
Query Match          5.7%; Score 70; DB 6; Length 3130;
Best Local Similarity 25.6%; Pred. No. 7.4e+02;
Matches 30; Conservative 14; Mismatches 49; Indels 24; Gaps 3;

QY  25 NLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHWPYNDLLVDLGSKDATNKYKGKK 84
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 2894 NGRPINTAREPPLTQALIPGDVFAKNS-LWKGAY-----EYQGGK 2932
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
```

```
QY  85 VDLYGAYGYQCAGGTPNKKTACMYGSGVTLHDNNRLTEKKVPINLWIDGKQTTVPID 141
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 2933 QPAMLRVTGFGQVANSKVNATMIDHSGVELH---LAGTYKKEDFHLLLVQVYITGPVE 2986
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

RESULT 75
US-10-453-372-40
; Sequence 40, Application US/10453372
; Publication No. US20060003323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 40
; LENGTH: 3483
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-40

Query Match          5.7%; Score 70; DB 6; Length 3483;
Best Local Similarity 25.6%; Pred. No. 8.4e+02;
Matches 30; Conservative 14; Mismatches 49; Indels 24; Gaps 3;

QY  25 NLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHWPYNDLLVDLGSKDATNKYKGKK 84
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 3247 NGRPINTAREPPLTQALIPGDVFAKNS-LWKGAY-----EYQGGK 3285
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:

QY  85 VDLYGAYGYQCAGGTPNKKTACMYGSGVTLHDNNRLTEKKVPINLWIDGKQTTVPID 141
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db 3286 QPAMLRVTGFGQVANSKVNATMIDHSGVELH---LAGTYKKEDFHLLLVQVYITGPVE 3339
    ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
```

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Job time : 9.66409 secs